

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KLVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	4	AAB48483
2	29	100.0	6	4	AAB48474
3	29	100.0	6	4	AAB82623
4	29	100.0	6	4	AAB82631
5	29	100.0	6	5	AAU96819
6	29	100.0	6	5	AAU96811
7	29	100.0	6	5	AAU11657
8	29	100.0	6	5	AAU11648
9	29	100.0	6	6	AAE35446
10	29	100.0	6	6	AAE35438
11	29	100.0	6	8	ADQ37322
12	29	100.0	6	8	ADQ37270
13	29	100.0	6	8	ADQ37313
14	29	100.0	6	8	ADQ37262
15	29	100.0	6	9	ADY37921
16	29	100.0	6	9	ADY37929
17	29	100.0	99	4	ABG25598
18	28	96.6	6	4	AAB48482
19	28	96.6	6	4	AAB48490
20	28	96.6	6	4	AAB82630
21	28	96.6	6	4	AAB82638
22	28	96.6	6	5	AAU96818
23	28	96.6	6	5	AAU96826
24	28	96.6	6	5	AAU11664

25	28	96.6	6	5	AAU11656	Aau11656	Peptide #
26	28	96.6	6	6	AAE35452	Aae35452	Abeta pep
27	28	96.6	6	8	ADQ37277	Adq37277	Vaccine a
28	28	96.6	6	8	ADQ37321	Adq37321	Antifibri
29	28	96.6	6	8	ADQ37328	Adq37328	Antifibri
30	28	96.6	6	9	ADY37928	Ady37928	Amyloid-t
31	28	96.6	6	9	ADY37936	Ady37936	Amyloid-t
32	28	96.6	22	8	ADQ09761	Adq09761	Rice 26kD
33	28	96.6	23	8	ADY93984	Ady93984	Rice 26 k
34	28	96.6	37	3	AAE05910	Aae05910	Mouse ind
35	28	96.6	37	8	ADK34080	Adk34080	Human nNO
36	28	96.6	37	8	ADL70727	Adl70727	Mouse iNO
37	28	96.6	77	3	AAE02840	Aae02840	Human sec
38	28	96.6	175	4	AAO11219	Aao11219	Human pol
39	28	96.6	186	7	ADC07962	Adc07962	Rice prot
40	28	96.6	186	7	ADC07948	Adc07948	Rice prot
41	28	96.6	190	4	AAE83792	Aae83792	Human imm
42	28	96.6	564	4	ABE61977	AbE61977	Drosophila
43	28	96.6	854	8	ADG66704	Adg66704	Novel hum
44	28	96.6	922	8	ABM83252	Abm83252	Human dia
45	28	96.6	925	7	ADF76335	Adf76335	Novel hum
46	28	96.6	925	7	ADJ70225	Adj70225	Human hea
47	28	96.6	925	8	ADJ75428	Adj75428	Marker ge
48	28	96.6	925	8	ADJ75495	Adj75495	Marker ge
49	28	96.6	925	8	ADN04860	Adn04860	Antipeori
50	28	96.6	925	8	ADR14233	Adr14233	Human NF-
51	28	96.6	925	8	ADP25011	Adp25011	PRO polyp
52	28	96.6	925	8	ADR97294	Adr97294	Human RIG
53	28	96.6	925	9	ADY17516	Ady17516	PRO polyp
54	28	96.6	925	9	AEA23525	Aea23525	Human PRO
55	28	96.6	1144	2	AAE77360	Aae77360	Inducible
56	28	96.6	1144	2	AAW51246	Aaw51246	Inducible
57	28	96.6	1144	4	AAE64500	Aae64500	Mouse ind
58	28	96.6	1144	7	ABU79138	Abu79138	Inducible
59	28	96.6	1144	7	ADF43404	Adf43404	iNOS poly
60	28	96.6	1144	7	ADF77432	Adf77432	Mouse ind
61	28	96.6	1144	8	ADJ76212	Adj76212	Marker ge
62	28	96.6	1144	8	ADJ76136	Adj76136	Marker ge
63	28	96.6	1144	9	AEA03075	Aea03075	VEGF amin.
64	28	96.6	1443	4	ABE68472	AbE68472	Drosophila
65	27	93.1	6	2	AAW02314	Aaw02314	Beta-amyl
66	27	93.1	6	2	AAW89378	Aaw89378	Beta-amyl
67	27	93.1	6	4	AAE48484	Aae48484	Antifibri
68	27	93.1	6	4	AAE48476	Aae48476	Antifibri
69	27	93.1	6	4	AAE82632	Aae82632	Antifibri
70	27	93.1	6	5	ABG71009	Abg71009	All-D pep
71	27	93.1	6	5	ABO05157	AbO05157	Beta amyl
72	27	93.1	6	5	AAU96820	Aau96820	Amyloid t
73	27	93.1	6	5	ABE83305	AbE83305	Amyloid-b
74	27	93.1	6	5	AAU11658	Aau11658	Peptide #
75	27	93.1	6	5	AAU11650	Aau11650	Peptide #
76	27	93.1	6	6	AAE35445	Aae35445	Abeta pep
77	27	93.1	6	6	AAE35434	Aae35434	Abeta pep
78	27	93.1	6	6	ADJ64060	Adj64060	Human bet
79	27	93.1	6	8	ADQ37271	Adq37271	Vaccine a
80	27	93.1	6	8	ADQ37315	Adq37315	Antifibri
81	27	93.1	6	8	ADQ37368	Adq37368	Beta-amyl
82	27	93.1	6	8	ADQ37269	Adq37269	Vaccine a
83	27	93.1	6	8	ADQ37292	Adq37292	Vaccine a
84	27	93.1	6	8	ADQ37258	Adq37258	Vaccine a
85	27	93.1	6	8	ADQ37353	Adq37353	Beta-amyl
86	27	93.1	6	8	ADQ37323	Adq37323	Antifibri
87	27	93.1	6	9	ADY37930	Ady37930	Amyloid-t
88	27	93.1	6	9	ADY37948	Ady37948	Amyloid-t
89	27	93.1	6	9	ADY37947	Ady37947	Amyloid-t
90	27	93.1	6	9	AEA23039	Aea23039	Human bet
91	27	93.1	7	2	AAE88300	Aae88300	Non-amnes
92	27	93.1	7	2	AAE87921	Aae87921	Test pept
93	27	93.1	7	2	AAW02312	Aaw02312	Beta-amyl
94	27	93.1	7	2	AAE89376	Aae89376	Beta-amyl
95	27	93.1	7	4	AAE67281	Aae67281	Residues
96	27	93.1	7	4	AAE48475	Aae48475	Antifibri
97	27	93.1	7	4	AAE48492	Aae48492	Antifibri

98	27	93.1	7	4	AB4848491	AB4848491	Antifibri	171	27	93.1	10	4	AB46226	AB46226	Human APP
99	27	93.1	7	4	AB82624	AB82624	All-D pep	172	27	93.1	10	4	AB46225	AB46225	Human APP
100	27	93.1	7	4	AB82624	AB82624	All-D pep	173	27	93.1	10	4	AB46228	AB46228	Human APP
101	27	93.1	7	4	AB82639	AB82639	All-D pep	174	27	93.1	10	4	AB46224	AB46224	Human APP
102	27	93.1	7	5	AB821007	AB821007	Long form	175	27	93.1	10	4	AB46227	AB46227	Human APP
103	27	93.1	7	5	AB805155	AB805155	Beta amyl	176	27	93.1	10	4	AB82641	AB82641	All-D pep
104	27	93.1	7	5	AB805155	AB805155	Beta amyl	177	27	93.1	10	5	AB82629	AB82629	Amlyoid t
105	27	93.1	7	5	AB805155	AB805155	Beta amyl	178	27	93.1	10	6	AB82641	AB82641	All-D pep
106	27	93.1	7	5	AB805155	AB805155	Beta amyl	179	27	93.1	10	6	AB82641	AB82641	All-D pep
107	27	93.1	7	5	AB805155	AB805155	Beta amyl	180	27	93.1	10	6	AB82641	AB82641	All-D pep
108	27	93.1	7	5	AB805155	AB805155	Beta amyl	181	27	93.1	10	8	ADQ37280	ADQ37280	Vaccine a
109	27	93.1	7	5	AB805155	AB805155	Beta amyl	182	27	93.1	10	8	ADQ37371	ADQ37371	Amlyoid-b
110	27	93.1	7	5	AB805155	AB805155	Beta amyl	183	27	93.1	10	8	ADQ37374	ADQ37374	Amlyoid-b
111	27	93.1	7	6	AB82630	AB82630	Peptide #	184	27	93.1	10	9	ADY37939	ADY37939	Amlyoid-t
112	27	93.1	7	6	AB82630	AB82630	Peptide #	185	27	93.1	11	2	AAW32560	AAW32560	Anti-amyl
113	27	93.1	7	6	AB82630	AB82630	Peptide #	186	27	93.1	11	5	AAW52586	AAW52586	Peptide #
114	27	93.1	7	6	AB82630	AB82630	Peptide #	187	27	93.1	11	5	AAU99431	AAU99431	Human amyl
115	27	93.1	7	6	AB82630	AB82630	Peptide #	188	27	93.1	11	5	AAE29504	AAE29504	Amlyoid b
116	27	93.1	7	6	AB82630	AB82630	Peptide #	189	27	93.1	11	6	ABU79013	ABU79013	Amlyoidog
117	27	93.1	7	7	AD20746	AD20746	Anti-Abet	190	27	93.1	11	7	ABR4683	ABR4683	Aggreca
118	27	93.1	7	7	AD20746	AD20746	Anti-Abet	191	27	93.1	11	7	ABW00147	ABW00147	Amlyoid-b
119	27	93.1	7	8	ADP64058	ADP64058	Human cal	192	27	93.1	12	6	AAE35464	AAE35464	Abeta pep
120	27	93.1	7	8	ADP64058	ADP64058	Human cal	193	27	93.1	12	6	AAE35464	AAE35464	Abeta pep
121	27	93.1	7	8	ADP64058	ADP64058	Human cal	194	27	93.1	12	6	AAE35466	AAE35466	Abeta pep
122	27	93.1	7	8	ADQ37278	ADQ37278	Vaccine a	195	27	93.1	12	7	ADD20745	ADD20745	Human bet
123	27	93.1	7	8	ADQ37278	ADQ37278	Vaccine a	196	27	93.1	12	8	ADJ71476	ADJ71476	N-termina
124	27	93.1	7	8	ADQ37278	ADQ37278	Vaccine a	197	27	93.1	12	8	ADQ37407	ADQ37407	Amlyoid-b
125	27	93.1	7	8	ADQ37330	ADQ37330	Antifibri	198	27	93.1	12	8	ADQ37289	ADQ37289	Vaccine a
126	27	93.1	7	8	ADQ37330	ADQ37330	Antifibri	199	27	93.1	12	8	ADQ37259	ADQ37259	Vaccine a
127	27	93.1	7	8	ADQ37331	ADQ37331	Antifibri	200	27	93.1	12	9	ADZ08890	ADZ08890	Human bet
128	27	93.1	7	9	ADY37922	ADY37922	Amlyoid-t	201	27	93.1	12	9	ADZ08892	ADZ08892	Human bet
129	27	93.1	7	9	ADY37922	ADY37922	Amlyoid-t	202	27	93.1	13	6	AAE35465	AAE35465	Abeta pep
130	27	93.1	7	9	ADY37937	ADY37937	Amlyoid-t	203	27	93.1	13	6	AAE35467	AAE35467	Abeta pep
131	27	93.1	7	9	ADY37937	ADY37937	Amlyoid-t	204	27	93.1	13	6	ADA37467	ADA37467	Human amyl
132	27	93.1	8	2	AAW02310	AAW02310	Beta-amyl	205	27	93.1	13	8	ADJ71477	ADJ71477	N-termina
133	27	93.1	8	2	AAW45967	AAW45967	Peptide d	206	27	93.1	13	8	ADJ71464	ADJ71464	N-termina
134	27	93.1	8	2	AAW32551	AAW32551	Amlyoidog	207	27	93.1	13	8	ADQ37408	ADQ37408	Amlyoid-b
135	27	93.1	8	2	AAW89374	AAW89374	Beta-amyl	208	27	93.1	13	8	ADQ37290	ADQ37290	Vaccine a
136	27	93.1	8	4	AAE01663	AAE01663	Human amyl	209	27	93.1	14	6	ADA89887	ADA89887	Beta-A4 s
137	27	93.1	8	4	AAE02615	AAE02615	Human amyl	210	27	93.1	14	6	ADJ71452	ADJ71452	N-termina
138	27	93.1	8	5	ABG71005	ABG71005	Long form	211	27	93.1	14	8	ADJ71465	ADJ71465	N-termina
139	27	93.1	8	5	ABG71005	ABG71005	Long form	212	27	93.1	14	8	ADJ71478	ADJ71478	N-termina
140	27	93.1	8	5	ABG71005	ABG71005	Long form	213	27	93.1	14	9	ADZ08889	ADZ08889	Human bet
141	27	93.1	8	6	ABW05153	ABW05153	Beta amyl	214	27	93.1	15	2	AAW02334	AAW02334	Beta-amyl
142	27	93.1	8	6	ABW05153	ABW05153	Beta amyl	215	27	93.1	15	2	AAW02334	AAW02334	Beta-amyl
143	27	93.1	8	6	ABW05153	ABW05153	Beta amyl	216	27	93.1	15	2	AAW02334	AAW02334	Beta-amyl
144	27	93.1	8	8	ADJ64056	ADJ64056	Human bet	217	27	93.1	15	5	ABG71014	ABG71014	Long form
145	27	93.1	8	8	ADQ37385	ADQ37385	Antifibri	218	27	93.1	15	5	ABW05162	ABW05162	Beta amyl
146	27	93.1	8	8	ADQ37349	ADQ37349	Beta-amyl	219	27	93.1	15	5	AAE26271	AAE26271	Human bet
147	27	93.1	8	9	ADZ08900	ADZ08900	Human bet	220	27	93.1	15	6	ABU79057	ABU79057	Aggregati
148	27	93.1	8	9	AAE51423	AAE51423	C-Abeta 1	221	27	93.1	15	6	ABU79064	ABU79064	Aggregati
149	27	93.1	8	9	AAE51420	AAE51420	A 16-22-C	222	27	93.1	15	6	ABU79059	ABU79059	Aggregati
150	27	93.1	8	9	AAE51420	AAE51420	A 16-22-C	223	27	93.1	15	6	ABU79055	ABU79055	Aggregati
151	27	93.1	8	9	AAE62834	AAE62834	Immunoco	224	27	93.1	15	6	ABU79055	ABU79055	Aggregati
152	27	93.1	9	2	AAE62834	AAE62834	Immunoco	225	27	93.1	15	6	ABU79056	ABU79056	Aggregati
153	27	93.1	9	2	AAE62834	AAE62834	Immunoco	226	27	93.1	15	6	ABU79062	ABU79062	Aggregati
154	27	93.1	9	5	AAU11667	AAU11667	Peptide #	227	27	93.1	15	7	ABW00190	ABW00190	Peptide #
155	27	93.1	9	6	ABP57517	ABP57517	Differen	228	27	93.1	15	7	ABW00198	ABW00198	Peptide #
156	27	93.1	9	6	ABU79063	ABU79063	Aggregati	229	27	93.1	15	7	ABW00189	ABW00189	Peptide #
157	27	93.1	9	6	ABU79063	ABU79063	Aggregati	230	27	93.1	15	7	ABW00193	ABW00193	Peptide #
158	27	93.1	9	7	AAE35436	AAE35436	Abeta pep	231	27	93.1	15	7	ABW00191	ABW00191	Peptide #
159	27	93.1	9	8	ADY37937	ADY37937	Amlyoid t	232	27	93.1	15	7	ABW00196	ABW00196	Peptide #
160	27	93.1	9	8	ADY37937	ADY37937	Amlyoid t	233	27	93.1	15	7	ABW00196	ABW00196	Peptide #
161	27	93.1	9	8	ADY37937	ADY37937	Amlyoid t	234	27	93.1	15	7	ABW00196	ABW00196	Peptide #
162	27	93.1	9	8	ADY37937	ADY37937	Amlyoid t	235	27	93.1	15	7	ADK82697	ADK82697	Beta-amyl
163	27	93.1	9	8	ADY37937	ADY37937	Amlyoid t	236	27	93.1	15	7	ADK82697	ADK82697	Beta-amyl
164	27	93.1	9	8	ADY37937	ADY37937	Amlyoid t	237	27	93.1	15	7	ADK82697	ADK82697	Beta-amyl
165	27	93.1	9	8	ADY37937	ADY37937	Amlyoid t	238	27	93.1	15	7	ADK82697	ADK82697	Beta-amyl
166	27	93.1	9	9	AAE51414	AAE51414	A 16-23-C	239	27	93.1	15	8	ADJ71466	ADJ71466	N-termina
167	27	93.1	9	9	AAE51417	AAE51417	C-A 16-23	240	27	93.1	15	8	ADJ71453	ADJ71453	N-termina
168	27	93.1	9	9	AAE62825	AAE62825	Immunoco	241	27	93.1	15	8	ADJ71479	ADJ71479	N-termina
169	27	93.1	9	9	AAE62828	AAE62828	Immunoco	242	27	93.1	15	8	ADJ71440	ADJ71440	N-termina
170	27	93.1	10	3	AAE79938	AAE79938	Beta-amyl	243	27	93.1	15	8	ADJ64065	ADJ64065	Human bet

244 AAE26330 Human bet
 245 ADJ71454 N-termina
 246 ADJ71480 N-termina
 247 ADJ71441 N-termina
 248 ADJ71467 N-termina
 249 ADJ71428 N-termina
 250 AAR54703 Beta-amyl
 251 AAW18880 Beta-amyl
 252 AAB91774 Amyloid b
 253 AAB91807 Amyloid b
 254 AAB48346 Beta-amyl
 255 ABB04911 Human amy
 256 AAE35468 Beta pep
 257 ABB99611 Peptide d
 258 ADG93165 Novel exp
 259 ADJ65843 Amyloid B
 260 ADM02827 Mammalian
 261 ADG37291 Vaccine a
 262 ADB18447 Amyloid-b
 263 AAB10963 Beta-amyl
 264 AAW18882 AEDANS-Beta-
 265 AAW18881 Trp-Beta-
 266 AAY79935 Beta-amyl
 267 AAB49097 Human amy
 268 AAB46201 Human APP
 269 ADU24440 Novel glu
 270 ADU24442 Novel glu
 271 ADU46714 Amyloid b
 272 ADU46716 Gln3 amyl
 273 ADZ71366 Human bet
 274 ADZ71368 Human bet
 275 AEA35401 Novel QC
 276 AEA35399 Novel QC
 277 AEB92572 Glutaminyl
 278 AEB92574 Glutaminyl
 279 AAY79934 Beta-amyl
 280 ABB06431 Beta-secr
 281 AAY30941 Human sec
 282 ADU24439 Novel glu
 283 ADU46713 Amyloid b
 284 ADV86872 Beta-amyl
 285 ADZ71365 Human bet
 286 AEA35398 Novel QC
 287 AEB92571 Glutaminyl
 288 ADR83670 Amyloidog
 289 AAR52569 Alzheimer
 290 ADW8085 T668 phos
 291 AEB09195 Human bet
 292 AEB09194 Human bet
 293 AAW47229 Beta-amyl
 294 AAY33408 Human amy
 295 ABU63718 Rat amylo
 296 ADF55647 Human A b
 297 ADY72250 N-termina
 298 AAY33409 Human amy
 299 AAP70594 Sequence
 300 AAP90381 Synthetic

ALIGNMENTS

RESULT 1
 AAB48483
 ID AAB48483 standard; peptide; 6 AA.
 AC AAB48483;
 XX
 XX 02-MAR-2001 (first entry)
 DT
 XX Antifibrillogenic peptide #10.
 DE
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW

KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 XX Modified-site 6 /note= "C-terminal amide"
 PT
 XX WO200068263-A2.
 XX 16-NOV-2000.
 XX
 XX 04-MAY-2000; 2000WO-CA000515.
 XX 05-MAY-1999; 99US-0132592P.
 XX (NEUR-) NEUROCHEM INC.
 XX Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 PT
 PS Claim 7; Page 25; 46pp; English.
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 DB 1 KIVFFFA 6
 RESULT 2
 AAB48474
 ID AAB48474 standard; peptide; 6 AA.
 XX
 XX AAB48474;
 AC
 XX 02-MAR-2001 (first entry)
 DT
 XX Antifibrillogenic peptide #1.
 DE
 XX
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX Homo sapiens.
 OS
 XX WO200068263-A2.
 XX 16-NOV-2000.
 XX
 XX 04-MAY-2000; 2000WO-CA000515.
 XX 05-MAY-1999; 99US-0132592P.
 XX (NEUR-) NEUROCHEM INC.
 PA

XX Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AA48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db |||||
 1 KIVFFA 6
 RESULT 3
 AAB82623
 ID AAB82623 standard; peptide; 6 AA.
 AC AAB82623;
 XX 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1..6
 FT /note= "all D-form residues"
 FT
 XX WO200139796-A2.
 XX 07-JUN-2001.
 PD 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 XX Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 DR Preventing/treating amyloid-related disease, especially Alzheimer's
 XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX Disclosure; Page 10; 31pp; English.
 PS The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self',
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db |||||
 1 KIVFFA 6
 RESULT 4
 AAB82631
 ID AAB82631 standard; peptide; 6 AA.
 AC AAB82631;
 XX 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1..6
 FT /note= "all D-form residues"
 FT Modified-site 6
 FT /note= "C-terminal amide"
 XX WO200139796-A2.
 XX 07-JUN-2001.
 PD 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 XX Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 DR Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 DB 1 KIVFFPA 6

RESULT 5
 AAU96819
 ID AAU96819 standard; peptide; 6 AA.

XX AAU96819;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #9.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

XX Key Difference 1..6 /note= "Preferably D-form residue"

XX Modified-site 6 /note= "Ala is amidated"

XX WO200207781-A2.

XX 31-JAN-2002.

XX

PF 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

PA Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid

PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A-t-(A₁n₁k)-z-A₁a₁b₁(i) where z = 0 - 1;
 CC A₁t = an amyloid targeting moiety; A₁n₁k = a linker moiety; and A₁a₁b₁
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (i) to the patient, and ultrasound imaging (i) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (i), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

DB 1 KIVFFPA 6

RESULT 6

AAU96811

ID AAU96811 standard; peptide; 6 AA.

XX AAU96811;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #1.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;

XX transmissible cerebral amyloidosis; transmissible virus dementia;

XX scrapie; transmissible mink encephalopathy; BSE; type II diabetes;

XX bovine spongiform encephalopathy; inflammation associated amyloid;

XX primary amyloidosis; feline spongiform encephalopathy;

XX Alzheimer's disease; prion-mediated disease; blood-brain barrier;

XX dialysis-related amyloidosis; light chain-related amyloidosis;

XX cerebral amyloid angiopathy.

XX Synthetic.

XX

```

FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "Preferably D-form residue"
XX
XX WO200207781-A2.
XX 31-JAN-2002.
XX
XX 25-JUL-2001; 2001WO-CA001071.
XX
XX 25-JUL-2000; 2000US-0220808P.
XX 24-JUL-2001; 2001US-00915092.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2002-371447/40.
XX
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX plaques and/or for the treatment of amyloidosis disorders.
XX
XX Claim 49; Page 21; 57pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent comprising an
XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX agent is of general formula A_t-(A_l)_n_k-z-A_l_a_b (i) where z = 0 - 1;
XX A_t = an amyloid targeting moiety; A_l)_n_k = a linker moiety; and A_l_a_b
XX = a labelling moiety. Also included are imaging amyloid deposition or
XX diagnosing an amyloid-related condition in a patient involving
XX administering (i) to the patient, and ultrasound imaging (i) in the
XX patient to determine the presence of amyloid or amyloid-related condition
XX ; and a kit for preparing a radiopharmaceutical preparation comprising
XX (i), a reducing agent, a buffering agent, a transchelating agent, and
XX instructions for the preparation and use of the radiopharmaceutical in
XX the imaging of amyloid or an amyloid-related condition. The agents are
XX used for imaging amyloid deposition and for diagnosing an amyloid related
XX condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX cerebral amyloidosis (transmissible virus dementia), familial CJD,
XX scrapie, transmissible mink encephalopathy, bovine spongiform
XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX primary amyloidosis, feline spongiform encephalopathy, non-transmissible
XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX amyloid angiopathy. The agents are capable of crossing the blood-brain
XX barrier and are capable of binding specifically to amyloid plaques. The
XX present sequence is a peptide forming the amyloid targeting moiety of the
XX agent of the invention
XX
XX Sequence 6 AA;
XX
XX Query Match 100.0%; Score 29; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 KIVFFA 6
XX |||||
XX Db 1 KIVFFA 6
XX
XX RESULT 7
XX AAU11657
XX ID AAU11657 standard; peptide; 6 AA.
XX
XX AC AAU11657;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Peptide #10, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; nontropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX OS Synthetic.
XX
XX PN WO200185093-A2.
XX
XX 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Green AM, Gervais F;
XX
XX WPI; 2002-075222/10.
XX
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX inhibitor.
XX
XX Disclosure; Page 10; 69pp; English.
XX
XX The present invention relates to a new method of inhibiting cerebral
XX amyloid angiopathy. The new method of the invention involves contacting a
XX blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX can be used for treating disease states characterised by cerebral amyloid
XX angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX The present sequence represents one of a group of peptides (AAU11648-
XX AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX was used in the invention to treat a disease state characterised by
XX cerebral amyloid angiopathy (CAA)
XX
XX Sequence 6 AA;
XX
XX Query Match 100.0%; Score 29; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 KIVFFA 6
XX |||||
XX Db 1 KIVFFA 6
XX
XX RESULT 8
XX AAU11648
XX ID AAU11648 standard; peptide; 6 AA.
XX
XX AC AAU11648;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Peptide #1, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; nontropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX OS Synthetic.
XX
XX PN WO200185093-A2.
XX
XX 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.
XX
XX

```

XX PA (NEUR-) NEUROCHEM INC.
 XX PI Green AM, Gervais F;
 XX PT WPI; 2002-075222/10.
 XX DR
 XX XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.
 XX PS Disclosure; Page 10; 68pp; English.
 XX CC The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11659, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX CC
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Mismatches 0; Gaps 0;
 Matches 6; Conservative 0; Indels 0;
 QY 1 KIVFFPA 6
 DB 1 KIVFFPA 6
 RESULT 9
 AAE35446
 ID AAE35446 standard; peptide; 6 AA.
 XX AC AAE35446;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #17.
 XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1. .6
 FT /note= "D-form residues"
 FT Modified-site 6
 FT /note= "C-terminal amide"
 XX WO200296937-A2.
 XX PD 05-DEC-2002.
 XX PF 29-MAY-2002; 2002WO-CA000763.
 XX PR 29-MAY-2001; 2001US-00867847.
 XX PA (NEUR-) NEUROCHEM INC.
 XX PI Gervais F, Hebert L, Chalifour RJ, Kong X;

XX DR WPI; 2003-201269/19.
 XX PT Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX PS Claim 1; Page 59; 44pp; English.
 XX CC The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D-
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal, and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, Bechet's syndrome and Crohn's
 CC Reiter's syndrome, Adult Still's disease, a result of chronic microbial
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Mismatches 0; Gaps 0;
 Matches 6; Conservative 0; Indels 0;
 QY 1 KIVFFPA 6
 DB 1 KIVFFPA 6
 RESULT 10
 AAE35438
 ID AAE35438 standard; peptide; 6 AA.
 XX AC AAE35438;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #9.
 XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1. .6
 FT /note= "D-form residues"
 XX WO200296937-A2.
 XX PD 05-DEC-2002.
 XX PF 29-MAY-2002; 2002WO-CA000763.
 XX PR 29-MAY-2001; 2001US-00867847.
 XX PA (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 XX Claim 1; Page 58; 44pp; English.
 XX
 CC The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 1 KIVFFA 6
 |||||
 |||||
 RESULT 11
 ADQ37322
 ID ADQ37322 standard; peptide; 6 AA.
 XX
 AC ADQ37322;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Antifibrillogenic amyloidosis inhibiting peptide.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6
 FT /note= "amidated"
 XX
 XX WO2004058239-A1.

15-JUL-2004.
 24-DEC-2003; 2003WO-CA002021.
 24-DEC-2002; 2002US-0436379P.
 23-JUN-2003; 2003US-0482214P.
 (NEUR-) NEUROCHEM INT LTD.
 Gervais F, Bellini F;
 WPI; 2004-543342/52.
 Composition for treating e.g. Alzheimer's disease comprises first agent
 that prevents or treats amyloid-beta related disease and second agent
 that is either a peptide or peptidomimetic or an immune system modulator.
 Disclosure; Page 69; 143pp; English.
 The present invention describes compositions (C) comprising: (a) a first
 agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 a second agent (a2) that is: (i) a peptide or peptidomimetic that
 modulates amyloid-beta fibril formation or induces a prophylactic or
 therapeutic immune response against amyloid-beta fibril formation; or
 (ii) an immune system modulator that prevents or inhibits amyloid-beta
 fibril formation. Also described is a kit comprising (C). (C) have
 neurotropic, neuroprotective, cerebroprotective, haemostatic,
 ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 and can be used as amyloid-beta fibril formation modulators, and as
 immune system modulators. (C) can be used for preventing or treating an
 amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 mild-to-moderate cognitive impairment, vascular dementia, cerebral
 amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 Down's syndrome, inclusion body myositis, age-related macular
 degeneration, or a condition associated with Alzheimer's disease
 (including hypothyroidism, cerebrovascular disease, cardiovascular
 disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 aggression, or incontinence), a neurological condition (e.g. Huntington's
 disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 field deficits, incoordination, gait disturbance, transient ischaemic
 attack or stroke, transient alertness, attention deficit, frequent falls
 syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 damage), or a psychological condition (e.g. depression, delusions,
 illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 excessive guilt)) in a subject e.g. human having a genomic mutation in an
 amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 having amyloid-beta deposits. The present sequence represents a peptide
 that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 in the exemplification of the present invention.
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 1 KIVFFA 6
 |||||
 |||||
 RESULT 12
 ADQ37270
 ID ADQ37270 standard; peptide; 6 AA.

XX ADQ37270;
 XX AC
 XX 07-OCT-2004 (first entry)
 DT
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment; vascular dementia;
 KW mild-to-moderate cognitive impairment; hereditary cerebral haemorrhage;
 KW cerebral amyloid angiopathy; Down's syndrome; inclusion body myositis;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "D-form residues"
 FT Modified-site 6 /note= "amidated"
 FT
 FT
 FT
 FT
 XX WO2004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 67; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,

CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |||||
 DB 1 KIVFFA 6

RESULT 13

ADQ37313

ID ADQ37313 standard; peptide; 6 AA.

XX AC

XX ADQ37313;

XX 07-OCT-2004 (first entry)

XX Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;

KW amyloid-beta fibril formation; immune response; neurotropic;

KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;

KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;

KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

KW cardiant; antidepressant; endocrine; hypnotic;

KW amyloid-beta fibril formation modulator; immune system modulator;

KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;

KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

KW senile dementia; Down's syndrome; inclusion body myositis;

KW age-related macular degeneration; hypothyroidism;

KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;

KW behavioural dysfunction; neurological condition; psychological condition;

KW vaccine antigen.

XX Synthetic.

XX WO2004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent

PT

PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX Disclosure; Page 69; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nontropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 1 KIVFFA 6

RESULT 14

ADQ37262

ID ADQ37262 standard; peptide; 6 AA.

AC ADQ37262;

XX 07-OCT-2004 (first entry)

XX Vaccine antigen amyloid-beta related amino acid sequence.

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nontropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 OS Synthetic.

XX Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "D-form residues"

XX WO2004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 PS Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nontropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.

```
XX SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |||||
Db 1 KIVFFA 6

RESULT 15
ADY37921
ID ADY37921 standard; peptide; 6 AA.
XX AC ADY37921;
XX DT 19-MAY-2005 (first entry)
XX DE Amyloid-targeting peptide, SEQ ID NO:1, for use in imaging agent.
XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
XX KW transmissible spongiform encephalopathy; scrapie; BSE;
XX KW Alzheimers disease; neurological disease; amyloidosis;
XX KW non-insulin dependent diabetes; metabolic disorder.
XX OS Synthetic.
XX PN US2005048000-A1.
XX PD 03-MAR-2005.
XX PF 03-DEC-2003; 2003US-00728028.
XX PR 25-JUL-2000; 2000US-0220808P.
XX PR 24-JUL-2001; 2001US-00915092.
XX PR 29-JAN-2003; 2003US-0443291P.
XX PA (NEUR-) NEUROCHEM INT LTD.
XX PI Gervais P, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.
XX PS New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
XX PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
XX PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX PS Disclosure; SEQ ID NO 1; 34pp; English.
XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
XX CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
XX CC a labeling moiety via a linking moiety, and is preferably able to cross
XX CC the blood-brain barrier. The invention also relates to a kit for
XX CC preparing a radiopharmaceutical preparation from the imaging agent of the
XX CC invention, a method for imaging amyloid deposition in a patient and a
XX CC method for diagnosing an amyloid-related condition in a patient. The
XX CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
XX CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
XX CC transmissible cerebral amyloidoses (also known as transmissible virus
XX CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
XX CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
XX CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
XX CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
XX CC mediated diseases, dialysis-related amyloidosis, light chain-related
XX CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
XX CC patient. The agent does not exhibit excessive toxicity or irritation,
XX CC amyloid-related conditions, thereby allowing earlier treatment and hence
XX CC prevention of the undesirable effects of such disorders. Sequences
XX CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
XX CC the amyloid-targeting moiety in an imaging agent of the invention.
```

```
XX SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |||||
Db 1 KIVFFA 6

RESULT 16
ADY37929
ID ADY37929 standard; peptide; 6 AA.
XX AC ADY37929;
XX DT 19-MAY-2005 (first entry)
XX DE Amyloid-targeting peptide, SEQ ID NO:9, for use in imaging agent.
XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
XX KW transmissible spongiform encephalopathy; scrapie; BSE;
XX KW Alzheimers disease; neurological disease; amyloidosis;
XX KW non-insulin dependent diabetes; metabolic disorder.
XX OS Synthetic.
XX PN US2005048000-A1.
XX PD 03-MAR-2005.
XX PF 03-DEC-2003; 2003US-00728028.
XX PR 25-JUL-2000; 2000US-0220808P.
XX PR 24-JUL-2001; 2001US-00915092.
XX PR 29-JAN-2003; 2003US-0443291P.
XX PA (NEUR-) NEUROCHEM INT LTD.
XX PI Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.
XX PS New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
XX PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
XX PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX PS Disclosure; SEQ ID NO 9; 34pp; English.
XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
XX CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
XX CC a labeling moiety via a linking moiety, and is preferably able to cross
XX CC the blood-brain barrier. The invention also relates to a kit for
XX CC preparing a radiopharmaceutical preparation from the imaging agent of the
XX CC invention, a method for imaging amyloid deposition in a patient and a
XX CC method for diagnosing an amyloid-related condition in a patient. The
XX CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
XX CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
XX CC transmissible cerebral amyloidoses (also known as transmissible virus
XX CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
XX CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
XX CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
XX CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
XX CC mediated diseases, dialysis-related amyloidosis, light chain-related
XX CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
XX CC patient. The agent does not exhibit excessive toxicity or irritation,
XX CC does not induce an allergic response, and permits an earlier diagnosis of
```

CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
| | | | |
Db 1 KIVFFA 6

RESULT 17
ABG26598
ID ABG26598 standard; protein; 99 AA.

XX AC ABG26598;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #26589.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX FN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS90785.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.

XX PS Claim 20; SEQ ID NO 56957; 103pp; English.
XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX CC sequences. (I) is useful as hybridisation probes, polymerase chain
XX CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX CC and in recombinant production of (II). The polynucleotides are also used
XX CC in diagnostics as expressed sequence tags for identifying expressed
XX CC genes. (I) is useful in gene therapy techniques to restore normal
XX CC activity of (II) or to treat disease states involving (II). (II) is
XX CC useful for generating antibodies against it, detecting or quantitating a
XX CC polypeptide in tissue, as molecular weight markers and as a food
XX CC supplement. (II) and its binding partners are useful in medical imaging
XX CC of sites expressing (II). (I) and (II) are useful for treating disorders
XX CC involving aberrant protein expression or biological activity. The
XX CC polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
XX CC amino acid sequences of the invention. Note: The sequence data for this
XX CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 99 AA;

Query Match 100.0%; Score 29; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
| | | | |
Db 63 KIVFFA 68

RESULT 18
AAB48482
ID AAB48482 standard; peptide; 6 AA.

XX AC AAB48482;
XX DT 02-MAR-2001 (first entry)
XX DE Antifibrillogenic peptide #9.
XX KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
XX KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
XX KW Alzheimer's disease.
XX OS Homo sapiens.
XX FN WO200068263-A2.
XX PD 16-NOV-2000.
XX PF 04-MAY-2000; 2000WO-CA000515.
XX PR 05-MAY-1999; 99US-0132592P.
XX PA (NEUR-) NEUROCHEM INC.
XX PI Chalifour R, Gervais F, Gupta A;
XX DR WPI; 2001-031852/04.

XX PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
XX PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
XX PT its isomer or peptidomimetic.
XX PS Claim 7; Page 25; 46pp; English.

XX CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
XX CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
XX CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
XX CC useful for treating amyloidosis disorders such as Alzheimer's disease.
XX CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
XX CC binding region and the prot-prot interaction region of the human amyloid
XX CC protein
XX SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
| | | | |
Db 1 KIVFFA 6

RESULT 19
AAB48490
ID AAB48490 standard; peptide; 6 AA.

XX

AC AAB48490;
 XX 02-MAR-2001 (first entry)
 XX Antifibrillogenic peptide #17.
 DE Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Modified-site 6
 FT /note= "C-terminal amide"
 XX
 XX WO200068263-A2.
 XX 16-NOV-2000.
 XX 04-MAY-2000; 2000WO-CA000515.
 XX 05-MAY-1999; 99US-0132592P.
 XX (NEUR-) NEUROCHEM INC.
 XX Chalifour R, Gervais P, Gupta A;
 XX WPI; 2001-031852/04.
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX Sequence 6 AA;
 SQ
 Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 Db 1 KVVFFFA 6
 RESULT 20
 AAB82630
 ID AAB82630 standard; peptide; 6 AA.
 AC AAB82630;
 XX 02-OCT-2001 (first entry)
 XX All-D peptide used in Alzheimer's disease vaccine.
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Misc-difference 1..6
 FT /note= "all D-form residues"
 FT

XX WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 XX Chalifour R, Hebert L, Kong X, Gervais P;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX Disclosure; Page 11; 31pp; English.
 XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX Sequence 6 AA;
 SQ
 Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 Db 1 KVVFFFA 6
 RESULT 21
 AAB82638
 ID AAB82638 standard; peptide; 6 AA.
 XX AAB82638;
 AC AAB82638;
 XX 02-OCT-2001 (first entry)
 XX All-D peptide used in Alzheimer's disease vaccine.
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX

OS Synthetic.

XX Key Location/Qualifiers

FH Misc-difference 1..6

FT /note= "all D-form residues"

FT Modified-site 6

FT /note= "C-terminal amide"

XX WO200139796-A2.

XX 07-JUN-2001.

XX 29-NOV-2000; 2000WO-CA001413.

XX 29-NOV-1999; 99US-0168594P.

PR 28-NOV-2000; 2000US-00724842.

XX (NEUR-) NEUROCHEM INC.

PA Chalifour R, Hebert L, Kong X, Gervais F;

PI WPI; 2001-441458/47.

DR Preventing/treating amyloid-related disease, especially Alzheimer's

PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and

PT associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

PS The present sequence is that of an all-D peptide suitable for use in

XX preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of

CC amyloid-beta peptide (see AAB82622), and may be modified by removing or

CC inserting 1 or more amino acid residues, or by substituting 1 or more

CC amino acid residues with other amino acid residues or non-amino acid

CC fragments. Vaccines of the invention are produced using 'non-self'

CC peptides synthesised from the unnatural D-configuration amino acids to

CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be

CC aggregated to be operative or immunogenic. They preferably interact with

CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or

CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic

CC fragments, protein conjugates, immunogenic derivative peptides and

CC immunogenic peptidomimetics. Examples include all-D peptides

CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and

CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given

CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,

CC preventing fibrillogenesis and associated cellular toxicity. The amyloid

CC related diseases may be localised amyloidosis, e.g. diabetes type II,

CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,

CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and

CC prion protein related disorders, or systemic amyloidosis associated with

CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.

CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic

CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

XX Query Match 96.6%; Score 28; DB 4; Length 6;

XX Best Local Similarity 83.3%; Pred. No. 2e+06;

XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db |:||||

1 KVVFFA 6

RESULT 22

AAU96818

ID AAU96818 standard; peptide; 6 AA.

AC AAU96818;

XX

DT 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #8.

DE Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;

XX transmissible cerebral amyloidosis; transmissible virus dementia;

KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;

KW bovine spongiform encephalopathy; inflammation associated amyloid;

KW primary amyloidosis; feline spongiform encephalopathy;

KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;

KW dialysis-related amyloidosis; light chain-related amyloidosis;

KW cerebral amyloid angiopathy.

XX Synthetic.

OS Key Location/Qualifiers

XX Misc-difference 1..6

FH /note= "Preferably D-form residue"

FT WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

PF 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

PA Gervais F, Kong X, Chalifour R, Migneault D;

PI WPI; 2002-371447/40.

DR New amyloid-targeting imaging agents useful for in vivo imaging amyloid

PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an

CC amyloid targeting moiety, a linker moiety and a labelling moiety. The

CC agent is of general formula A_t-(A_1)_n_K)-A_1_a_b (I) where z = 0 - 1;

CC A_t = an amyloid targeting moiety; A_1)_n_K) = a linker moiety; and A_1_a_b

CC = a labelling moiety. Also included are imaging amyloid deposition or

CC diagnosing an amyloid-related condition in a patient involving

CC administering (I) to the patient, and ultrasound imaging (I) in the

CC patient to determine the presence of amyloid or amyloid-related condition

CC ; and a kit for preparing a radiopharmaceutical preparation comprising

CC (I), a reducing agent, a buffering agent, a transchelating agent, and

CC instructions for the preparation and use of the radiopharmaceutical in

CC the imaging of amyloid or an amyloid-related condition. The agents are

CC used for imaging amyloid deposition and for diagnosing an amyloid related

CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible

CC cerebral amyloidosis (transmissible virus dementia), familial CJD,

CC scrapie, transmissible mink encephalopathy, bovine spongiform

CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,

CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible

CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,

CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral

CC amyloid angiopathy. The agents are capable of crossing the blood-brain

CC barrier and are capable of binding specifically to amyloid plaques. The

CC present sequence is a peptide forming the amyloid targeting moiety of the

XX agent of the invention

XX Sequence 6 AA;

XX Query Match 96.6%; Score 28; DB 5; Length 6;

XX Best Local Similarity 83.3%; Pred. No. 2e+06;

XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db |:||||

1 KVVFFA 6

RESULT 23
AAU96826
ID AAU96826 standard; peptide; 6 AA.
XX
AC AAU96826;
XX
DT 30-JUL-2002 (first entry)
XX
DE Amyloid targeting peptide #16.
XX
KW Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
transmissible cerebral amyloidosis; transmissible virus dementia;
scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
bovine spongiform encephalopathy; inflammation associated amyloid;
primary amyloidosis; feline spongiform encephalopathy;
Alzheimer's disease; prion-mediated disease; blood-brain barrier;
dialysis-related amyloidosis; light chain-related amyloidosis;
cerebral amyloid angiopathy.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..6 /note= "Preferably D-form residue"
FT Modified-site 6
FT /note= "Ala is amidated"
XX
PN WO200207781-A2.
XX
PD 31-JAN-2002.
XX
PP 25-JUL-2001; 2001WO-CA001071.
XX
PR 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Gervais P, Kong X, Chalifour R, Migneault D;
XX
DR WPI; 2002-371447/40.
XX
PT New amyloid-targeting imaging agents useful for in vivo imaging amyloid
plaques and/or for the treatment of amyloidosis disorders.
XX
PS Claim 49; Page 21; 57pp; English.
XX
CC The invention relates to an amyloid-targeting imaging agent comprising an
amyloid targeting moiety, a linker moiety and a labelling moiety. The
agent is of general formula A-t-(A₁ n k) z-A₁ a b (I) where z = 0 - 1;
A₁ t = an amyloid targeting moiety; A₁ n k = a linker moiety; and A₁ a b
= a labelling moiety. Also included are imaging amyloid deposition or
diagnosing an amyloid-related condition in a patient involving
administering (I) to the patient, and ultrasound imaging (I) in the
patient to determine the presence of amyloid or amyloid-related condition
; and a kit for preparing a radiopharmaceutical preparation comprising
(I), a reducing agent, a buffering agent, a transchelating agent, and
instructions for the preparation and use of the radiopharmaceutical in
the imaging of amyloid or an amyloid-related condition. The agents are
used for imaging amyloid deposition and for diagnosing an amyloid related
condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
cerebral amyloidosis (transmissible virus dementia), familial CJD,
scrapie, transmissible mink encephalopathy, bovine spongiform
encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
primary amyloidosis, feline spongiform encephalopathy, non-transmissible
cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
amyloid angiopathy. The agents are capable of crossing the blood-brain
barrier and are capable of binding specifically to amyloid plaques. The
present sequence is a peptide forming the amyloid targeting moiety of the
agent of the invention

XX Sequence 6 AA;
SQ
Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 1 KVVFFA 6
|:|||||
|:|||||
RESULT 24
AAU11664
ID AAU11664 standard; peptide; 6 AA.
XX
AC AAU11664;
XX
DT 09-APR-2002 (first entry)
XX
DE Peptide #17, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "C-terminal amide"
FT
XX
PN WO200185093-A2.
XX
PD 15-NOV-2001.
XX
PP 22-DEC-2000; 2000WO-IB002078.
XX
PR 23-DEC-1999; 99US-0171877P.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Green AM, Gervais P;
XX
DR WPI; 2002-075222/10.
XX
PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
disease comprises contacting blood vessel wall cell with amyloid-beta 40
inhibitor.
XX
PS Disclosure; Page 10; 68pp; English.
XX
CC The present invention relates to a new method of inhibiting cerebral
amyloid angiopathy. The new method of the invention involves contacting a
blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
can be used for treating disease states characterised by cerebral amyloid
angiopathy, particularly Alzheimer's disease, hereditary cerebral
haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
The present sequence represents one of a group of peptides (AAU11648-
AAU11669, AAU11910 & AAU11911) that were used in the invention as a
carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
was used in the invention to treat a disease state characterised by
cerebral amyloid angiopathy (CAA)
XX
SQ Sequence 6 AA;
Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 1 KVVFFA 6
|:|||||
|:|||||

RESULT 25
 AAU11656
 ID AAU11656 standard; peptide; 6 AA.
 AC AAU11656;
 XX
 DT 09-APR-2002 (first entry)
 DE
 DE Peptide #9, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
 XX
 XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
 XX
 XX Synthetic.
 OS
 XX WO2000185093-A2.
 FN
 XX
 XX 15-NOV-2001.
 PD
 XX 22-DEC-2000; 2000WO-IB002078.
 PF
 XX 23-DEC-1999; 99US-0171877P.
 PR
 XX (NEUR-) NEUROCHEM INC.
 PA
 XX Green AM, Gervais F;
 PI
 XX WPI; 2002-075222/10.
 DR
 XX
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.
 PT
 XX Disclosure; Page 10; 68pp; English.
 PS
 XX
 CC The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CNA)
 XX
 SQ Sequence 6 AA;
 Query Match 96.6%; Score 28; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db |:|||||
 1 KVVFFA 6
 RESULT 26
 AA335452
 ID AA335452 standard; peptide; 6 AA.
 AC AA335452;
 XX
 DT 17-JUN-2003 (first entry)
 DE
 DE Abeta peptide #23.
 XX
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW

KW peoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX
 OS Unidentified.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1. .6
 FT /note= "D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX WO200296937-A2.
 PN
 XX 05-DEC-2002.
 PD
 XX 29-MAY-2002; 2002WO-CA000763.
 PF
 XX 29-MAY-2001; 2001US-00867847.
 PR
 XX (NEUR-) NEUROCHEM INC.
 PA
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;
 FI WPI; 2003-201269/19.
 DR
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 PT
 XX Claim 1; Page 59; 44pp; English.
 PS
 XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 6 AA;
 Query Match 96.6%; Score 28; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db |:|||||
 1 KVVFFA 6
 RESULT 27
 ADQ37277
 ID ADQ37277 standard; peptide; 6 AA.
 XX
 AC ADQ37277;
 XX
 DT 07-OCT-2004 (first entry)
 DE Vaccine antigen amyloid-beta related amino acid sequence.

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.
 OS
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1. .6 /note= "D-form residues"
 FT Modified-site 6 /note= "amidated"
 FT
 XX
 XX WO2004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 67; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX
 XX Sequence 6 AA;
 Query Match 96.6%; Score 28; DB 8; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 1 KIVFFPA 6
 ID ADQ37321 standard; peptide; 6 AA.
 XX
 XX ADQ37321;
 XX
 XX 07-OCT-2004 (first entry)
 XX
 XX Antifibrillogenic amyloidosis inhibiting peptide.
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.
 OS
 XX
 XX WO2004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 69; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first

CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C): (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

Db 1 KVVFFPA 6

RESULT 29

ADQ37329

ID ADQ37329 standard; peptide; 6 AA.

XX AC ADQ37329;

XX DT 07-OCT-2004 (first entry)

XX DE Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;

KW vaccine antigen.
 XX Synthetic.

XX Key Location/Qualifiers
 XX Modified-site 6 /note= "amidated"

FT W02004058239-A1.

XX 15-JUL-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 23-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52.

XX Composition for treating e.g. Alzheimer's disease comprises first agent
 XX that prevents or treats amyloid-beta related disease and second agent
 XX that is either a peptide or peptidomimetic or an immune system modulator.
 XX Disclosure; Page 70, 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C): (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 30

ADY37928
ID ADY37928 standard; peptide; 6 AA.

XX AC ADY37928;

XX DT 19-MAY-2005 (first entry)

XX DE Amyloid-targeting peptide, SEQ ID NO:8, for use in imaging agent.

XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimers disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX PN US2005048000-A1.

XX PD 03-MAR-2005.

XX PF 03-DEC-2003; 2003US-00728028.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PR 29-JAN-2003; 2003US-0443291P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Kong X, Chalifour R, Migneault D;

XX DR WPI; 2005-212201/22.

XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.

XX PS Disclosure; SEQ ID NO 8; 34pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementia), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.

XX SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 9; Length 6;

Best Local Similarity 83.3%; Pred. No. 2e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 31

ADY37936
ID ADY37936 standard; peptide; 6 AA.

XX AC ADY37936;

XX DT 19-MAY-2005 (first entry)

XX DE Amyloid-targeting peptide, SEQ ID NO:16, for use in imaging agent.

XX KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimers disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.

XX OS Synthetic.

XX PN US2005048000-A1.

XX PD 03-MAR-2005.

XX PF 03-DEC-2003; 2003US-00728028.

XX PR 25-JUL-2000; 2000US-0220808P.

XX PR 24-JUL-2001; 2001US-00915092.

XX PR 29-JAN-2003; 2003US-0443291P.

XX PA (NEUR-) NEUROCHEM INT LTD.

XX PI Gervais F, Kong X, Chalifour R, Migneault D;

XX DR WPI; 2005-212201/22.

XX PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.

XX PS Disclosure; SEQ ID NO 16; 34pp; English.

XX CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementia), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.

XX SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KWVFFA 6

RESULT 32
ADQ09761
ID ADQ09761 standard; peptide; 22 AA.
XX
AC ADQ09761;
XX
DT 23-SEP-2004 (first entry)
XX
DE Rice 26kDa globulin signal sequence SEQ ID NO:117.
XX
KW prolamine; rice; plant; seed; transgenic plant; signal.
XX
OS Oryza sativa.
XX
FN W02004056993-A1.
XX
PD 08-JUL-2004.
XX
PF 09-DEC-2003; 2003WO-JP015753.
XX
PR 20-DEC-2002; 2002JP-00369700.
XX
FA (NAAQ-) NAT AGRIC & BIO-ORIENTED RES ORG.
XX
PI Kuroda M;
XX
DR WPI; 2004-525439/50.
DR N-FSDB; ADQ09760.
XX
PT Novel nucleic acid molecule antisense to nucleic acid sequence encoding
PT prolamine, useful for reducing expression dose of protein in seed, and
PT for producing transgenic plant, preferably rice plant having reduced
PT storage protein.
XX
PS Example 13; SEQ ID NO 117; 272pp; Japanese.
XX
CC The present invention describes a nucleic acid molecule (I) comprising a
CC consecutive nucleic acid sequence (S1) of at least 15 bp in length and
CC complementary with a nucleic acid sequence encoding a prolamine
CC polypeptide or a nucleic acid sequence having a homology of at least
CC about 70% to (S1). Also described: (1) a nucleic acid molecule (N1)
CC comprising a nucleic acid sequence (A) having about 70% homology to a
CC nucleic acid sequence encoding a prolamine polypeptide and a nucleic acid
CC acid sequence encoding a prolamine polypeptide; (2) a factor (II) capable
CC of causing RNA interference of the gene sequence encoding a prolamine
CC polypeptide; (3) a nucleic acid cassette (III) containing (1); (4)
CC producing (III); (5) a vector (IV) comprising (1); (6) a plant cell (V)
CC comprising (1); (7) a plant tissue (VI) comprising (V); (8) a plant (VII)
CC containing (1) or (V); (9) a seed (VIII) produced by (VII); (10) starch
CC preparation produced from (VII) or (VIII); and (11) a composition
CC containing gene product of foreign gene produced from (VII) or (VIII).
CC (1) is useful for decreasing the expression level of a protein in the
CC seed of a plant, for expressing a foreign gene in the seed of a plant and
CC for decreasing the expression of a natural protein in the seed of a
CC plant. The method of decreasing the amount of expression level of a
CC protein in the seed of a plant involves providing (I), introducing (I)
CC into the cell of the plant, redifferentiating the cell, producing a
CC transgenic plant, and obtaining the seed from the transgenic plant. The
CC method after the step of introduction, further involves selecting the
CC cell introduced with (1), by determining resistance with respect to
CC antibiotics. The method of expressing a foreign gene in the seed of a
CC plant, involves providing (I) and the nucleic acid molecule encoding a

foreign gene product, introducing (I) and the nucleic acid molecule
encoding a foreign gene product into cell of the plant, re-
differentiating the cell, producing a transgenic plant, and obtaining the
seed from the transgenic plant. The method further involves isolating the
gene product of the foreign gene from the seed. (1) is useful for
producing transgenic plants having reduced expression of storage proteins
and for reducing the expression dose of a protein in a seed of a plant.
The present sequence represents a rice 26kDa globulin signal sequence,
which is used in the exemplification of the present invention.

Sequence 22 AA;
Query Match 96.6%; Score 28; DB 8; Length 22;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KWVFFA 9

RESULT 33
ADT93984
ID ADT93984 standard; peptide; 23 AA.
XX
AC ADT93984;
XX
DT 27-JAN-2005 (first entry)
XX
DE Rice 26 kDa peptide.
XX
KW Storage protein; allergen specific T cell epitope;
KW vesicle anchoring signal; transgenic plant; rice albumen;
KW T cell epitope-attached peptide; 7crp; seed; glutelin; edible vaccine;
KW Japanese cedar pollen antigen; CryJ1; CryJ2; allergic disease; hay fever;
KW antiallergic; plant; 26 kDa.
XX
OS Oryza sativa.
XX
FN W02004094637-A1.
XX
PD 04-NOV-2004.
XX
PF 23-APR-2004; 2004WO-JP005938.
XX
PR 24-APR-2003; 2003JP-00120639.
XX
FA (NORQ) NAT INST AGROBIOLOGICAL SCI.
XX
PI Takaiwa F, Takagi H;
XX
DR WPI; 2004-784905/77.
XX
PT Novel DNA having sequence encoding allergen specific T-cell epitope
PT peptide, useful for accumulating T-cell epitope peptide in plants and for
PT treating allergic diseases such as pollinosis.
XX
PS Disclosure; SEQ ID NO 5; 79pp; Japanese.
XX
CC This invention relates to a DNA (I) having a sequence under the control
CC of a storage protein promoter, chosen from a sequence encoding storage
CC protein signal sequence at the 5' end of a sequence encoding allergen
CC specific T cell epitope peptide and/or a sequence encoding vesicle
CC anchoring signal sequence at the 3' end, and a DNA sequence encoding a
CC polypeptide having allergen specific T-cell epitope peptide inserted in
CC the variable region of a storage protein. Also disclosed is a vector (II)
CC for T-cell epitope accumulated plant preparation, and a method of
CC accumulating allergen specific T-cell epitope in a plant. The method
CC involves introducing (I) or (II) to a plant, obtaining DNA encoding
CC allergen specific T-cell epitope peptide, adding a DNA encoding a storage
CC protein signal sequence to the 5' end and/or a vesicle anchoring signal
CC sequence to the 3' end of the obtained DNA, and expressing the DNA in a
CC plant under the control of a storage protein promoter, or obtaining DNA

CC encoding allergen specific T-cell epitope peptide, inserting a DNA into
 CC the variable region of storage protein of the plant and expressing the
 CC peptide in the transgenic plant. The invention describes the accumulation
 CC of human T cell epitope in rice albumen, a method of accumulating T cell
 CC epitope-attached peptide (7crp) in seeds, a method of inserting the 7crp
 CC into the variable region of glutelin (the major storage protein of rice),
 CC and expressing and accumulating 7crp as part of the glutelin. The rice
 CC capable of producing the 7crp is useful as an edible vaccine against
 CC Japanese (Cryptomeria japonica) cedar pollen antigen. The pollen allergen
 CC is Cryj1 or Cryj2. The T-cell epitope is integrated on an edible region
 CC such as the seed of a plant. The method of the invention is useful for
 CC producing a plant accumulated with allergen specific T-cell epitope, and
 CC manufacturing a transgenic plant, preferably rice, integrated with T-cell
 CC epitope. The method is useful for preventing or treating allergic disease
 CC such as hay fever. The method enables the production of allergen specific
 CC T-cell epitope at a low cost and also reduces the amount for
 CC administration. The allergen specific T-cell epitope accumulated in a
 CC seed is stable for storage. This sequence represents rice 26 kDa peptide.
 XX
 XX Sequence 23 AA;

Query Match 96.6%; Score 28; DB 8; Length 23;
 Best Local Similarity 83.3%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
 Db 4 KVVFFFA 9
 |:|||||

RESULT 34
 AAB05910
 ID AAB05910 standard; peptide; 37 AA.

AC AAB05910;

DT 16-OCT-2000 (first entry)

DE Mouse inducible nitric oxide synthase calmodulin-binding region.

XX Mouse; inducible nitric oxide synthase; iNOS;
 KW endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;
 KW AMP-activated protein kinase; AMPK; calmodulin; Cam;
 KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;
 KW obstructive airways disease.

OS Mus sp.

PN WO200028076-A1.

PD 18-MAY-2000.

PP 05-NOV-1999; 99WO-AU000968.

PR 06-NOV-1998; 98AU-00006976.

XX (SVIN-) ST VINCENTS INST MEDICAL RES.

XX Stapleton DI, Chen Z, Michell BJ, Kemp BE, Mitchellhill KI;

XX WPI; 2000-376583/32.

XX Identifying modulators of AMP-activated protein kinase-mediated
 PT activation of a nitric oxide synthase (NOS), for use in ischemic heart
 PT disease, comprises testing for the increase or decrease in
 PT phosphorylation of NOS.

XX Example 4; Fig 5; 4lpp; English.

XX The present sequence is the calmodulin (Cam)-binding region of mouse
 CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of
 CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-
 CC arginine. The sequence is provided for comparison with endothelial nitric

CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is
 CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of
 CC Ca²⁺-Cam. Phosphorylation results in inhibition of eNOS. In the presence
 CC of Ca²⁺-Cam, phosphorylation by AMPK occurs predominantly at Ser-1177 and
 CC eNOS is activated. Modulators which activate AMPK may be used in the
 CC treatment of ischaemic heart disease by promoting glucose and fatty acid
 CC metabolism, and improving nutrient and oxygen supply to the myocytes.
 CC They may also be used for the treatment of pulmonary hypertension and
 CC obstructive airways disease

XX Sequence 37 AA;

Query Match 96.6%; Score 28; DB 3; Length 37;
 Best Local Similarity 83.3%; Pred. No. 32;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
 Db 18 KVVFFFA 23
 |:|||||

RESULT 35
 ADK34080
 ID ADK34080 standard; peptide; 37 AA.

AC ADK34080;

DT 20-MAY-2004 (first entry)

DE Human nNOS calmodulin binding domain peptide seqid 7.

XX vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;
 KW eNOS; endothelial nitric oxide synthase; angiogenesis;
 KW microvascular dysfunction; human; calmodulin binding domain;
 KW neuronal nitric oxide; nNOS.

OS Homo sapiens.

PN WO2004016761-A2.

PD 26-FEB-2004.

PP 15-AUG-2003; 2003WO-US025626.

PR 16-AUG-2002; 2002US-0403637P.

XX (SCHD) SCHERING AG.

XX Dole WP, Kauser K, Qian HS, Rubanyi G;

XX WPI; 2004-203789/19.

XX Treating critical limb ischemia (CLI), or angiogenesis comprises
 PT administering to a patient a polynucleotide encoding a mammalian
 PT endothelial nitric oxide synthase (eNOS) polypeptide.

XX Example 1; SEQ ID NO 7; 82pp; English.

XX The invention describes a method of creating critical limb ischaemia
 CC (CLI) comprising administering to a patient a polynucleotide encoding a
 CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also
 CC described are: a method for treating angiogenesis by administering to a
 CC patient a polynucleotide encoding eNOS; and ameliorating microvascular
 CC dysfunction by administering to the patient the polynucleotide encoding
 CC the eNOS polypeptide. The method is useful for treating critical limb
 CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.
 CC This is the amino acid sequence of a human neuronal nitric synthase
 CC (nNOS) calmodulin binding domain peptide.

XX Sequence 37 AA;

Query Match 96.6%; Score 28; DB 8; Length 37;
 Best Local Similarity 83.3%; Pred. No. 32;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
18 KVVFFA 23

Db

RESULT 36
ADL70727
ID ADL70727 standard; peptide; 37 AA.

XX
AC ADL70727;
XX
DT 20-MAY-2004 (first entry)
XX
DE Mouse iNOS calmodulin-binding site amino acid sequence SEQ ID NO:7.
XX
KW mouse; endothelial nitric oxide synthase; eNOS; enzyme; mutant;
KW calmodulin-binding domain; vasotropic; antiarteriosclerotic; hypotensive;
KW antidiabetic; vulnerable; antilipidemic; anorectic;
KW reduced calcium dependence; ischaemia; atherosclerosis; hypertension;
KW diabetes; Raynaud's phenomenon; poor wound healing; hyperlipidaemia;
KW obesity; iNOS.
XX
OS Mus musculus.
XX
XN WO2004016764-A2.
XX
PD 26-FEB-2004.
XX
XX 15-AUG-2003; 2003WO-US025745.
XX
PR 16-AUG-2002; 2002US-0403638P.
XX
PA (SCHD) SCHERING AG.
XX
PI Blasko E, Kausser K, Parkinson J;
XX
XX WPI; 2004-203792/19.
XX
XX New isolated endothelial nitric oxide synthase polypeptide mutant, useful
PT for diagnosing or treating ischemia, atherosclerosis, hypertension, and
PT diabetes, Raynaud's phenomenon, poor wound healing, hyperlipidemia or
PT obesity.
XX
PS Example 1; SEQ ID NO 7; 57pp; English.

CC The present sequence represents the calmodulin-binding site of mouse iNOS
CC amino acid sequence. The present invention describes endothelial nitric
CC oxide synthase (eNOS) mutants having one or more mutations in an amino
CC acid sequence corresponding to a functional domain of a mammalian eNOS.
CC At least one of the mutations is at a position corresponding to an amino
CC acid residue in a calmodulin-binding domain that is phosphorylated in
CC mammalian cells, and not an amino acid substitution to Ala or Asp. Also
CC described: (1) an isolated eNOS polypeptide mutant that is substantially
CC homologous, or has a 95-99% sequence identity to the amino acid sequence
CC of the novel eNOS polypeptide mutant; (2) an isolated polynucleotide
CC encoding the polypeptide mutant; (3) a recombinant vector comprising the
CC polynucleotide operably linked to at least one regulatory sequence; (4) a
CC pharmaceutical composition comprising the polypeptide mutant or the
CC polynucleotide; (5) a binding partner of the polypeptide mutant; (6)
CC modulating eNOS activity in a cell by administering to the cell the
CC polypeptide mutant; (7) modulating eNOS activity in a cell by
CC administering the polypeptide mutant or the polynucleotide to the cell,
CC such that the polypeptide mutant is expressed in the cell; (8) diagnosing
CC a condition associated with aberrant eNOS activity by contacting a cell
CC of a patient with the polynucleotide, and detecting a level of eNOS
CC activity indicative of the medical condition; and (9) prophylactic and
CC therapeutic methods of treating a condition associated with aberrant eNOS
CC activity by administering the polypeptide mutant or polynucleotide to the
CC patient. The eNOS mutant has vasotropic, antiarteriosclerotic, and
CC hypotensive, antidiabetic, vulnerable, antilipidemic and anorectic
CC activities, and has reduced calcium dependence and increased activity.

CC The polypeptide mutant, polynucleotide and methods are useful for
CC diagnosing or treating a condition associated with aberrant eNOS
CC activity, e.g. ischaemia, atherosclerosis, hypertension, diabetes,
CC Raynaud's phenomenon, poor wound healing, hyperlipidaemia or obesity.

XX Sequence 37 AA;

Query Match 96.6%; Score 28; DB 8; Length 37;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
18 KVVFFA 23

Db

RESULT 37
AAG02840
ID AAG02840 standard; protein; 77 AA.
XX
AC AAG02840;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 6921.
XX
KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
XX
XN EP1033401-A2.
XX
PD 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
PF
PR 26-FEB-1999; 99US-0122487P.
XX
XX (GEST) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI
XX WPI; 2000-500381/45.
DR
XX N-PSDB; AAC02846.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
PS Claim 13; SEQ ID NO 6921; 71pp + Sequence Listing; English.

CC The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors

XX Sequence 77 AA;

Query Match 96.6%; Score 28; DB 3; Length 77;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
KW gene; ds; plant.

XX Oryza sativa.

XX WO2003000905-A2.

XX 03-JAN-2003.

XX 21-JUN-2002; 2002WO-IB002450.

XX 22-JUN-2001; 2001US-0300112P.

XX 26-SEP-2001; 2001US-0325277P.

XX 20-DEC-2001; 2001US-0342327P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
PI Glazebrook J, Katagiri F, Krepis J, Provart N, Ricke D;

XX WPI; 2003-229341/22.

XX N-PSDB; AUC07947.

XX New plant genes encoding polypeptides having an activity involved in or
PT associated with the synthesis, metabolism or degradation of carbohydrates
PT in the plant grain useful in generating plants having improved
PT nutritional properties.

XX Claim 15; SEQ ID NO 214; 130pp; English.

XX This invention, in the area of plant biotechnology, relates to novel
CC polynucleotides comprising a nucleotide sequence encoding a protein which
CC is involved in or associated with the synthesis, metabolism or
CC degradation of carbohydrates in the plant grain and the expression of
CC which is up-regulated during grain filling. The plant is selected from
CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
CC sugarbeet, wheat, and rice. The invention may be useful for the
CC improvement of protein, oil, starch, fibre and moisture content of the
CC cereal grains. In addition, carbohydrate levels may be modified to a more
CC desirable level using the present invention. The present sequence is the
CC amino acid sequence of a rice protein of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedseq_sequences.

XX SQ Sequence 186 AA;

Query Match 96.6%; Score 28; DB 7; Length 186;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFPA 6
|:||||
Db 4 KVVFFPA 9

RESULT 41

AAW83792
ID AAW83792 standard; protein; 190 AA.

XX AAW83792;

XX AC AAW83792;

XX DT 07-NOV-2001 (first entry)

XX Human immune/haematopoietic antigen SEQ ID NO:11385.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis.

XX Homo sapiens.

XX WO200157182-A2.
XX 09-AUG-2001.
XX 17-JAN-2001; 2001WO-US001354.
XX 31-JAN-2000; 2000US-0179065P.
XX 04-FEB-2000; 2000US-0180628P.
XX 24-FEB-2000; 2000US-0184664P.
XX 02-MAR-2000; 2000US-0186350P.
XX 16-MAR-2000; 2000US-0189874P.
XX 17-MAR-2000; 2000US-0190076P.
XX 18-APR-2000; 2000US-0198123P.
XX 19-MAY-2000; 2000US-0205151P.
XX 07-JUN-2000; 2000US-0209467P.
XX 28-JUN-2000; 2000US-0214886P.
XX 30-JUN-2000; 2000US-0215135P.
XX 07-JUL-2000; 2000US-0216647P.
XX 07-JUL-2000; 2000US-0216880P.
XX 11-JUL-2000; 2000US-0217487P.
XX 11-JUL-2000; 2000US-0217496P.
XX 14-JUL-2000; 2000US-0218290P.
XX 26-JUL-2000; 2000US-0220963P.
XX 26-JUL-2000; 2000US-0220964P.
XX 14-AUG-2000; 2000US-0224518P.
XX 14-AUG-2000; 2000US-0224519P.
XX 14-AUG-2000; 2000US-0225213P.
XX 14-AUG-2000; 2000US-0225214P.
XX 14-AUG-2000; 2000US-0225266P.
XX 14-AUG-2000; 2000US-0225267P.
XX 14-AUG-2000; 2000US-0225268P.
XX 14-AUG-2000; 2000US-0225270P.
XX 14-AUG-2000; 2000US-0225447P.
XX 14-AUG-2000; 2000US-0225757P.
XX 14-AUG-2000; 2000US-0225758P.
XX 14-AUG-2000; 2000US-0225759P.
XX 18-AUG-2000; 2000US-0226279P.
XX 22-AUG-2000; 2000US-0226681P.
XX 22-AUG-2000; 2000US-0226686P.
XX 22-AUG-2000; 2000US-0227182P.
XX 23-AUG-2000; 2000US-0227009P.
XX 30-AUG-2000; 2000US-0228924P.
XX 01-SEP-2000; 2000US-0229287P.
XX 01-SEP-2000; 2000US-0229343P.
XX 01-SEP-2000; 2000US-0229344P.
XX 01-SEP-2000; 2000US-0229345P.
XX 05-SEP-2000; 2000US-0229509P.
XX 05-SEP-2000; 2000US-0229513P.
XX 06-SEP-2000; 2000US-0230437P.
XX 06-SEP-2000; 2000US-0230438P.
XX 08-SEP-2000; 2000US-0231242P.
XX 08-SEP-2000; 2000US-0231243P.
XX 08-SEP-2000; 2000US-0231244P.
XX 08-SEP-2000; 2000US-0231413P.
XX 08-SEP-2000; 2000US-0231414P.
XX 08-SEP-2000; 2000US-0232080P.
XX 08-SEP-2000; 2000US-0232081P.
XX 12-SEP-2000; 2000US-0232081P.
XX 14-SEP-2000; 2000US-0232397P.
XX 14-SEP-2000; 2000US-0232398P.
XX 14-SEP-2000; 2000US-0232399P.
XX 14-SEP-2000; 2000US-0232400P.
XX 14-SEP-2000; 2000US-0232401P.
XX 14-SEP-2000; 2000US-0233063P.
XX 14-SEP-2000; 2000US-0233064P.
XX 14-SEP-2000; 2000US-0233065P.
XX 21-SEP-2000; 2000US-0234223P.
XX 21-SEP-2000; 2000US-0234274P.
XX 25-SEP-2000; 2000US-0234997P.
XX 25-SEP-2000; 2000US-0234998P.
XX 26-SEP-2000; 2000US-0235484P.
XX 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239353P.
PR 13-OCT-2000; 2000US-0239373P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 08-DEC-2000; 2000US-0250391P.
PR 08-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
DR N-PSDB; AAK56573.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Claim 11; SEQ ID NO 11385; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX Sequence 190 AA;
SQ Query Match 96.6%; Score 28; DB 4; Length 190;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 14 KIVFFA 19
RESULT 42
ABB61977
ID ABB61977 standard; protein; 564 AA.
XX AC ABB61977;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 12723.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX OS pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR N-PSDB; ABL06080.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.

XX PS Disclosure; SEQ ID NO 12723; 2lpp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent

XX CC capable of detecting 1000 or more genes from *Drosophila*. The invention is

XX CC useful in developmental biology and in elucidating cell signalling and

XX CC cell-cell interactions in higher eukaryotes for the development of

XX CC insecticides, therapeutics and pharmaceutical drugs. The invention

XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-

XX CC ABB72072). The sequence data for this patent did not form part of the

XX CC printed specification, but was obtained in electronic format directly

XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 564 AA;

Query Match 96.6%; Score 28; DB 4; Length 564;

Best Local Similarity 83.3%; Pred. No. 4.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6

Db 53 KIIFFA 58

RESULT 43

ADQ66704

ID ADQ66704 standard; protein; 854 AA.

XX AC ADQ66704;

XX DT 07-OCT-2004 (first entry)

XX DE Novel human protein sequence #1677.

XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

XX KW gene therapy; diagnostic marker; morbid state; osteoporosis;

XX KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

XX KW cancer.

XX OS Homo sapiens.

XX PN EP1440981-A2.

XX PD 28-JUL-2004.

XX PF 21-JAN-2004; 2004EP-00001196.

XX PR 21-JAN-2003; 2003JP-00102206.

XX PR 09-MAY-2003; 2003JP-00131392.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

XX PI Yamamoto J, Isono Y, Nagai K, Irie R;

XX DR WPI; 2004-535376/52.

XX DR N-PSDB; ADQ64516.

XX PT Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,

XX PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX FS Claim 1; SEQ ID NO 3865; 2449pp; English.

XX CC The invention relates to 2495 novel polynucleotides (I) and their encoded

XX CC polypeptides, sequences hybridizing to these nucleotides, sequences

XX CC encoding partial polypeptides and sequences having 70% or 90% identity to

XX CC the nucleotide and protein sequences. The nucleotides and polypeptides

XX CC are useful as diagnostic markers or therapeutic target for the diseases

XX CC or morbid states. They are also useful for treating osteoporosis,

XX CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,

XX CC dementia and various cancers. This sequence corresponds to a protein

XX CC sequence of the invention.

XX SQ Sequence 854 AA;

Query Match 96.6%; Score 28; DB 8; Length 854;

Best Local Similarity 83.3%; Pred. No. 7.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6

Db 221 KVVFFA 226

RESULT 44

ABM83252

ID ABM83252 standard; protein; 922 AA.

XX AC ABM83252;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:3501.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX OS Homo sapiens.

XX PN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;

XX PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;

XX PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

XX PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

XX PI Lagace RE, Spiro FA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

XX PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX PI Patury S, Shi X, Suarez CJ;

XX DR WPI; 2004-329368/30.

XX DR N-PSDB; ACN41904.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful

XX PT in diagnosing a condition, disease or disorder associated with human

XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

XX PT in gene mapping.

XX FS Claim 27; Page; 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides

XX CC selected from one of the 2722 sequences defined in the specification. A

XX CC polynucleotide of the invention may have a use in gene therapy. The human

XX CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

XX CC used to diagnose a particular condition, disease or disorder associated

XX CC with human molecules, e.g. cell proliferative disorders,

XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine

XX CC disorder, neurological disorders, gastrointestinal disorders, or

XX CC infections caused by virus, bacteria, fungi or parasite. The dithp

XX CC molecules may also be used in genetic mapping, in identifying individuals

XX CC from minute biological samples, in detecting single nucleotide

XX CC polymorphisms, as molecular weight markers, and for somatic or germline

XX CC gene therapy. The present sequence represents a dithp protein of the

XX CC invention. Note: The sequence data for this patent is not represented in

XX CC the printed specification, but was obtained in electronic format directly

XX CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SQ Sequence 922 AA;
 Query Match 96.6%; Score 28; DB 8; Length 922;
 Best Local Similarity 83.3%; Pred. NO. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 |:|||||
 Db 291 KVVFFA 296
 RESULT 45
 ADP76335
 ID ADF76335 standard; protein; 925 AA.
 XX AC ADP76335;
 DT 26-FEB-2004 (first entry)
 XX DE Novel human secreted and transmembrane protein SeqID 8.
 XX KW human; PRO; membrane bound protein; membrane bound receptor;
 KW cell proliferation; cell migration; cell differentiation;
 KW mitogenic factor; survival factor; cytotoxic factor;
 KW differentiation factor; neurotrophic; hormone; cell receptor;
 KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
 XX OS Homo sapiens.
 XX KW WO2003072035-A2.
 PN 04-SEP-2003.
 PD 21-FEB-2003; 2003WO-US005241.
 XX PF 22-FEB-2002; 2002US-0359461P.
 PR (GETH) GENENTECH INC.
 PA Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
 PI Williams PM, Wood WI, Wu TD;
 XX WPI; 2003-721702/58.
 DR N-PSDB; ADF76334.
 XX New PRO polypeptides, useful for diagnosing and treating an immune
 PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
 PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
 PT diabetes mellitus.
 XX Claim 10; SEQ ID NO 8; 918pp; English.
 PS This invention relates to novel nucleic acids encoding human PRO secreted
 CC and transmembrane proteins. Extracellular proteins play important roles
 CC in the formation, differentiation and maintenance of multicellular
 CC organisms. The fate of many individual cells (for example proliferation,
 CC migration or differentiation) is typically governed by information
 CC received from other cells and the immediate environment. The information
 CC is often transmitted by secreted polypeptides (for example mitogenic
 CC factors, survival factors, cytotoxic factors, differentiation factors,
 CC neurotrophic factors or hormones) which are received and interpreted by diverse
 CC cell receptors or membrane bound proteins. These membrane bound proteins
 CC and receptors may be of use as pharmaceutical and diagnostic agents, such
 CC as in the blocking of receptor-ligand interactions. The current invention
 CC provides the amino acid sequences of novel human membrane bound receptors
 CC and proteins, along with the cDNA sequences encoding them. The novel
 CC proteins of the invention may have cytostatic activities through the
 CC stimulation of chondrocytes. The nucleic acids of the invention may be
 CC useful for the manufacture of a medicament for diagnosing or treating a
 CC tumour in a mammal. In addition, they may be useful for measuring or
 CC detecting the expression of a tumour associated gene. The present
 CC sequence is the amino acid sequence of a human PRO protein of the
 CC invention.
 XX
 XX SQ Sequence 925 AA;
 Query Match 96.6%; Score 28; DB 7; Length 925;
 Best Local Similarity 83.3%; Pred. NO. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 |:|||||
 Db 292 KVVFFA 297
 RESULT 46
 ADJ70225
 ID ADJ70225 standard; protein; 925 AA.
 XX AC ADJ70225;
 DT 06-MAY-2004 (first entry)
 XX DE Human heat mitochondrial protein as a therapeutic target SeqID2031.
 XX KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX OS Homo sapiens.
 XX KW WO2003087768-A2.
 PN 23-OCT-2003.
 PD 04-APR-2003; 2003WO-US010870.
 XX PF 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 XX PR 20-SEP-2002; 2002US-0412418P.
 XX (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX WPI; 2003-845369/78.
 DR Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX Claim 1; SEQ ID NO 2031; 180pp; English.
 PS This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nontropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytostatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 CC

SQ Sequence 925 AA;
 Query Match 96.6%; Score 28; DB 7; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 |:|||||
 Db 292 KVVFFA 297
 RESULT 47
 ADJ75428
 ID ADJ75428 standard; protein; 925 AA.
 XX AC ADJ75428;
 XX DT 20-MAY-2004 (first entry)
 XX DE Marker gene related amino acid sequence SEQ ID NO:680.
 XX KW bronchial asthma; chronic obstructive pulmonary disease;
 XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 XX KW gene therapy; marker.
 XX OS Homo sapiens.
 XX PN EP1394274-A2.
 XX PD 03-MAR-2004.
 XX PF 04-AUG-2003; 2003EP-00254857.
 XX PR 06-AUG-2002; 2002JJP-00229312.
 XX PR 20-MAR-2003; 2003JP-00077212.
 XX PA (GENO-) GENOX RES INC.
 XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuohara K;
 XX WPI; 2004-193155/19.
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX Example 11; SEQ ID NO 680; 241pp; English.
 PS The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a

CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.
 XX Sequence 925 AA;
 Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 |:|||||
 Db 292 KVVFFA 297
 RESULT 48
 ADJ75495
 ID ADJ75495 standard; protein; 925 AA.
 XX AC ADJ75495;
 XX DT 20-MAY-2004 (first entry)
 XX DE Marker gene related amino acid sequence SEQ ID NO:747.
 XX KW bronchial asthma; chronic obstructive pulmonary disease;
 XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 XX KW gene therapy; marker.
 XX OS Homo sapiens.
 XX PN EP1394274-A2.
 XX PD 03-MAR-2004.
 XX PF 04-AUG-2003; 2003EP-00254857.
 XX PR 06-AUG-2002; 2002JJP-00229312.
 XX PR 20-MAR-2003; 2003JP-00077212.
 XX PA (GENO-) GENOX RES INC.
 XX PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuohara K;
 XX WPI; 2004-193155/19.
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX Example 11; SEQ ID NO 747; 241pp; English.
 PS The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial

CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 925 AA;

SQ Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. NO. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 Db 292 KIVFFA 297

RESULT 49

ID ADN04860 standard; protein; 925 AA.

XX AC ADN04860;

XX 01-JUL-2004 (first entry)

XX Antipsoriatic protein sequence #610.

XX antipsoriatic; gene therapy; psoriasis; diagnosis.

XX Homo sapiens.

XX WO2004028479-A2.

XX 08-APR-2004.

XX 25-SEP-2003; 2003WO-US030907.

XX 25-SEP-2002; 2002US-0414006P.

XX (GETH) GENENTECH INC.

XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 PI Wu TD;

XX WPI; 2004-305105/28.

XX N-PSDB; ADN04859.

XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.

XX Claim 9; SEQ ID NO 1254; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.

XX Sequence 925 AA;

SQ Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. NO. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|:|

Db 292 KIVFFA 297

RESULT 50

ADN14233

ID ADN14233 standard; protein; 925 AA.

XX AC ADN14233;

XX 21-OCT-2004 (first entry)

XX Human NF-kappaB pathway-associated protein SeqID234.

XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnary; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.

XX Homo sapiens.

XX WO2004065577-A2.

XX 05-AUG-2004.

XX 13-JAN-2004; 2004WO-US000798.

XX 14-JAN-2003; 2003US-0440068P.

XX 12-MAY-2003; 2003US-0469757P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Nadler SG, Neubauer MG, Feder JN, Carman J;

XX WPI; 2004-562168/54.

XX N-PSDB; ADN14232.

XX New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.

XX Claim 6; SEQ ID NO 234; 237pp; English.

XX This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,
 CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnary activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper

CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NP-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.

XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|||||
 Db 292 KVVFFA 297

RESULT 51
 ADP25011
 ID ADP25011 standard; protein; 925 AA.

XX AC ADP25011;

XX DT 18-NOV-2004 (first entry)

XX DE PRO polypeptide SEQ ID NO:2189.

XX KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 XX osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 XX antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX OS Unidentified.

XX FN WO2004041170-A2.

XX PD 21-MAY-2004.

XX PF 30-OCT-2003; 2003WO-US034312.

XX PR 01-NOV-2002; 2002US-0423394P.

XX PA (GETH) GENENTECH INC.

XX PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI,
 XX Wu TD;

XX DR WPI; 2004-419628/39.

XX DR N-PSDB; ADP25010.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 XX erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 XX renal disease, or demyelinating diseases of the central or peripheral
 XX nervous system.

XX Claim 7; SEQ ID NO 2189; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
 XX polypeptide encoded by it. A protein of the invention has
 XX antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 XX osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 XX antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 XX of the invention may have a use in gene therapy. The PRO polypeptide, its
 XX agonist, antagonist, or antibody that specifically binds to the
 XX polypeptide is useful for treating an immune related disorder such as
 XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|||||
 Db 292 KVVFFA 297

RESULT 52

ADR97294

ID ADR97294 standard; protein; 925 AA.

XX AC ADR97294;

XX DT 02-DEC-2004 (first entry)

XX DE Human RIG-I-DEAD/H box protein, an apoptosis related target Seq 2.

XX KW human; enzyme; apoptosis; cancer; inflammation; autoimmune;
 XX neurodegenerative disorder; cytostatic; antiinflammatory;
 XX immunosuppressive; neuroprotective; gene therapy; RIG-I-DEAD/H box.

XX OS Homo sapiens.

XX FN WO2004078783-A2.

XX PD 16-SEP-2004.

XX PF 05-MAR-2004; 2004WO-GB000957.

XX PR 07-MAR-2003; 2003GB-00005267.

XX PA (EIRX-) EIRX THERAPEUTICS LTD.

XX PI Murphy FJ, Sheehan DE, Keating KE, Hayes I, Seera L;
 XX WPI; 2004-662402/64.

XX DR N-PSDB; ADR97293.

XX Identifying an agent that modulates the function of an apoptosis-
 XX associated polypeptide, useful for diagnosing or treating e.g. cancer,
 XX comprises comparing the binding of the polypeptide to the candidate agent
 XX and to a control agent.

XX Claim 1; SEQ ID NO 2; 304pp; English.

XX This invention relates to novel agents that modulates the function of
 XX human apoptosis-associated proteins specified within the specification.
 XX Specifically, it refers to a method for the identification of target
 XX genes whose expression is correlated with an early stage in the
 XX regulation of apoptosis. The present invention describes a method of
 XX contacting either candidate agents or control agents to the target genes
 XX and assessing the difference of binding and inhibitory activity, where
 XX the candidate agent is selected from a low molecular weight organic
 XX molecule, an antibody or fragment thereof, an antisense oligonucleotide,

CC a small inhibitory dRNA, or a ribozyme. As such, the compositions and
 CC methods are useful for diagnosing and treating diseases or conditions
 CC associated with abnormal apoptosis in mammalian tissue, such as cancer,
 CC inflammation, autoimmune or neurodegenerative disorders. Accordingly,
 CC they exhibit cytostatic, antiinflammatory, immunosuppressive and
 CC neuroprotective activities. These may also be used for drug screening
 CC purposes and in gene therapy. This polypeptide sequence is a human target
 CC protein, an enzyme associated with the regulation of apoptosis whose
 CC expression is modulated by novel agents of the invention.
 XX
 XX Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;

Best Local Similarity 83.3%; Pred. No. 7.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

Db 292 KIVFFPA 297

RESULT 53

ADV17516

ID ADV17516 standard; protein; 925 AA.

XX

AC

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Db 292 KIVFFPA 297

RESULT 54

AEA23525

ID AEA23525 standard; protein; 925 AA.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Db 292 KIVFFPA 297

RESULT 54

AEA23525

ID AEA23525 standard; protein; 925 AA.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

Db 292 KIVFFPA 297

RESULT 54

AEA23525

ID AEA23525 standard; protein; 925 AA.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

```

DE Inducible nitrogen monoxide synthase.
XX
KW nitrogen monoxide synthase; inducible; treatment; prevention;
KW vascular disease; restenosis.
XX
OS Mus musculus.
XX
FN DE4411402-A1.
XX
PD 05-OCT-1995.
XX
PF 31-MAR-1994; 94DE-04411402.
XX
PR 31-MAR-1994; 94DE-04411402.
XX
PA (SCHR/) SCHRADER J.
XX
PI Schrader J, Goedecke A;
XX
DR WPI; 1995-345550/45.
XX
DR N-PSDB; AAQ94252.
XX
PT Eukaryotic expression vector for nitrogen-monoxide synthase gene -
PT useful in the treatment and prevention of diseases of blood vessels by
PT gene therapy.
XX
PS Claim 5; Fig 1; 28pp; German.
XX
CC Inducible nitrogen monoxide synthase (iNOS) was isolated from mice, and
CC is encoded by AAQ94252. iNOS is homodimer with a mol. wt. of 130 kDa per
CC subunit. The activity of iNOS is independent of calmodulin and cellular
CC calcium levels. Vectors contg. the DNA are used in the treatment or
CC prevention of vascular diseases, high blood pressure, arteriosclerosis,
CC stenosis or restenosis of blood vessels, esp. coronary vessels after
CC percutane transluminal coronary angioplasty. See AAR77363 and AAR77362
CC for endothelial and brain-derived NOS
XX
SQ Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 56
AAG64500
ID AAG64500 standard; protein; 1144 AA.
XX
AC AAG64500;
XX
DT 02-OCT-2001 (first entry)
XX
DE Mouse inducible nitric oxide synthase 2.
XX
KW Antisense oligonucleotide; inducible nitric oxide synthase;
KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
KW cardiant; neuroprotective; vasotropic; ischaemia; reperfusion injury;
KW 2'-O-methoxyethyl; phosphorothioate; mouse.
XX
OS Mus sp.
XX
FN WO200152902-A1.
XX
PD 26-JUL-2001.
XX
PF 15-JAN-2001; 2001WO-US001381.
XX
PR 24-JAN-2000; 2000US-00490208.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dean NM, Cowseert LM;
XX
DR WPI; 2001-465340/50.
XX
DR N-PSDB; AAH47974.
XX
PT New antisense oligonucleotides for modulating the expression of inducible
PT nitric oxide synthase in cells or tissues, particularly useful for
PT treating e.g. immunological, cardiovascular or neurological disorders, or
PT ischemia.
XX
PS Example 17; Page 110-114; 144pp; English.
XX
CC The invention relates to antisense compounds, especially
CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
CC nitric oxide synthase and which specifically hybridise to and modulate

```

```

DE Inducible nitrogen monoxide synthase.
XX
KW nitrogen monoxide synthase; inducible; treatment; prevention;
KW vascular disease; restenosis.
XX
OS Mus musculus.
XX
FN DE4411402-A1.
XX
PD 05-OCT-1995.
XX
PF 31-MAR-1994; 94DE-04411402.
XX
PR 31-MAR-1994; 94DE-04411402.
XX
PA (SCHR/) SCHRADER J.
XX
PI Schrader J, Goedecke A;
XX
DR WPI; 1995-345550/45.
XX
DR N-PSDB; AAQ94252.
XX
PT Eukaryotic expression vector for nitrogen-monoxide synthase gene -
PT useful in the treatment and prevention of diseases of blood vessels by
PT gene therapy.
XX
PS Claim 5; Fig 1; 28pp; German.
XX
CC Inducible nitrogen monoxide synthase (iNOS) was isolated from mice, and
CC is encoded by AAQ94252. iNOS is homodimer with a mol. wt. of 130 kDa per
CC subunit. The activity of iNOS is independent of calmodulin and cellular
CC calcium levels. Vectors contg. the DNA are used in the treatment or
CC prevention of vascular diseases, high blood pressure, arteriosclerosis,
CC stenosis or restenosis of blood vessels, esp. coronary vessels after
CC percutane transluminal coronary angioplasty. See AAR77363 and AAR77362
CC for endothelial and brain-derived NOS
XX
SQ Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 56
AAW51246
ID AAW51246 standard; protein; 1144 AA.
XX
AC AAW51246;
XX
DT 25-MAR-2003 (revised)
DT 12-AUG-1998 (first entry)
XX
DE Inducible nitric oxide synthase, long isoform.
XX
KW Inducible nitric oxide synthase; iNOS; recombinant protein; cDNA library;
KW isoform.
XX
OS Mus sp.
XX
FN US5766909-A.
XX
PD 16-JUN-1998.
XX
PF 05-NOV-1993; 93US-00147812.
XX
PR 04-FEB-1992; 92US-00841641.
XX
PA (MERI ) MERCK & CO INC.

```

CC expression of inducible nitric oxide synthase. The antisense compounds
 CC have immunomodulator, antidiabetic, cardiovascular, cardiant,
 CC neuroprotective, disorder and vasotropic activity. The antisense
 CC oligonucleotides are useful for inhibiting the expression of inducible
 CC nitric oxide synthase in cells or tissues. In particular, the antisense
 CC oligonucleotides are useful for treating diseases or disorders associated
 CC with inducible nitric oxide synthase, e.g. diabetes, immunological
 CC disorder, cardiovascular disorder, neurological disorder or
 CC ischaemia/reperfusion injury. The antisense oligonucleotides are also
 CC useful for research and diagnostics. The present sequence is that of
 CC mouse inducible nitric oxide synthase
 XX
 SQ Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 4; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 Db 514 KVVFFPA 519
 |:.|||

RESULT 58
 ABU79138
 ID ABU79138 standard; protein; 1144 AA.
 XX
 AC ABU79138;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE Inducible nitric oxide synthase protein.
 XX
 KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.
 XX
 OS Unidentified.
 XX
 PN US2002177551-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 30-MAY-2001; 2001US-00870759.
 XX
 PR 31-MAY-2000; 2000US-0208128P.
 XX
 PA (TERM/) TERMAN D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 2003-361759/34.
 DR N-PSDB; ACA64740.
 XX
 XX A mammalian cell receptor, useful in the treatment of cancer by binding
 FT to tumor associated lipids where the binding induces anergy or apoptosis
 PT in T cells and antigen presenting cells.
 XX
 PS Example 2; Page; 167pp; English.
 XX
 CC The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a

CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal (by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents an anti-tumour protein which is co-administered with
 CC or incorporated into a fusion construct with a superantigen. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from the US patent
 CC office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 SQ Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 6; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 Db 514 KVVFFPA 519
 |:.|||

RESULT 59
 ADP43404
 ID ADP43404 standard; protein; 1144 AA.
 XX
 AC ADP43404;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE INOS polypeptide seqid 124.
 XX
 KW receptor; lipid-based tumour associated antigen; cytostatic;
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
 KW infectious disease; iNOS.
 XX
 OS Unidentified.
 XX
 PN US2003157113-A1.
 XX
 PD 21-AUG-2003.
 XX
 PF 28-DEC-2000; 2000US-00751708.
 XX
 PR 28-DEC-1999; 99US-0173371P.
 XX

PA (TERM//) Terman D S.
 XX Terman DS;
 XX WPI; 2003-787326/74.
 DR N-PSDB; ADF43403.
 XX
 PT New receptor in a mammalian cell that inhibits regular activation by
 PT receptors specific for lipid-based tumor associated antigens, useful for
 PT treating a neoplastic disease or tumor, and infectious diseases.
 XX
 PS Example 3; SEQ ID NO 124; 151pp; English.
 XX
 CC The invention describes a receptor in a mammalian cell that inhibits
 CC regular activation by receptors specific for lipid-based tumour
 CC associated antigen. The receptor has cytostatic and antimicrobial
 CC properties and is suitable for use in gene therapy. The receptors,
 CC methods and compositions are useful for treating a neoplastic disease or
 CC tumour (cancer), and infectious diseases. This sequence represents INOS
 CC polypeptide, a cell surface moiety, the DNA of which can be transfected
 CC into a cell with superantigen DNA to generate antitumour immunity.
 XX
 SQ Sequence 1144 AA;
 Query Match 96.6%; Score 28; DB 7; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVRFA 6
 Db 514 KVVFFA 519
 |:|||||
 |:|||||
 RESULT 60
 ADF77432
 ID ADF77432 standard; protein; 1144 AA.
 XX
 AC ADF77432;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Mouse inducible nitric oxide synthase, INOS.
 XX
 KW Mouse; inducible nitric oxide synthase; INOS; cardiac; vasodilator;
 KW cytosolic; gynaecological; restenotic response; angioplasty;
 KW vasodilation; angina; cancer; cell death; premature labour; tumour;
 KW nervous system; brain; erectile dysfunction; uterus; lung; vascular tone;
 KW regional blood flow.
 XX
 OS Mus musculus.
 XX
 PN US6620616-B1.
 XX
 PD 16-SEP-2003.
 XX
 PF 13-SEP-2000; 2000US-00661259.
 XX
 PR 13-SEP-2000; 2000US-00661259.
 XX
 PA (CLEV-) CLEVELAND CLINIC FOUND.
 XX
 STuehr DJ, Adak S;
 WPI; 2003-895427/82.
 DR
 XX New isolated polynucleotide encoding a variant of a corresponding wild-
 PT type nitric oxide synthase, useful for reducing the restenotic response
 PT after angioplasty, or for inhibiting the development or onset of
 PT premature labor.
 XX
 PS Disclosure; SEQ ID NO 5; 35pp; English.
 XX
 CC The invention relates to an isolated polynucleotide encoding a variant of

CC a corresponding wild-type nitric oxide synthase (NOS). The variant has
 CC the tryptophan in the alpha 3 helix substituted by tyrosine or
 CC phenylalanine. Also included are a nucleic acid construct comprising the
 CC nucleotide sequence that encodes a variant of a corresponding wild-type
 CC nitric oxide synthase and a promoter operably linked to the encoding
 CC sequence of the variant and a transformed cell comprising the construct,
 CC where the cell expresses the nitric oxide synthase variant. The variant
 CC has an in vitro enzymatic activity that is greater than the in vitro
 CC enzymatic activity of the corresponding wild-type nitric oxide synthase.
 CC The variant can preferably be of a corresponding wild-type endothelial
 CC nitric oxide synthase (eNOS), neuronal nitric oxide synthase (nNOS), or
 CC inducible nitric oxide synthase (iNOS). The polynucleotides are useful
 CC for reducing the restenotic response after angioplasty, or related
 CC interventional procedures, or to enhance the vasodilation response in
 CC treating angina, for anticancer therapy to promote cell death, and for
 CC inhibiting the development or onset of premature labour. The
 CC polynucleotides are useful to achieve or augment expression of NOS
 CC variant proteins or polypeptides in vivo to increase NOS production in
 CC target tissue, tumour tissue, tissue of the nervous system, including
 CC brain, penis (e.g. in erectile dysfunction) and uterine tissue, and lung
 CC tissue. NOS is useful for maintaining vascular tone and regulating
 CC regional blood flow. The present sequence is wild-type mouse INOS.
 XX
 SQ Sequence 1144 AA;
 Query Match 96.6%; Score 28; DB 7; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVRFA 6
 Db 514 KVVFFA 519
 |:|||||
 |:|||||
 RESULT 61
 ADF76212
 ID ADJ76212 standard; protein; 1144 AA.
 XX
 AC ADJ76212;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Marker gene related amino acid sequence SEQ ID NO:1464.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 OS Mus musculus.
 XX
 PN EPI394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 PF 04-AUG-2003; 2003EP-00254857.
 XX
 PR 06-AUG-2002; 2002JP-00229312.
 XX
 PR 20-MAR-2003; 2003JP-00077212.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 WPI; 2004-193155/19.
 DR
 XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 PS Claim 16; SEQ ID NO 1464; 241pp; English.
 XX
 CC The present invention describes a method of testing for bronchial asthma

CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

SQ Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 8; Length 1144;

Best Local Similarity 83.3%; Pred. No. 9.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 514 KVVFFA 519

RESULT 62

ADJ76136

ID ADJ76136 standard; protein; 1144 AA.

XX AC

XX ADJ76136;

XX 20-MAY-2004 (first entry)

XX DE Marker gene related amino acid sequence SEQ ID NO:1388.

XX KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.

XX OS Mus musculus.

XX XX EP1394274-A2.

XX XX 03-MAR-2004.

XX XX 04-AUG-2003; 2003EP-00254857.

XX XX 06-AUG-2002; 2002JP-00229312.

XX XX 20-MAR-2003; 2003JP-00077212.

XX XX (GENO-) GENOX RES INC.

XX XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX XX WPI; 2004-193155/19.

XX XX Testing for bronchial asthma or chronic obstructive pulmonary disease by

XX XX comparing the expression level of a marker gene in a biological sample

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

XX XX

PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.

XX Claim 16; SEQ ID NO 1388; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (1) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (1) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 8; Length 1144;

Best Local Similarity 83.3%; Pred. No. 9.8e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 514 KVVFFA 519

RESULT 63

AEA03075

ID AEA03075 standard; protein; 1144 AA.

XX AC

XX AEA03075;

XX 28-JUL-2005 (first entry)

XX DE VEGF amino acid sequence SEQ ID NO:101.

XX KW tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
 KW vascular endothelial cell growth factor.

XX OS Unidentified.

XX XX US2005112141-A1.

XX XX 26-MAY-2005.

XX XX 08-SEP-2004; 2004US-00937758.

XX XX 30-AUG-2000; 2000US-00650884.

XX XX (TERM/) Terman D S.

XX XX Terman DS;

XX XX

DR WPI; 2005-394926/40.
 DR N-PSDB; AEA03074.
 XX
 PT New composition for treating a tumor or neoplastic disease in a subject
 PT comprises conjugates comprising superantigen polypeptides or nucleic
 PT acids with other molecules that produce a tumoricidal response.
 XX
 PS Example 3; SEQ ID NO 101; 125pp; English.
 XX
 CC The invention relates to a composition for treating a tumor or neoplastic
 CC disease in a subject. Also described: (1) a mammalian cell comprising an
 CC exogenous nucleic acid encoding a superantigen expressed in the cell,
 CC which cell also produces or expresses all alpha-anomers of
 CC monoglycosylceramide or diglycosylceramide, where expression of the
 CC superantigen and the mono- or diglycosylceramide is capable of eliciting
 CC an antitumor immune response in a mammal into which the cell is
 CC introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
 CC preparing a population of immunotherapeutic T or natural killer T (NKT)
 CC cells useful to treat a tumor or neoplastic disease in a subject; (4) an
 CC apoptotic cell preparation or lysate useful for treating a tumor or
 CC neoplastic disease in a subject, comprising a cell population that has
 CC been transfected with naked DNA encoding a superantigen, and treated to
 CC undergo apoptosis or lysis; and (5) a cell that has ingested or been
 CC transfected with the above apoptotic preparation or lysate, thus,
 CC rendering the cell effective in presenting material expressed from
 CC transfecting nucleic acid or material ingested to the immune system of a
 CC mammal to elicit an anti-tumor immune response. The composition and
 CC methods are useful for treating tumors or neoplastic diseases. The
 CC present sequence represents a VEGF protein sequence, which is used in an
 CC example from the present invention. Note - The sequence data for this
 CC patent is not represented in the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site.
 XX
 SQ Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 9; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFFA 6
 Db 514 KVVFFFA 519
 :|||||
 :|||||

RESULT 64
 ABB68472
 ID ABB68472 standard; protein; 1443 AA.
 XX
 AC ABB68472;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 32208.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 XX WO200171042-A2.
 XX
 FN 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US009231.
 XX
 XX 23-MAR-2000; 2000US-0191637P.
 XX
 PR 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EM;
 XX
 XX WPI; 2001-656860/75.
 XX
 PS

DR N-PSDB; ABL12575.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 32208; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
 CC AB872072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1443 AA;

Query Match 96.6%; Score 28; DB 4; Length 1443;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFFA 6
 Db 1204 KIIFFFA 1209
 :|||||
 :|||||

RESULT 65
 AAW02314
 ID AAW02314 standard; peptide; 6 AA.
 XX
 AC AAW02314;
 XX
 DT 02-MAY-1997 (first entry)
 XX
 DE Beta-amyloid modulator peptide #5.
 XX
 KW Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
 KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 XX
 OS Synthetic.
 XX
 XX WO9628471-A1.
 XX
 PD 19-SEP-1996.
 XX
 PF 14-MAR-1996; 96WO-US003492.
 XX
 XX 14-MAR-1995; 95US-00404831.
 XX
 PR 07-JUN-1995; 95US-00475579.
 XX
 PR 27-OCT-1995; 95US-00548998.
 XX
 XX (PHAR-) PHARM PEPTIDES INC.
 XX
 XX Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
 PI Kaaman L, Musso G, Signer ER, Wakefield J, Reed MJ, Molineaux S;
 PI Kubasek W, Chin J, Lee J, Kelley M;
 XX
 XX WPI; 1996-433762/43.
 DR
 XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 PT protein coupled (in)directly to at least 1 modifying gp., useful in
 PT treatment of Alzheimer's disease.
 XX
 XX Claim 16; Page 91; 106pp; English.
 PS

AAW02310-W02332 represent the peptide portions of the beta-amyloid modulator compounds of the invention. Beta-amyloid peptide is a 4 kilodalton peptide that is the major protein component of amyloid plaques. Amyloid plaques are present both in the brain lesions, and in the walls of cerebral blood vessels in Alzheimer's disease patients. The amyloid modulators of the invention comprise an amyloidogenic protein or peptide (such as this sequence) coupled directly or indirectly to at least one modifying group. The modifying group is preferably a cyclic, heterocyclic, or polycyclic group, such as declain, a cholanyl group, a biotin containing group, or a fluorescein containing group. These compounds then modulate the aggregation of these sequences to natural amyloid proteins or peptides when contacted with the natural amyloidogenic proteins or peptides. The modulator compounds can be used in the treatment of disorders associated with amyloidosis, such as familial amyloid polynuropathy, familial amyloid cardiomyopathy, isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie, bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset diabetes, insulinoma, familial Mediterranean fever, familial amyloid nephropathy with urticaria and deafness, hereditary cerebral haemorrhage and other types of amyloidosis. The modulators are also useful for the treatment of disorders associated with beta-amyloidosis, especially Alzheimer's disease

Query Match	93.1%	Score 27	DB 2	Length 6
Best Local Similarity	83.3%	Pred. No. 2e+06		
Matches 5: Conservative	1: Mismatches	0: Indels	0: Gaps	0

RESULT 66	
AAW89378	
ID	AAW89378 standard; peptide; 6 AA.
XX	
XX	
AC	AAW89378;
XX	
XX	
DT	02-MAR-1999 (first entry)
XX	
DE	Beta-amyloid peptide derivative A-beta-16-21.
XX	
XX	Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW	aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW	familial amyloid polynuropathy; bovine spongiform encephalopathy;
KW	Creutzfeldt-Jakob disease; BAP.
XX	
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
XX	
PN	US5854204-A.
XX	
FD	29-DEC-1998.
XX	
XX	
PF	14-MAR-1996; 96US-00612785.
XX	
XX	
PR	14-MAR-1995; 95US-00404831.
PR	07-JUN-1995; 95US-00475579.
PR	27-OCT-1995; 95US-00548998.
XX	
PA	(PRAE-) PRAECIS PHARM INC.
XX	
PI	Hundal A, Gefter ML, Kasman L, Musso G, Molineaux S, Benjamin H;
PI	Findeis MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;
PI	Garnick MB, Kubasek W, Signer ER,
XX	
DR	WPI; 1999-094964/08.
XX	
PT	New peptide(s) derived from beta-amyloid peptide that inhibit amyloid
PT	accretion - and neurotoxicity. specifically for treatment and

```

PT prevention of Alzheimer's disease.
XX
XX Example 12; Col 64; 52pp; English.
XX
XX The present invention describes beta-amyloid peptide (bAP) derivatives.
XX The bAP derivatives inhibit aggregation of amyloidogenic proteins and
XX peptides, specifically bAP, and their neurotoxicity, so are useful for
XX treating and preventing any disease involving amyloidosis, specifically
XX Alzheimer's disease but also Down's syndrome, familial amyloid
XX polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
XX Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
XX these diseases, in vitro or in vivo, by detecting binding of bAP to
XX labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
XX even when bAP is present in molar excess. The present sequence represents
XX a bAP derivative
XX
XX Sequence 6 AA;
XX
XX Query Match          93.1%; Score 27; DB 2; Length 6;
XX Best Local Similarity 83.3%; Fred. No. 2e+06;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0
XX
Qy 1 KLVFFA 6
Db 1 KLVFFA 6
|:||||
|:||||

RESULT 67
AAB48484
ID AAB48484 standard; peptide; 6 AA.
XX
XX AAB48484;
XX
DT 02-MAR-2001 (first entry)
XX
DE Antifibrillogenic peptide #11.
XX
KW Neotropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KW Alzheimer's disease.
XX
XX Homo sapiens.
XX
XX OS
XX
XX Key Location/Qualifiers
FT Modified-site 6 /note= "C-terminal amide"
FT
XX
XX WO2000068263-A2.
XX
XX 16-NOV-2000.
XX
XX 04-MAY-2000; 2000WO-CA000515.
XX
XX 05-MAY-1999; 99US-0132592P.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Chalifour R, Gervais F, Gupta A;
XX
XX WPI; 2001-031852/04.
XX
XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
XX cytoprotection for treating amyloidosis disorders, comprises a peptide,
XX its isomer or peptidomimetic.
XX

```



```

CC protein
XX
SQ Sequence 6 AA;

Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
Db 1 KLVFFA 6

RESULT 69
ID AAB48476 standard; peptide; 6 AA.
XX
AC AAB48476;
XX
DT 02-MAR-2001 (first entry)
XX
DE Antifibrillogenic peptide #3.
XX
KW Neotropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200068263-A2.
XX
PD 16-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-CA000515.
XX
PR 05-MAY-1999; 99US-0132592P.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Chalifour R, Gervais F, Gupta A;
XX
DR WPI; 2001-031852/04.
XX
PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT its isomer or peptidomimetic.
XX
PS Claim 7; Page 25; 46pp; English.
XX
CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC useful for treating amyloidosis disorders such as Alzheimer's disease.
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
CC binding region and the prot-prot interaction region of the human amyloid
CC protein
XX
SQ Sequence 6 AA;

Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
Db 1 KLVFFA 6

RESULT 69
ID AAB82632 standard; peptide; 6 AA.
XX
AC AAB82632;
XX
DT 02-OCT-2001 (first entry)
XX
DE All-D peptide used in Alzheimer's disease vaccine.
XX
KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
KW therapy; antigen.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..6
FT Modified-site 6 /note= "all D-form residues"
FT Modified-site 6 /note= "C-terminal amide"
XX
PN WO200139796-A2.
XX
PD 07-JUN-2001.
XX
PF 29-NOV-2000; 2000WO-CA001413.
XX
PR 29-NOV-1999; 99US-0168594P.
XX
PR 28-NOV-2000; 2000US-00724842.
XX
PA (NEUR-) NEUROCHEM INC.
XX
PI Chalifour R, Hebert L, Kong X, Gervais F;
XX
DR WPI; 2001-441458/47.
XX
PT Preventing/treating amyloid-related disease, especially Alzheimer's
PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
PT which elicits production of antibodies to prevent fibrillogenesis and
PT associated cellular toxicity.
XX
PS Disclosure; Page 11; 31pp; English.
XX
CC The present sequence is that of an all-D peptide suitable for use for
CC preparing vaccines for preventing or treating Alzheimer's disease and
CC other amyloid related disorders in humans. It is based on a portion of
CC amyloid-beta peptide (see AAB82632), and may be modified by removing or
CC inserting 1 or more amino acid residues, or by substituting 1 or more
CC amino acid residues with other amino acid residues or non-amino acid
CC fragments. Vaccines of the invention are produced using 'non-self'
CC peptides synthesised from the unnatural D-configuration amino acids to
CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
CC aggregated to be operative or immunogenic. They preferably interact with
CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
CC fragments, protein conjugates, immunogenic derivative peptides and
CC immunogenic peptidomimetics. Examples include all-D peptides
CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
CC in AAB82632-64. The vaccine elicits a preferential TH-2 or TH-1 response,
CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
CC related diseases may be localised amyloidosis, e.g. diabetes type II,
CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
CC prion protein related disorders, or systemic amyloidosis associated with
CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
CC amyloidosis found in long-term haemodialysis patients. The present all-D
CC peptide was demonstrated to elicit antibody production in rabbits, and
CC provided greater anti-fibrillogenic activity than its all-L equivalent
XX
SQ Sequence 6 AA;

Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6

```

Db 1 KLVFFA 6

RESULT 70
ABG71009

ID ABG71009 standard; peptide; 6 AA.
XX AC ABG71009;
XX DT 05-DEC-2002 (first entry)
XX DE Long form beta-amyloid protein fragment #6.
XX KW Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis; familial amyloid polyneuropathy; familial amyloid cardiomyopathy; isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma; bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease; adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome; insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis; macroglobulinaemia-associated amyloidosis; reactive amyloidosis; primary localised cutaneous nodular amyloidosis; Sjogren's syndrome; hereditary cerebral haemorrhage with amyloidosis; Muckle-Wells syndrome; hereditary non-neuropathic systemic amyloidosis; familial Mediterranean Fever.
XX OS Homo sapiens.
XX PN US2002098173-A1.
XX PD 25-JUL-2002.
XX PF 04-OCT-2001; 2001US-00972475.
XX PR 14-MAR-1995; 95US-00404831.
XX PR 07-JUN-1995; 95US-00475579.
XX PR 27-OCT-1995; 95US-00548998.
XX PR 14-MAR-1996; 96US-00617267.
XX PA (PRAE-) PRAECIS PHARM INC.
XX PI Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
XX PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX WP1; 2002-697709/75.
XX PT Amyloid modulator useful for treating a disorder associated with amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment coupled to a modifying group.
XX PS Example 12; Page 35; 41pp; English.
XX CC The invention describes an amyloid modulator comprising an amyloidogenic protein and/or peptide fragment coupled to a modifying group so that the compound modulates the aggregation of natural amyloid proteins or peptides. The modulator is used for treating a disorder associated with amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese and Swedish types), familial amyloid cardiomyopathy (Danish type), isolated cardiac amyloid, systemic senile amyloidosis, scrapie, bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or macroglobulinaemia-associated amyloidosis, primary localised cutaneous nodular amyloidosis associated with Sjogren's syndrome, reactive (secondary) amyloidosis, familial Mediterranean Fever and familial amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome), hereditary cerebral haemorrhage with amyloidosis of Icelandic type, amyloidosis associated with long term haemodialysis, hereditary non-neuropathic systemic amyloidosis (familial amyloid polyneuropathy III), familial amyloidosis of Finnish type, amyloidosis associated with medullary carcinoma of the thyroid, fibrinogen-associated hereditary renal amyloidosis and lyszyme-associated hereditary systemic amyloidosis. The compound is capable of altering and inhibiting beta-

CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins or peptides when contacted with a molar excess amount of natural beta-APs relative to the modulator. This sequence represents a fragment of the long form of beta-amyloid used in the creation of an amyloid modulator

XX SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY 1 KLVFFA 6
DB 1 KLVFFA 6

RESULT 71
ABB05157

ID ABB05157 standard; peptide; 6 AA.
XX AC ABB05157;
XX DT 02-APR-2002 (first entry)
XX DE Beta amyloid peptide (16-21) SEQ ID NO:9.
XX KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta; APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease; neurotropic; neuroprotective; immunosuppressive; antimicrobial; auditory; antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic; amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome; amyloidogenic disease; beta amyloid deposition; amyloidosis; hereditary cerebral haemorrhage; familial amyloid polyneuropathy.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN US6319498-B1.
XX PD 20-NOV-2001.
XX PR 14-MAR-1996; 96US-00617267.
XX PR 14-MAR-1995; 95US-00404831.
XX PR 07-JUN-1995; 95US-00475579.
XX PR 27-OCT-1995; 95US-00548998.
XX PA (PRAE-) PRAECIS PHARM INC.
XX PI Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
XX PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX WP1; 2002-146668/19.
XX PT Amyloid modulator compound useful for treatment of an amyloidogenic disease such as Alzheimer's disease comprises an aggregation core domain and a modifying group attached to it.
XX PS Disclosure; Col 18; 54pp; English.
XX CC The present invention describes an amyloid modulator compound (I) comprising an aggregation core domain and a modifying group attached to it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial, antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic and auditory activities, and can be used as a natural amyloid aggregation inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide (beta-AP). (I) are used in the manufacture of a medicament for the diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's disease and other clinical occurrences of beta amyloid deposition such as Down's syndrome individuals and in patients with hereditary cerebral haemorrhage with amyloidosis, and for treating a disorder associated with amyloidosis such as familial amyloid polyneuropathy. (I) reduces the toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)

CC not only reduces the formation of neurotoxic aggregates but also have the
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
 CC present sequence represents a beta-AP peptide, which is used in the
 CC exemplification of the present invention

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
 |:|||||
 Db 1 KLVFFA 6

RESULT 72

AAU96820
 ID AAU96820 standard; peptide; 6 AA.

AC AAU96820;

DT 30-JUL-2002 (first entry)

DE Amyloid targeting peptide #10.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

Key Location/Qualifiers

FT Misc-difference 1..6

FT /note= "Preferably D-form residue"

FT Modified-site 6

FT /note= "Ala is amidated"

XX WO200207781-A2.

PN 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 XX plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A_t-(A₁)_n-k-2-A₁-a₁-b₁ (I) where z = 0 - 1;
 CC A_t = an amyloid targeting moiety; A₁-n-k = a linker moiety; and A₁-a₁-b₁
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and

CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 XX agent of the invention

SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
 |:|||||

Db 1 KLVFFA 6

RESULT 73

ABB83305

ID ABB83305 standard; peptide; 6 AA.

AC ABB83305;

XX 29-AUG-2002 (first entry)

XX Amyloid-beta (Abeta) peptide fragment.

XX Human; islet amyloid polypeptide; IAPP; antifibrillogenic; amylin;
 KW fibrillar accumulation; amyloidosis; diabetes; cytoprotection; neurotropic;
 KW chronic infection; tuberculosis; inflammation; rheumatoid arthritis;
 KW fever; neurodegenerative disease; scrapie; neuroprotective; antipyrretic;
 KW bovine spongy form encephalitis; Creutzfeldt-Jacob disease; amyloid-beta;
 KW Alzheimer's disease; cerebral amyloid angiopathy; anti-diabetic;
 KW tuberculostatic; antiarthritic; antirheumatic; cerebroprotective.

XX Unidentified.

XX WO200224727-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-CA001333.

XX 19-SEP-2000; 2000US-0233482P.

XX (UTOR) UNIV TORONTO.

XX Fraser P;

XX WPI; 2002-519078/55.

XX New antifibrillogenic peptide useful for inhibiting amyloidosis and/or
 XX for cytoprotection in the treatment of amyloidosis disorders e.g. type I
 XX or type II.

XX Disclosure; Page 5; 77pp; English.

XX The present invention relates to antifibrillogenic agents (ABB83281-
 CC ABB83298), derived from human islet amyloid polypeptide (IAPP, ABB83307).
 CC The present sequence is a peptide fragment of the amyloid-beta (Abeta)
 CC peptide. Aggregation of IAPP also known as amylin, or Abeta results in
 CC fibrillar accumulations, leading to amyloidosis. The antifibrillogenic
 CC peptides prevent fibril formation and amyloidosis and hence control
 CC folding or deposition of amyloid proteins. The antifibrillogenic peptides

CC of the invention are useful in the manufacture of a medicament for
 CC inhibiting or treating amyloidosis or amyloid deposits e.g. Type I and
 CC Type II diabetes and/or for cytoprotection. They are also useful for
 CC treating secondary amyloidosis associated with chronic infection e.g.
 CC tuberculosis and chronic inflammation e.g. rheumatoid arthritis, and
 CC familial inflammation, fever, neurodegenerative diseases e.g. scrapie,
 CC bovine spongy form encephalitis, Creutzfeldt-Jacob disease, Alzheimer's
 CC disease, cerebral amyloid angiopathy

XX SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIVFFA 6
 Db 1 KLVFFA 6

RESULT 74

AAU11658
 ID AAU11658 standard; peptide; 6 AA.

XX AC AAU11658;

XX DT 09-APR-2002 (first entry)

XX DE Peptide #11, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
 XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 XX KW CAA; nontropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 XX FT Modified-site 6 /note= "C-terminal amide"

XX PN WO200185093-A2.

XX PD 15-NOV-2001.

XX PF 22-DEC-2000; 2000WO-IB002078.

XX PR 23-DEC-1999; 99US-0171877P.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Green AM, Gervais F;

XX DR WPI; 2002-075222/10.

XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 XX PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 XX PT inhibitor.

XX PS Disclosure; Page 10; 68pp; English.

XX CC The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)

XX SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIVFFA 6
 Db 1 KLVFFA 6

RESULT 75

AAU11650
 ID AAU11650 standard; peptide; 6 AA.

XX AC AAU11650;

XX DT 09-APR-2002 (first entry)

XX DE Peptide #3, used as a carrier for amyloid-beta40 (Abeta40) inhibitor.

XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 XX KW CAA; nontropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX OS Synthetic.

XX PN WO200185093-A2.

XX PD 15-NOV-2001.

XX PF 22-DEC-2000; 2000WO-IB002078.

XX PR 23-DEC-1999; 99US-0171877P.

XX PA (NEUR-) NEUROCHEM INC.

XX PI Green AM, Gervais F;

XX DR WPI; 2002-075222/10.

XX PT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 XX PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 XX PT inhibitor.

XX PS Disclosure; Page 10; 68pp; English.

XX CC The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)

XX SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIVFFA 6
 Db 1 KLVFFA 6

Search completed: December 29, 2005, 17:33:10

Job time : 90.7742 secs

THIS PAGE BLANK (USPTO)

TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-63

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 5 KLVFFA 10

RESULT 74
US-08-766-596A-65
; Sequence 65, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-65

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 5 KLVFFA 10

RESULT 75

US-09-264-709A-2
; Sequence 2, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; TITLE OF INVENTION: Improve the Quality of Life
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-2

Query Match 93.1%; Score 27; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 5 KLVFFA 10

Search completed: December 29, 2005, 17:52:31
Job time : 22.1323 secs

STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-60

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 72
US-08-766-596A-61
Sequence 61, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-61

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 73
US-08-766-596A-63
Sequence 63, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELEPHONE: 202-628-5197

US-08-766-596A-56

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 69

US-08-766-596A-57
; Sequence 57, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-57

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 70

US-08-766-596A-58

; Sequence 58, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-58

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 71

US-08-766-596A-60
; Sequence 60, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLY APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match 93.1%; Score 27; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 6 KLVFFA 11

RESULT 67
US-08-617-267C-14
Sequence 14, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-617-267C-14

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 1 KLVFFA 6

RESULT 68
US-08-766-596A-56
Sequence 56, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 63

US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-594-366-5

Query Match 93.1%; Score 27; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 64

US-09-992-800-5
; Sequence 5, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-800-5

Query Match 93.1%; Score 27; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 65

US-08-612-785B-14
; Sequence 14, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:

APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-14

Query Match 93.1%; Score 27; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 66

US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:

APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-14

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 60
US-09-988-842-9
; Sequence 9, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 61
US-09-988-842-25
; Sequence 25, Application US/09988842
; Patent No. 6716589
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION

; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 62
PCT-US96-10220-14
; Sequence 14, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US96-10220-14

Query Match 93.1%; Score 27; DB 4; Length 11;

```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 2 KLVFFA 7

RESULT 57
US-09-724-940-24
; Sequence 24, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-24

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 58
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
```

```
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-630-645-14

Query Match          93.1%; Score 27; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 2 KLVFFA 7

RESULT 59
US-08-766-596A-14
; Sequence 14, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
```

; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-20

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 54
US-09-724-940-21
; Sequence 21, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-21

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 55
US-09-724-940-22
; Sequence 22, Application US/09724940
; Patent No. 6905686

; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-22

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 56
US-09-724-940-23
; Sequence 23, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence

```
; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 4 KLVFFA 9

RESULT 50
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 3 KLVFFA 8

RESULT 51
US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-23

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 3 KLVFFA 8

RESULT 52
US-09-724-551-24
; Sequence 24, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 53
US-09-724-940-20
; Sequence 20, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
```


; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
US-09-580-018-22 peptide)

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 46

US-09-580-018-23
; Sequence 23, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-23

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 47

US-09-580-018-24
; Sequence 24, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)

US-09-580-018-24

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 48

US-09-724-551-20
; Sequence 20, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-20

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 49

US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)

Query Match 93.1%; Score 27; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:||||
 Db 2 KLVFFA 7

RESULT 42

US-09-724-961-24
 ; Sequence 24, Application US/09724961
 ; Patent No. 6743427
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Bard, Frederique
 ; APPLICANT: Vasquez, Nickl
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-004750UC
 ; CURRENT APPLICATION NUMBER: US/09/724,961
 ; CURRENT FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: US 09/580,015
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/322,289
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: US 09/201,430
 ; PRIOR FILING DATE: 1998-11-30
 ; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
 ; PRIOR FILING DATE: 1998-11-30
 ; PRIOR APPLICATION NUMBER: US 60/080,970
 ; PRIOR FILING DATE: 1998-04-07
 ; PRIOR APPLICATION NUMBER: US 60/067,740
 ; PRIOR FILING DATE: 1997-12-02
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
 ; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid peptide)
 ; OTHER INFORMATION: peptide)
 US-09-724-961-24

Query Match 93.1%; Score 27; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:||||
 Db 1 KLVFFA 6

RESULT 43

US-09-580-018-20
 ; Sequence 20, Application US/09580018
 ; Patent No. 6761888
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Bard, Frederique
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-004760US
 ; CURRENT APPLICATION NUMBER: US/09/580,018
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/322,289
 ; PRIOR FILING DATE: 1999-05-28
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 10

; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
 ; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid peptide)
 ; OTHER INFORMATION: peptide)
 US-09-580-018-20

Query Match 93.1%; Score 27; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:||||
 Db 5 KLVFFA 10

RESULT 44

US-09-580-018-21
 ; Sequence 21, Application US/09580018
 ; Patent No. 6761888
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Bard, Frederique
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-004760US
 ; CURRENT APPLICATION NUMBER: US/09/580,018
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/322,289
 ; PRIOR FILING DATE: 1999-05-28
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 21
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
 ; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid peptide)
 ; OTHER INFORMATION: peptide)
 US-09-580-018-21

Query Match 93.1%; Score 27; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 5.6;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:||||
 Db 4 KLVFFA 9

RESULT 45

US-09-580-018-22
 ; Sequence 22, Application US/09580018
 ; Patent No. 6761888
 ; GENERAL INFORMATION:
 ; APPLICANT: Schenk, Dale B.
 ; APPLICANT: Bard, Frederique
 ; APPLICANT: Yednock, Ted
 ; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
 ; FILE REFERENCE: 15270J-004760US
 ; CURRENT APPLICATION NUMBER: US/09/580,018
 ; CURRENT FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/322,289
 ; PRIOR FILING DATE: 1999-05-28
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-20

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5,6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:|
Db 5 KLVFFA 10

RESULT 39
US-09-724-961-21
; Sequence 21, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-21

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5,6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:|
Db 4 KLVFFA 9

RESULT 40
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
```

```
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5,6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:|
Db 3 KLVFFA 8

RESULT 41
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-23
```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/630,645

; FILING DATE: 10-APR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/478,326

; FILING DATE: 06-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: YUN, Allen C.

; REGISTRATION NUMBER: 37,971

; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 202-628-5197

; TELEFAX: 202-737-3528

; INFORMATION FOR SEQ ID NO: 64:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-766-596A-64

Query Match 93.1%; Score 27; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 2 KLVFFA 7

RESULT 36

US-09-747-408-20

; Sequence 20, Application US/09747408

; Patent No. 6670399

; GENERAL INFORMATION:

; APPLICANT: Green, Allan M.

; APPLICANT: Gervais, Francine

; TITLE OF INVENTION: Compounds And Methods For Modulating

; TITLE OF INVENTION: Cerebral Amyloid Angiopathy

; FILE REFERENCE: NBI-088

; CURRENT APPLICATION NUMBER: US/09/747,408

; CURRENT FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/171,877

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 20

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-747-408-20

Query Match 93.1%; Score 27; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 4 KLVFFA 9

RESULT 37

US-08-970-833-3

; Sequence 3, Application US/08970833

; Patent No. 602859

; GENERAL INFORMATION:

; APPLICANT: Kiessling, Laura L.

; APPLICANT: Murphy, Regina M.

; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Quarles & Brady

; STREET: 411 East Wisconsin Avenue

; CITY: Milwaukee

; STATE: Wisconsin

; COUNTRY: U.S.A.

; ZIP: 53202-4497

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/970,833

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Baker, Jean C.

; REGISTRATION NUMBER: 35,433

; REFERENCE/DOCKET NUMBER: 960296.94291

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (414) 277-5709

; TELEFAX: (414) 271-3552

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-970-833-3

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6

Db 1 KLVFFA 6

RESULT 38

US-09-724-961-20

; Sequence 20, Application US/09724961

; Patent No. 6743427

; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.

; APPLICANT: Bard, Frederique

; APPLICANT: Vasquez, Nicki

; APPLICANT: Yednock, Ted

; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease

; FILE REFERENCE: 152703-004750UC

; CURRENT APPLICATION NUMBER: US/09/724,961

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: US 09/580,015

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/322,289

; PRIOR FILING DATE: 1999-05-28

; PRIOR APPLICATION NUMBER: US 09/201,430

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: WO PCT/US00/14810

; PRIOR FILING DATE: 1998-11-30

; PRIOR APPLICATION NUMBER: US 60/080,970

; PRIOR FILING DATE: 1998-04-07

; PRIOR APPLICATION NUMBER: US 60/067,740

; PRIOR FILING DATE: 1997-12-02

; NUMBER OF SEQ ID NOS: 77

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 10

```
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-766-596A-1

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KLVFFA 6

RESULT 33
US-09-668-314C-73
; Sequence 73, Application US/09668314C
; Patent No. 6844148
; GENERAL INFORMATION:
; APPLICANT: Gurney, et al
; TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
; FILE REFERENCE: 28341/5280NCP
; CURRENT APPLICATION NUMBER: US/09/668,314C
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 60/169,232
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/416,901
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 60/155,493
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 09/404,133
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: PCT/US99/20881
; PRIOR FILING DATE: 1999-09-23
; PRIOR APPLICATION NUMBER: US 60/101,594
; PRIOR FILING DATE: 1998-09-24
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 8
; TYPE: PPT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; US-09-668-314C-73

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KLVFFA 6

RESULT 34
PCT-US96-10220-1
; Sequence 1, Application PC/TUS9610220
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10220
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US96-10220-1

Query Match 93.1%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KLVFFA 6

RESULT 35
US-08-766-596A-64
; Sequence 64, Application US/08766596A
; Patent No. 6452171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-28

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 30
US-08-617-267C-5
Sequence 5, Application US/08617267C
Patent No. 6319498

GENERAL INFORMATION:
APPLICANT: Findexis, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995

ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PFI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-5

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||

Db 3 KLVFFA 8

RESULT 31

US-09-095-106A-44
Sequence 44, Application US/09095106A
Patent No. 6331440

GENERAL INFORMATION:
APPLICANT: NORDSTEDT, Christer
APPLICANT: NASLUND, Jan
APPLICANT: THYBERG, Johan

APPLICANT: TJERNBERG, Lars O.
APPLICANT: TERNIUS, Lars
TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA

FILE REFERENCE: 000500-124
CURRENT APPLICATION NUMBER: US/09/095,106A
CURRENT FILING DATE: 1998-06-10

PRIOR APPLICATION NUMBER: US 60/009,386
PRIOR FILING DATE: 1995-12-29
PRIOR APPLICATION NUMBER: PCT/SE96/01621

PRIOR FILING DATE: 1996-12-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44

LENGTH: 8
TYPE: PRT
ORGANISM: Amyloidosis
US-09-095-106A-44

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 32

US-08-766-596A-1

Sequence 1, Application US/08766596A
Patent No. 6462171

GENERAL INFORMATION:

APPLICANT: SOTO-JARA, Claudio

APPLICANT: BAUMANN, Marc

APPLICANT: FRANGIONE, Blas

TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL

TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE

TITLE OF INVENTION: DEPOSITS

NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 400

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/766,596A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/630,645

FILING DATE: 10-APR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/478,326

FILING DATE: 06-JUN-1995

```

;
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PFI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-612-785B-5

Query Match 93.1%; Score 27; DB 1; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 3 KLVFFA 8

RESULT 28
US-08-630-645-1
; Sequence 1, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Bias
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

;
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-630-645-1

Query Match 93.1%; Score 27; DB 1; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 1 KLVFFA 6

RESULT 29
US-08-703-675C-28
; Sequence 28, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2

```


; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-2

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 24

US-09-747-408-18
; Sequence 18, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 25

US-09-747-408-19
; Sequence 19, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 26

PCT-US94-10475-14
; Sequence 14, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Amnestic
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSES: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: None
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 626-3564 or 783-6030
; TELEFAX: (202) 783-6031
; TELEX: None
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
PCT-US94-10475-14

Query Match 93.1%; Score 27; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 27

US-08-612-785B-5
; Sequence 5, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation

```

; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703.675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-703-675C-30

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 21
US-08-617-267C-7
; Sequence 7, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-703-675C-30

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 22
US-09-264-709A-13
; Sequence 13, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-264-709A-13

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 23
US-09-747-408-2
; Sequence 2, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23

```

;; CURRENT FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/171,877
;; PRIOR FILING DATE: 1999-12-23
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 11
;; LENGTH: 6
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 18
US-08-127-904-14
; Sequence 14, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:

;; APPLICANT: Eugene Roberts
;; TITLE OF INVENTION: Method For Antagonizing
;; TITLE OF INVENTION: Amnesic Effects of Amyloid n
;; TITLE OF INVENTION: Protein and Improving the
;; TITLE OF INVENTION: Quality of Life in Individuals
;; TITLE OF INVENTION: With Alzheimer Disease
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: City of Hope
;; STREET: 1500 East Duarte Road
;; CITY: Duarte
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 91010-0269

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
;; COMPUTER: Wang PC
;; OPERATING SYSTEM: MS DOS Version 3.20
;; SOFTWARE: Microsoft

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/127,904
;; FILING DATE: 29 September 1993
;; CLASSIFICATION: 424

;; PRIOR APPLICATION DATA: No. 5470951e
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Irons, Edward S.
;; REGISTRATION NUMBER: 16,541

;; REFERENCE/DOCKET NUMBER: No. 5470951e
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 783-6040
;; TELEFAX: (202) 783-6031

;; TELEX: No. 5470951e
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 7
;; TYPE: Amino Acid

;; STRANDEDNESS:
;; TOPOLOGY: Unknown
US-08-127-904-14

Query Match 93.1%; Score 27; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 19
US-08-612-785B-7
; Sequence 7, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:

;; APPLICANT: Findeis, Mark A. et al.
;; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
;; TITLE OF INVENTION: Aggregation
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 28 State Street, Suite 510
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA

;; ZIP: 02109-1875

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/612,785B

;; FILING DATE: Herewith

;; CLASSIFICATION: 514

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: USSN 08/404,831
;; FILING DATE: 14-MAR-1995

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: USSN 08/475,579
;; FILING DATE: 07-JUN-1995

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: USSN 08/548,998
;; FILING DATE: 27-OCT-1995

;; ATTORNEY/AGENT INFORMATION:

;; NAME: DeConti, Giulio A.

;; REGISTRATION NUMBER: 31,503

;; REFERENCE/DOCKET NUMBER: PPI-002CP3

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617)227-7400

;; TELEFAX: (617)742-4214

;; INFORMATION FOR SEQ ID NO: 7:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 7 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: peptide

US-08-612-785B-7

Query Match 93.1%; Score 27; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

Qy 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 20

US-08-703-675C-30

; Sequence 30, Application US/08703675C

; Patent No. 6303567

; GENERAL INFORMATION:

;; APPLICANT: Findeis, Mark A. et al.

;; TITLE OF INVENTION: Modulators of -Amyloid Peptide

;; NUMBER OF SEQUENCES: 46

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: LAHIVE & COCKFIELD, LLP

;; STREET: 28 State Street

;; CITY: Boston

;; STATE: Massachusetts

;; COUNTRY: USA

Aggregation Comprising D-

```
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-703-675C-32

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 15
US-08-617-267C-9
; Sequence 9, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findex, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
```

```
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-617-267C-9

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 16
US-09-747-408-3
; Sequence 3, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 17
US-09-747-408-11
; Sequence 11, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
```

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/809,917
;; APPLICATION NUMBER: US/08/809,917
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; PRIOR APPLICATION NUMBER: PCT/US95/13198
;; FILING DATE:
;; APPLICATION NUMBER: US 08/361,063
;; FILING DATE: 21-DEC-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/319,866
;; FILING DATE: 07-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Granahan, Patricia
;; REGISTRATION NUMBER: 32,227
;; REFERENCE/DOCKET NUMBER: CSHL94-03A2 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 861-6240
;; TELEFAX: (617) 861-9540
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1144 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-809-917-12

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 514 KLVFFA 519

RESULT 12
US-09-419-371-12
;; Sequence 12, Application US/09419371
;; Patent No. 6890516
;; GENERAL INFORMATION:
;; APPLICANT: Tully, Timothy P.
;; TITLE OF INVENTION: Cloning and Characterizing of Genes
;; TITLE OF INVENTION: Associated With Long-Term Memory
;; FILE REFERENCE: CSHL94-03A3Z
;; CURRENT APPLICATION NUMBER: US/09/419,371
;; CURRENT FILING DATE: 1999-10-14
;; PRIOR APPLICATION NUMBER: 08/809,917
;; PRIOR FILING DATE: 1997-07-07
;; PRIOR APPLICATION NUMBER: PCT/US95/13198
;; PRIOR FILING DATE: 1995-10-06
;; PRIOR APPLICATION NUMBER: 08/361,063
;; PRIOR FILING DATE: 1994-12-21
;; PRIOR APPLICATION NUMBER: 08/319,866
;; PRIOR FILING DATE: 1994-10-07
;; NUMBER OF SEQ ID NOS: 25
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 12
;; LENGTH: 1144
;; TYPE: PRT
;; ORGANISM: mouse
US-09-419-371-12

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||

Db 514 KLVFFA 519
RESULT 13
US-08-612-785B-9
;; Sequence 9, Application US/08612785B
;; Patent No. 5854204
;; GENERAL INFORMATION:
;; APPLICANT: Findeis, Mark A. et al.
;; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
;; NUMBER OF SEQUENCES: 40
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 28 State Street, Suite 510
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109-1875
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/612,785B
;; FILING DATE: Herewith
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/404,831
;; FILING DATE: 14-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/475,579
;; FILING DATE: 07-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/548,998
;; FILING DATE: 27-OCT-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeConti, Giulio A.
;; REGISTRATION NUMBER: 31,503
;; REFERENCE/DOCKET NUMBER: PPI-002CP3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)742-4214
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-612-785B-9

Query Match 93.1%; Score 27; DB 1; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 14
US-08-703-675C-32
;; Sequence 32, Application US/08703675C
;; Patent No. 6303567
;; GENERAL INFORMATION:
;; APPLICANT: Findeis, Mark A. et al.
;; TITLE OF INVENTION: Modulators of -Amyloid Peptide
;; NUMBER OF SEQUENCES: 46
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD, LLP
;; STREET: 28 State Street
;; CITY: Boston

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,866
; FILING DATE: 7-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-03
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-319-866-12

Query Match          96.6%; Score 28; DB 1; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      514 KVVFFA 519

RESULT 8
US-09-123-708-2
; Sequence 2, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GOECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; FILE REFERENCE: 511169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Cytomegalovirus
; US-09-123-708-2

Query Match          96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      514 KVVFFA 519

RESULT 9
US-09-123-624-2
; Sequence 2, Application US/09123624
; Patent No. 6149936
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Jurgen
; APPLICANT: GOECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC
```

```
;
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2004
; CURRENT APPLICATION NUMBER: US/09/123,624
; CURRENT FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 08/553,503
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 4411402.8
; PRIOR FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-123-624-2

Query Match          96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      514 KVVFFA 519

RESULT 10
US-09-661-258-5
; Sequence 5, Application US/09661258
; Patent No. 6620616
; GENERAL INFORMATION:
; APPLICANT: Stuehr, Dennis J.
; APPLICANT: Adak, Subrata
; TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants
; FILE REFERENCE: 26473/04028
; CURRENT APPLICATION NUMBER: US/09/661,258
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-661-258-5

Query Match          96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      514 KVVFFA 519

RESULT 11
US-08-809-917-12
; Sequence 12, Application US/08809917
; Patent No. 6689557
; GENERAL INFORMATION:
; APPLICANT: APPLICANT
; APPLICANT: APPLICANT
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
```

Qy 1 KIVFFA 6
|:||||
Db 1 KWFFA 6

RESULT 4

US-09-747-408-17
; Sequence 17, Application US/09747408
; Patent No. 6670399

GENERAL INFORMATION:

; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match 96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KWFFA 6

RESULT 5

US-09-513-999C-6921
; Sequence 6921, Application US/09513999C
; Patent No. 6783961

GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6921
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6921

Query Match 96.6%; Score 28; DB 2; Length 77;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 38 KWFFA 43

RESULT 6

US-08-147-812-5
; Sequence 5, Application US/08147812
; Patent No. 5766909

GENERAL INFORMATION:

; APPLICANT: Xie, Qiao-wen
; APPLICANT: Nathan, Carl F.
; APPLICANT: Mumford, Richard A.
; APPLICANT: Calaycay, Jimmy Ramos
; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 East Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh Centris650
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,812
; FILING DATE: No. 5766909 Available
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/841,641
; FILING DATE: 02-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W III
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 186581A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-147-812-5

Query Match 96.6%; Score 28; DB 1; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 514 KWFFA 519

RESULT 7

US-08-319-866-12
; Sequence 12, Application US/08319866
; Patent No. 5929223

GENERAL INFORMATION:

; APPLICANT: Tully, Timothy P.
; APPLICANT: Yin, Jerry C.
; APPLICANT: Regulski, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30


```
247 27 93.1 42 2 US-09-005-215-20
248 27 93.1 42 2 US-09-242-724-23
249 27 93.1 42 2 US-08-922-930-2
250 27 93.1 42 2 US-09-660-954-1
251 27 93.1 42 2 US-08-923-055-2
252 27 93.1 42 2 US-08-922-885-2
253 27 93.1 42 2 US-09-731-460-1
254 27 93.1 42 2 US-09-133-866-2
255 27 93.1 42 2 US-09-723-384-1
256 27 93.1 42 2 US-09-724-961-42
257 27 93.1 42 2 US-09-724-552-1
258 27 93.1 42 2 US-09-580-018-42
259 27 93.1 42 2 US-10-455-218-2
260 27 93.1 42 2 US-09-723-927-1
261 27 93.1 42 2 US-09-724-489-1
262 27 93.1 42 2 US-09-724-477-1
263 27 93.1 42 2 US-09-723-762-1
264 27 93.1 42 2 US-09-201-430-1
265 27 93.1 42 2 US-09-724-551-42
266 27 93.1 42 2 US-10-815-353-1
267 27 93.1 42 2 US-10-278-181-1
268 27 93.1 42 2 US-10-816-529-1
269 27 93.1 42 2 US-09-623-548A-955
270 27 93.1 42 2 US-09-623-548A-961
271 27 93.1 42 2 US-09-623-548A-967
272 27 93.1 42 2 US-09-623-548A-988
273 27 93.1 42 2 US-09-623-548A-994
274 27 93.1 42 2 US-10-815-391-1
275 27 93.1 42 2 US-10-816-022-1
276 27 93.1 42 2 US-09-724-953-34
277 27 93.1 42 2 US-09-657-276-955
278 27 93.1 42 2 US-09-657-276-961
279 27 93.1 42 2 US-09-657-276-967
280 27 93.1 42 2 US-09-657-276-988
281 27 93.1 42 2 US-09-657-276-994
282 27 93.1 42 2 US-09-724-567-34
283 27 93.1 42 2 US-09-724-940-42
284 27 93.1 42 2 US-09-865-294A-65
285 27 93.1 42 2 US-09-979-953-34
286 27 93.1 42 2 US-09-585-817-34
287 27 93.1 42 2 US-09-962-955D-37
288 27 93.1 42 2 US-09-706-574A-20
289 27 93.1 42 2 US-10-934-609-1
290 27 93.1 42 2 PCT-US92-06700-2
291 27 93.1 42 4 PCT-US93-00325-1
292 27 93.1 42 4 PCT-US95-08302-5
293 27 93.1 42 6 5220013-12
294 27 93.1 42 6 5220013-14
295 27 93.1 42 6 5223482-12
296 27 93.1 42 6 5223482-12
297 27 93.1 43 1 US-08-235-400-1
298 27 93.1 43 1 US-08-437-067-1
299 27 93.1 43 1 US-08-302-808-6
300 27 93.1 43 1 US-08-079-511-1

ALIGNMENTS

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 2
US-09-747-408-10
; Sequence 10, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 3
US-09-747-408-9
; Sequence 9, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match 96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

101	27	93.1	20	2	US-09-724-953-33	Sequence 33, Appl	174	27	93.1	38	2	US-09-557-276-1002	Sequence 1002, Ap
102	27	93.1	20	2	US-09-724-567-33	Sequence 33, Appl	175	27	93.1	39	1	US-08-304-585-5	Sequence 5, Appl
103	27	93.1	20	2	US-09-973-952-33	Sequence 33, Appl	176	27	93.1	39	1	US-08-302-808-2	Sequence 2, Appl
104	27	93.1	20	2	US-09-585-817-33	Sequence 33, Appl	177	27	93.1	39	1	US-08-609-090-7	Sequence 7, Appl
105	27	93.1	26	1	US-08-304-585-7	Sequence 4, Appl	178	27	93.1	39	1	US-08-682-245A-1	Sequence 1, Appl
106	27	93.1	28	1	US-08-346-849-4	Sequence 4, Appl	179	27	93.1	39	1	US-08-986-948-2	Sequence 2, Appl
107	27	93.1	28	1	US-08-302-808-7	Sequence 7, Appl	180	27	93.1	40	1	US-07-744-767A-1	Sequence 1, Appl
108	27	93.1	28	1	US-08-609-090-2	Sequence 2, Appl	181	27	93.1	40	1	US-08-235-400-2	Sequence 2, Appl
109	27	93.1	28	1	US-08-986-948-7	Sequence 7, Appl	182	27	93.1	40	1	US-08-476-464A-2	Sequence 2, Appl
110	27	93.1	28	1	US-08-293-284A-4	Sequence 4, Appl	183	27	93.1	40	1	US-08-304-585-1	Sequence 1, Appl
111	27	93.1	28	1	US-08-461-216-2	Sequence 2, Appl	184	27	93.1	40	1	US-08-304-585-8	Sequence 8, Appl
112	27	93.1	28	2	US-09-388-890-3	Sequence 2, Appl	185	27	93.1	40	1	US-08-302-808-3	Sequence 3, Appl
113	27	93.1	28	2	US-09-388-890-2	Sequence 3, Appl	186	27	93.1	40	1	US-08-433-734-1	Sequence 1, Appl
114	27	93.1	28	2	US-09-388-890-4	Sequence 4, Appl	187	27	93.1	40	1	US-08-609-090-8	Sequence 8, Appl
115	27	93.1	28	2	US-09-388-890-5	Sequence 5, Appl	188	27	93.1	40	1	US-07-737-371B-69	Sequence 69, Appl
116	27	93.1	28	2	US-09-388-890-6	Sequence 6, Appl	189	27	93.1	40	1	US-08-682-245A-2	Sequence 2, Appl
117	27	93.1	28	2	US-09-388-890-7	Sequence 7, Appl	190	27	93.1	40	1	US-08-986-948-3	Sequence 3, Appl
118	27	93.1	28	2	US-09-388-890-8	Sequence 8, Appl	191	27	93.1	40	1	US-08-461-216-1	Sequence 1, Appl
119	27	93.1	28	2	US-09-388-890-9	Sequence 9, Appl	192	27	93.1	40	2	US-08-959-148-1	Sequence 1, Appl
120	27	93.1	28	2	US-09-388-890-10	Sequence 10, Appl	193	27	93.1	40	2	US-09-242-724-22	Sequence 22, Appl
121	27	93.1	28	2	US-09-388-890-12	Sequence 12, Appl	194	27	93.1	40	2	US-08-723-661B-1	Sequence 1, Appl
122	27	93.1	28	2	US-09-388-890-13	Sequence 13, Appl	195	27	93.1	40	2	US-09-062-365-3	Sequence 3, Appl
123	27	93.1	28	2	US-09-388-890-14	Sequence 14, Appl	196	27	93.1	40	2	US-09-133-866-1	Sequence 1, Appl
124	27	93.1	28	2	US-09-264-709A-1	Sequence 1, Appl	197	27	93.1	40	2	US-09-861-847A-7	Sequence 7, Appl
125	27	93.1	28	2	US-08-723-661B-2	Sequence 2, Appl	198	27	93.1	40	2	US-09-861-847A-8	Sequence 8, Appl
126	27	93.1	28	2	US-09-660-954-2	Sequence 2, Appl	199	27	93.1	40	2	US-09-988-842-3	Sequence 3, Appl
127	27	93.1	28	2	US-09-660-954-3	Sequence 3, Appl	200	27	93.1	40	2	US-10-455-218-1	Sequence 1, Appl
128	27	93.1	28	2	US-09-660-954-4	Sequence 4, Appl	201	27	93.1	40	2	US-10-151-614-1	Sequence 1, Appl
129	27	93.1	28	2	US-09-660-954-5	Sequence 5, Appl	202	27	93.1	40	2	US-09-623-548A-956	Sequence 956, App
130	27	93.1	28	2	US-09-660-954-6	Sequence 6, Appl	203	27	93.1	40	2	US-09-623-548A-962	Sequence 962, App
131	27	93.1	28	2	US-09-660-954-7	Sequence 7, Appl	204	27	93.1	40	2	US-09-623-548A-968	Sequence 968, App
132	27	93.1	28	2	US-09-660-954-8	Sequence 8, Appl	205	27	93.1	40	2	US-09-623-548A-978	Sequence 978, App
133	27	93.1	28	2	US-09-660-954-9	Sequence 9, Appl	206	27	93.1	40	2	US-09-623-548A-988	Sequence 988, App
134	27	93.1	28	2	US-09-660-954-10	Sequence 10, Appl	207	27	93.1	40	2	US-09-623-548A-995	Sequence 995, App
135	27	93.1	28	2	US-09-660-954-12	Sequence 12, Appl	208	27	93.1	40	2	US-09-623-548A-1005	Sequence 1005, Ap
136	27	93.1	28	2	US-09-660-954-13	Sequence 13, Appl	209	27	93.1	40	2	US-09-657-276-956	Sequence 956, App
137	27	93.1	28	2	US-09-660-954-14	Sequence 14, Appl	210	27	93.1	40	2	US-09-657-276-962	Sequence 962, App
138	27	93.1	28	2	US-08-898-300-4	Sequence 4, Appl	211	27	93.1	40	2	US-09-657-276-968	Sequence 968, App
139	27	93.1	28	2	US-08-824-513-4	Sequence 4, Appl	212	27	93.1	40	2	US-09-657-276-978	Sequence 978, App
140	27	93.1	28	2	US-09-623-548A-959	Sequence 959, App	213	27	93.1	40	2	US-09-657-276-989	Sequence 989, App
141	27	93.1	28	2	US-09-623-548A-965	Sequence 965, App	214	27	93.1	40	2	US-09-657-276-995	Sequence 995, App
142	27	93.1	28	2	US-09-623-548A-976	Sequence 976, App	215	27	93.1	40	2	US-09-657-276-1005	Sequence 1005, Ap
143	27	93.1	28	2	US-09-623-548A-992	Sequence 992, App	216	27	93.1	40	2	US-09-962-955D-36	Sequence 36, Appl
144	27	93.1	28	2	US-09-623-548A-1003	Sequence 1003, Ap	217	27	93.1	40	4	FCT-US92-08700-1	Sequence 1, Appl
145	27	93.1	28	2	US-09-657-276-959	Sequence 959, App	218	27	93.1	41	1	US-07-819-361-1	Sequence 1, Appl
146	27	93.1	28	2	US-09-657-276-965	Sequence 965, App	219	27	93.1	41	1	US-08-302-808-4	Sequence 4, Appl
147	27	93.1	28	2	US-09-657-276-976	Sequence 976, App	220	27	93.1	41	1	US-08-682-245A-3	Sequence 3, Appl
148	27	93.1	28	2	US-09-657-276-992	Sequence 992, App	221	27	93.1	41	1	US-08-986-948-4	Sequence 4, Appl
149	27	93.1	28	2	US-09-657-276-1003	Sequence 1003, Ap	222	27	93.1	42	1	US-07-744-767A-2	Sequence 2, Appl
150	27	93.1	28	2	US-09-865-294A-66	Sequence 66, Appl	223	27	93.1	42	1	US-08-179-574-1	Sequence 1, Appl
151	27	93.1	30	1	US-08-609-090-3	Sequence 3, Appl	224	27	93.1	42	1	US-08-271-162-5	Sequence 5, Appl
152	27	93.1	30	2	US-09-861-847A-1	Sequence 1, Appl	225	27	93.1	42	1	US-08-347-144-1	Sequence 1, Appl
153	27	93.1	33	1	US-08-609-090-4	Sequence 4, Appl	226	27	93.1	42	1	US-08-462-859A-19	Sequence 19, Appl
154	27	93.1	34	1	US-08-475-579A-4	Sequence 4, Appl	227	27	93.1	42	1	US-08-123-659A-19	Sequence 19, Appl
155	27	93.1	35	1	US-08-304-585-6	Sequence 6, Appl	228	27	93.1	42	1	US-08-464-247A-19	Sequence 19, Appl
156	27	93.1	35	1	US-08-612-785B-16	Sequence 16, Appl	229	27	93.1	42	1	US-08-464-248A-19	Sequence 19, Appl
157	27	93.1	35	1	US-08-612-785B-36	Sequence 36, Appl	230	27	93.1	42	1	US-08-476-464A-1	Sequence 1, Appl
158	27	93.1	35	1	US-08-612-785B-38	Sequence 38, Appl	231	27	93.1	42	1	US-08-304-585-2	Sequence 2, Appl
159	27	93.1	35	1	US-08-612-785B-40	Sequence 40, Appl	232	27	93.1	42	1	US-08-302-808-5	Sequence 5, Appl
160	27	93.1	35	2	US-08-617-267C-16	Sequence 16, Appl	233	27	93.1	42	1	US-08-268-348A-1	Sequence 1, Appl
161	27	93.1	35	2	US-09-623-548A-979	Sequence 979, App	234	27	93.1	42	1	US-08-268-348A-2	Sequence 2, Appl
162	27	93.1	35	2	US-09-623-548A-1006	Sequence 1006, Ap	235	27	93.1	42	1	US-08-268-348A-3	Sequence 3, Appl
163	27	93.1	35	2	US-09-657-276-979	Sequence 979, App	236	27	93.1	42	1	US-08-268-348A-4	Sequence 4, Appl
164	27	93.1	35	2	US-09-657-276-1006	Sequence 1006, Ap	237	27	93.1	42	1	US-08-268-348A-5	Sequence 5, Appl
165	27	93.1	36	1	US-08-609-090-6	Sequence 6, Appl	238	27	93.1	42	1	US-08-268-348A-6	Sequence 6, Appl
166	27	93.1	36	2	US-09-861-847A-6	Sequence 6, Appl	239	27	93.1	42	1	US-08-433-734-2	Sequence 2, Appl
167	27	93.1	36	2	US-09-861-847A-11	Sequence 11, Appl	240	27	93.1	42	1	US-08-609-090-9	Sequence 9, Appl
168	27	93.1	38	1	US-08-302-808-1	Sequence 1, Appl	241	27	93.1	42	1	US-07-737-371B-72	Sequence 72, Appl
169	27	93.1	38	1	US-07-737-371E-68	Sequence 68, Appl	242	27	93.1	42	1	US-08-422-333-4	Sequence 4, Appl
170	27	93.1	38	1	US-08-986-948-1	Sequence 1, Appl	243	27	93.1	42	1	US-08-682-245A-4	Sequence 4, Appl
171	27	93.1	38	2	US-09-623-548A-975	Sequence 975, App	244	27	93.1	42	1	US-08-986-948-5	Sequence 5, Appl
172	27	93.1	38	2	US-09-623-548A-1002	Sequence 1002, Ap	245	27	93.1	42	2	US-08-717-551A-2	Sequence 2, Appl
173	27	93.1	38	2	US-09-657-276-975	Sequence 975, App	246	27	93.1	42	2	US-09-388-890-1	Sequence 1, Appl

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-1
Perfect score: 29
Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database :

- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
- 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
- 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
- 4: /cgn2_6/prodata/1/iaa/PCITUS COMB.pep.*
- 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
- 6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	2	US-09-747-408-1
2	29	100.0	6	2	US-09-747-408-10
3	28	96.6	6	2	US-09-747-408-9
4	28	96.6	6	2	US-09-747-408-17
5	28	96.6	77	2	US-09-513-999C-6921
6	28	96.6	1144	1	US-08-147-812-5
7	28	96.6	1144	1	US-08-319-866-12
8	28	96.6	1144	2	US-09-123-708-2
9	28	96.6	1144	2	US-09-123-624-2
10	28	96.6	1144	2	US-09-661-258-5
11	28	96.6	1144	2	US-08-809-917-12
12	28	96.6	1144	2	US-09-419-371-12
13	27	93.1	6	1	US-08-612-785B-9
14	27	93.1	6	2	US-08-703-675C-32
15	27	93.1	6	2	US-08-617-267C-9
16	27	93.1	6	2	US-09-747-408-3
17	27	93.1	6	2	US-09-747-408-11
18	27	93.1	7	1	US-08-127-904-14
19	27	93.1	7	1	US-08-612-785B-7
20	27	93.1	7	2	US-08-703-675C-30
21	27	93.1	7	2	US-08-617-267C-7
22	27	93.1	7	2	US-09-264-709A-13
23	27	93.1	7	2	US-09-747-408-2
24	27	93.1	7	2	US-09-747-408-18
25	27	93.1	7	2	US-09-747-408-19
26	27	93.1	7	4	PCT-US94-10475-14
27	27	93.1	8	1	US-08-612-785B-5

28	27	93.1	8	1	US-08-630-645-1	Sequence 1, Appli
29	27	93.1	8	2	US-08-703-675C-28	Sequence 28, Appl
30	27	93.1	8	2	US-08-617-267C-5	Sequence 5, Appli
31	27	93.1	8	2	US-09-095-106A-44	Sequence 44, Appl
32	27	93.1	8	2	US-08-766-596A-1	Sequence 1, Appli
33	27	93.1	8	2	US-09-668-314C-73	Sequence 73, Appl
34	27	93.1	8	4	PCT-US96-10220-1	Sequence 1, Appli
35	27	93.1	9	2	US-08-766-596A-64	Sequence 64, Appl
36	27	93.1	9	2	US-09-747-408-20	Sequence 20, Appl
37	27	93.1	10	2	US-08-970-833-3	Sequence 3, Appli
38	27	93.1	10	2	US-09-724-961-20	Sequence 20, Appl
39	27	93.1	10	2	US-09-724-961-21	Sequence 21, Appl
40	27	93.1	10	2	US-09-724-961-22	Sequence 22, Appl
41	27	93.1	10	2	US-09-724-961-23	Sequence 23, Appl
42	27	93.1	10	2	US-09-724-961-24	Sequence 24, Appl
43	27	93.1	10	2	US-09-580-018-20	Sequence 20, Appl
44	27	93.1	10	2	US-09-580-018-21	Sequence 21, Appl
45	27	93.1	10	2	US-09-580-018-22	Sequence 22, Appl
46	27	93.1	10	2	US-09-580-018-23	Sequence 23, Appl
47	27	93.1	10	2	US-09-580-018-24	Sequence 24, Appl
48	27	93.1	10	2	US-09-724-551-20	Sequence 20, Appl
49	27	93.1	10	2	US-09-724-551-21	Sequence 21, Appl
50	27	93.1	10	2	US-09-724-551-22	Sequence 22, Appl
51	27	93.1	10	2	US-09-724-551-23	Sequence 23, Appl
52	27	93.1	10	2	US-09-724-551-24	Sequence 24, Appl
53	27	93.1	10	2	US-09-724-940-20	Sequence 20, Appl
54	27	93.1	10	2	US-09-724-940-21	Sequence 21, Appl
55	27	93.1	10	2	US-09-724-940-22	Sequence 22, Appl
56	27	93.1	10	2	US-09-724-940-23	Sequence 23, Appl
57	27	93.1	10	2	US-09-724-940-24	Sequence 24, Appl
58	27	93.1	11	1	US-08-630-645-14	Sequence 14, Appl
59	27	93.1	11	2	US-08-766-596A-14	Sequence 14, Appl
60	27	93.1	11	2	US-09-988-842-9	Sequence 9, Appli
61	27	93.1	11	2	US-09-988-842-25	Sequence 25, Appl
62	27	93.1	11	4	PCT-US96-10220-14	Sequence 14, Appl
63	27	93.1	14	2	US-09-594-366-5	Sequence 5, Appli
64	27	93.1	14	2	US-09-592-800-5	Sequence 5, Appli
65	27	93.1	15	1	US-08-612-785B-14	Sequence 14, Appl
66	27	93.1	15	1	US-08-612-785B-37	Sequence 37, Appl
67	27	93.1	15	2	US-08-617-267C-14	Sequence 14, Appl
68	27	93.1	15	2	US-08-766-596A-56	Sequence 56, Appl
69	27	93.1	15	2	US-08-766-596A-58	Sequence 58, Appl
70	27	93.1	15	2	US-08-766-596A-60	Sequence 60, Appl
71	27	93.1	15	2	US-08-766-596A-61	Sequence 61, Appl
72	27	93.1	15	2	US-08-766-596A-63	Sequence 63, Appl
73	27	93.1	15	2	US-08-766-596A-65	Sequence 65, Appl
74	27	93.1	17	2	US-09-264-709A-2	Sequence 2, Appli
75	27	93.1	17	2	US-09-594-366-3	Sequence 3, Appli
76	27	93.1	17	2	US-09-623-548A-950	Sequence 950, App
77	27	93.1	17	2	US-09-623-548A-983	Sequence 983, App
78	27	93.1	17	2	US-09-992-800-3	Sequence 3, Appli
79	27	93.1	17	2	US-09-657-276-950	Sequence 950, App
80	27	93.1	17	2	US-09-657-276-983	Sequence 983, App
81	27	93.1	17	2	US-08-970-833-11	Sequence 11, Appl
82	27	93.1	19	2	US-09-723-384-5	Sequence 5, Appli
83	27	93.1	19	2	US-09-724-961-75	Sequence 75, Appl
84	27	93.1	19	2	US-09-724-552-5	Sequence 5, Appli
85	27	93.1	19	2	US-09-580-018-75	Sequence 75, Appl
86	27	93.1	19	2	US-09-723-927-5	Sequence 5, Appli
87	27	93.1	19	2	US-09-724-489-5	Sequence 5, Appli
88	27	93.1	19	2	US-09-724-477-5	Sequence 5, Appli
89	27	93.1	19	2	US-09-723-762-5	Sequence 5, Appli
90	27	93.1	19	2	US-09-201-430-5	Sequence 5, Appli
91	27	93.1	19	2	US-09-724-551-75	Sequence 75, Appl
92	27	93.1	19	2	US-10-815-353-5	Sequence 5, Appli
93	27	93.1	19	2	US-10-816-529-5	Sequence 5, Appli
94	27	93.1	19	2	US-10-815-391-5	Sequence 5, Appli
95	27	93.1	19	2	US-10-816-022-5	Sequence 5, Appli
96	27	93.1	19	2	US-09-724-940-75	Sequence 75, Appl
97	27	93.1	19	2	US-09-724-609-5	Sequence 5, Appli
98	27	93.1	19	2	US-10-834-892-5	Sequence 5, Appli
99	27	93.1	20	2	US-08-970-833-10	Sequence 10, Appl
100	27	93.1	20	2		

```
; TITLE OF INVENTION:  USES THEREOF
; FILE REFERENCE:  NBI-139
; CURRENT APPLICATION NUMBER:  US/09/915,092
; CURRENT FILING DATE:  2001-07-24
; PRIOR APPLICATION NUMBER:  60/220,808
; PRIOR FILING DATE:  2000-07-25
; NUMBER OF SEQ ID NOS:  28
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH:  7
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-915-092-17
```

```
Query Match          93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |:||||
Db      1 KLVFFA 6
```

```
RESULT 75
US-09-915-092-18
; Sequence 18, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT:  Gervais, Francine
; APPLICANT:  Kong, Xianqi
; APPLICANT:  Chalifour, Robert
; APPLICANT:  Migneault, David
; TITLE OF INVENTION:  ANYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE:  NBI-139
; CURRENT APPLICATION NUMBER:  US/09/915,092
; CURRENT FILING DATE:  2001-07-24
; PRIOR APPLICATION NUMBER:  60/220,808
; PRIOR FILING DATE:  2000-07-25
; NUMBER OF SEQ ID NOS:  28
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH:  7
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-915-092-18
```

```
Query Match          93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |:||||
Db      1 KLVFFA 6
```

Search completed: December 29, 2005, 18:49:33
Job time : 70.2903 secs

```
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 71
US-09-867-847-28
; Sequence 28, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-867-847-28

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 72
US-09-972-475-7
; Sequence 7, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
```

```
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-972-475-7

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 73
US-09-915-092-2
; Sequence 2, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-2

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 74
US-09-915-092-17
; Sequence 17, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
```

```
RESULT 67
US-10-825-958-18
; Sequence 18, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR FILING DATE: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-18

Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 68
US-10-666-095-3
; Sequence 3, Application US/10666095
; Publication No. US20050119187A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Robert P.
; APPLICANT: Fu, Yanwen
; APPLICANT: Aucoin, Jed P.
; APPLICANT: Miller, Tod J.
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: McCarley, Robin L.
; TITLE OF INVENTION: Anti-fibril Peptides
; FILE REFERENCE: 0212.1 Hammer
; CURRENT APPLICATION NUMBER: US/10/666,095
; CURRENT FILING DATE: 2003-09-18
; PRIOR FILING DATE: 60/412,081
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-666-095-3

Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KLVFFA 6

RESULT 69
US-09-867-847-12
; Sequence 12, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR FILING DATE: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR FILING DATE: 09/724,842
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-12

Query Match          93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 70
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR FILING DATE: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR FILING DATE: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-27

Query Match          93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 2 KLVFFA 7
```

```
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-10
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:|||||
Db      1 KLVFFA 6
```

```
RESULT 64
US-10-728-028-27
; Sequence 27, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-27
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:|||||
Db      1 KLVFFA 6
```

```
RESULT 65
US-10-728-028-28
; Sequence 28, Application US/10728028
```

```
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-28
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:|||||
Db      1 KLVFFA 6
```

```
RESULT 66
US-10-825-958-7
; Sequence 7, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-7
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
        |:|||||
Db      1 KLVFFA 6
```



```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Antifibrillogenic agents
US-09-956-625-25

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 60
US-09-747-408-3
; Sequence 3, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 61
US-09-747-408-11
; Sequence 11, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 62
US-10-463-729-9
; Sequence 9, Application US/10463729
; Publication No. US20040005307A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,729
; FILING DATE: 17-JUNE-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-463-729-9

Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 63
US-10-728-028-10
; Sequence 10, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
```

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 56
US-09-972-475-9
; Sequence 9, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-972-475-9

Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 57
US-09-915-092-10
; Sequence 10, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139

; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-10

Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 58
US-09-915-092-28
; Sequence 28, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(6)
; OTHER INFORMATION: D-amino acids
US-09-915-092-28

Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 59
US-09-956-625-25
; Sequence 25, Application US/09956625
; Patent No. US2002011926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25

```
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32208
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: DROSOPHILA
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-10-097-143-32208

Query Match          96.6%; Score 28; DB 6; Length 1443;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1204 KIVFFA 1209

RESULT 53
US-10-437-963-109646
; Sequence 109646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Audrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109646
; LENGTH: 1640
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-10-437-963-109646

Query Match          96.6%; Score 28; DB 4; Length 1640;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1596 KIVFFA 1601
```

```
RESULT 54
US-09-867-847-7
; Sequence 7, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-7

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1 KIVFFA 6

RESULT 55
US-09-867-847-20
; Sequence 20, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-20

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Db 514 KVVFFA 519

RESULT 48

US-10-428-817A-120
; Sequence 120, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-428-817A-120

Query Match 96.6%; Score 28; DB 4; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 49

US-10-937-758A-101
; Sequence 101, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-937-758A-101

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 50

US-10-631-467-1388
; Sequence 1388, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1388
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1388

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 51

US-10-631-467-1464
; Sequence 1464, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for broncheal asthma, or chronic obstructive
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1464
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1464

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 52

US-11-097-143-32208
; Sequence 32208, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 8
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-8

Query Match 96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 44
US-10-631-467-680
; Sequence 680, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-680

Query Match 96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 45
US-10-631-467-747
; Sequence 747, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 742
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-631-467-747

; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 747
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-747

Query Match 96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 46
US-09-870-759-124
; Sequence 124, Application US/09870759
; Patent No. US2002017551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-124

Query Match 96.6%; Score 28; DB 3; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 47
US-09-751-708A-124
; Sequence 124, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-751-708A-124

Query Match 96.6%; Score 28; DB 3; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||

```

; FILE REFERENCE: A34614-A-PCT-USA-A-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 10/055,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-11-042-922-13

Query Match          96.6%; Score 28; DB 6; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      57 KVVFFA 62

RESULT 40
US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12723
; LENGTH: 564
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match          96.6%; Score 28; DB 6; Length 564;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      53 KIVFFA 58

RESULT 41
; FILE REFERENCE: A34614-A-PCT-USA-A-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 10/055,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-11-042-922-13

Query Match          96.6%; Score 28; DB 6; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      57 KVVFFA 62

RESULT 40
US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12723
; LENGTH: 564
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match          96.6%; Score 28; DB 6; Length 564;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      53 KIVFFA 58

RESULT 41
; FILE REFERENCE: A34614-A-PCT-USA-A-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 10/055,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-11-042-922-13

Query Match          96.6%; Score 28; DB 6; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      57 KVVFFA 62

RESULT 40
US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12723
; LENGTH: 564
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match          96.6%; Score 28; DB 6; Length 564;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      53 KIVFFA 58

RESULT 41
; FILE REFERENCE: A34614-A-PCT-USA-A-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 10/055,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-11-042-922-13

Query Match          96.6%; Score 28; DB 6; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      57 KVVFFA 62

RESULT 40
US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12723
; LENGTH: 564
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match          96.6%; Score 28; DB 6; Length 564;
Best Local Similarity 83.3%; Pred. No. 1e+0
```

; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172452
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70587C.1.pep
US-10-437-963-172452

Query Match 96.6%; Score 28; DB 4; Length 198;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 36
US-10-055-475-14
; Sequence 14, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-055-475-14

Query Match 96.6%; Score 28; DB 4; Length 416;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 57 KVVFFA 62

RESULT 37
US-11-042-922-14
; Sequence 14, Application US/11042922
; Publication No. US20050186211A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul

; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 10/055,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-042-922-14

Query Match 96.6%; Score 28; DB 6; Length 416;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 57 KVVFFA 62

RESULT 38
US-10-055-475-13
; Sequence 13, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-055-475-13

Query Match 96.6%; Score 28; DB 4; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 57 KVVFFA 62

RESULT 39
US-11-042-922-13
; Sequence 13, Application US/11042922
; Publication No. US20050186211A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalakrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT

Best Local Similarity 83.3%; Pred. No. 3.3e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 32

US-10-481-032A-214

; Sequence 214, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wenqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 214
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-214

Query Match 96.6%; Score 28; DB 5; Length 186;
Best Local Similarity 83.3%; Pred. No. 3.5e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 33

US-10-481-032A-228

; Sequence 228, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wenqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 228
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-228

Query Match 96.6%; Score 28; DB 5; Length 186;
Best Local Similarity 83.3%; Pred. No. 3.5e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 34

US-10-437-963-172476

; Sequence 172476, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172476
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Oryza sativa
; NAME/KEY: unsure
; LOCATION: (1)..(188)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70608C.1.pap
US-10-437-963-172476

Query Match 96.6%; Score 28; DB 4; Length 188;
Best Local Similarity 83.3%; Pred. No. 3.5e+02; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 35

US-10-437-963-172452

; Sequence 172452, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 28

US-10-437-963-133986
; Sequence 133986, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133986
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35803C.1.pap
US-10-437-963-133986

Query Match 96.6%; Score 28; DB 4; Length 87;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 6 KVVFFA 11

RESULT 29

US-10-437-963-105773
; Sequence 105773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105773
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102988C.1.pap
US-10-437-963-105773

Query Match 96.6%; Score 28; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 30

US-10-437-963-141578
; Sequence 141578, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141578
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42668C.1.pap
US-10-437-963-141578

Query Match 96.6%; Score 28; DB 4; Length 135;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 31

US-10-437-963-122124
; Sequence 122124, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122124
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(175)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25081C.1.pap
US-10-437-963-122124

Query Match 96.6%; Score 28; DB 4; Length 175;

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 24
US-10-825-958-24
; Sequence 24, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangl
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; FEATURE:
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-24

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 25
US-10-641-924-7
; Sequence 7, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kausser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 5303SAUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-924-7

Query Match 96.6%; Score 28; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 18 KVVFFA 23

RESULT 26
US-10-642-255-7
; Sequence 7, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kausser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubany1, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; TITLE OF INVENTION: eNOS
; FILE REFERENCE: 52339AUSM1
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-255-7

Query Match 96.6%; Score 28; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 18 KVVFFA 23

RESULT 27
US-10-437-963-173619
; Sequence 173619, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(532221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173619
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71639C.1.pep
US-10-437-963-173619

Query Match 96.6%; Score 28; DB 4; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 20

US-09-747-408-17
; Sequence 17, Application US/09747408
; Publication No. US2003003141A1

; GENERAL INFORMATION:

; APPLICANT: Green, Allan M.

; APPLICANT: Gervais, Francine

; TITLE OF INVENTION: Compounds And Methods For Modulating

; FILE OF INVENTION: Cerebral Amyloid Angiopathy

; FILE REFERENCE: NBI-088

; CURRENT APPLICATION NUMBER: US/09/747,408

; CURRENT FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/171,877

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-747-408-17

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 21

US-10-728-028-8
; Sequence 8, Application US/10728028
; Publication No. US20050048000A1

; GENERAL INFORMATION:

; APPLICANT: Gervais, Francine

; APPLICANT: KONG, Xianqi

; APPLICANT: CHALIFOUR, Robert

; APPLICANT: MIGNEAULT, David

; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND

; FILE OF INVENTION: USES THEREOF

; FILE REFERENCE: NBI-139CP

; CURRENT APPLICATION NUMBER: US/10/728,028

; CURRENT FILING DATE: 2003-12-03

; PRIOR APPLICATION NUMBER: 60/443291

; PRIOR FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: 09/915092

; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: 60/220808

; PRIOR FILING DATE: 2000-07-25

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

US-10-728-028-8

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 22

US-10-728-028-16

; Sequence 16, Application US/10728028

; Publication No. US20050048000A1

; GENERAL INFORMATION:

; APPLICANT: Gervais, Francine

; APPLICANT: KONG, Xianqi

; APPLICANT: CHALIFOUR, Robert

; APPLICANT: MIGNEAULT, David

; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND

; FILE OF INVENTION: USES THEREOF

; FILE REFERENCE: NBI-139CP

; CURRENT APPLICATION NUMBER: US/10/728,028

; CURRENT FILING DATE: 2003-12-03

; PRIOR APPLICATION NUMBER: 60/443291

; PRIOR FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: 09/915092

; PRIOR FILING DATE: 2001-07-24

; PRIOR APPLICATION NUMBER: 60/220808

; PRIOR FILING DATE: 2000-07-25

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

US-10-728-028-16

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 23

US-10-825-958-16

; Sequence 16, Application US/10825958

; Publication No. US20050090439A1

; GENERAL INFORMATION:

; APPLICANT: Chalifour, Robert

; APPLICANT: Hebert, Lise

; APPLICANT: Kong, Xianqi

; APPLICANT: Gervais, Francine

; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S

; FILE OF INVENTION: AND AMYLOID RELATED DISEASES

; FILE REFERENCE: 50291/004002

; CURRENT APPLICATION NUMBER: US/10/825,958

; CURRENT FILING DATE: 2004-04-16

; PRIOR APPLICATION NUMBER: 09/724,842

; PRIOR FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 60/168,594

; PRIOR FILING DATE: 1999-11-29

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: All D peptides

; OTHER INFORMATION: or peptidomimetics

US-10-825-958-16

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-18

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 16
US-09-867-847-26
; Sequence 26, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Hebert, Robert
; APPLICANT: Chalifour, Robert
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-26

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 17
US-09-915-092-8
; Sequence 8, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
```

```
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-8

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 18
US-09-915-092-16
; Sequence 16, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-16

Query Match          96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 19
US-09-747-408-9
; Sequence 9, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9
```

; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280164
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_187087C.1.pep
US-10-425-115-280164

Query Match 100.0%; Score 29; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 28 KIVFFA 33

RESULT 12
US-10-424-599-165325
; Sequence 165325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 165325
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120303C.1.pep
US-10-424-599-165325

Query Match 100.0%; Score 29; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 21 KIVFFA 26

RESULT 13
US-10-424-599-240310
; Sequence 240310, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240310
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59027C.1.pep
US-10-424-599-240310

Query Match 100.0%; Score 29; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 34 KIVFFA 39

RESULT 14
US-10-450-763-56957
; Sequence 56957, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354Z, p-value=2.452e-13, raw score
; OTHER INFORMATION: 9.06
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(99)
; OTHER INFORMATION: Xaa = X * as defined in Table 2
US-10-450-763-56957

Query Match 100.0%; Score 29; DB 5; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 63 KIVFFA 68

RESULT 15
US-09-867-847-18
; Sequence 18, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18

```
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-1

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6
|||||

RESULT 8
US-10-728-028-9
; Sequence 9, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-9

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6
|||||

RESULT 9
US-10-825-958-9
; Sequence 9, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-17

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6
|||||

RESULT 11
US-10-425-115-280164
; Sequence 280164, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
```

```

; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-1

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6

RESULT 4
US-09-915-092-9
; Sequence 9, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-9

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6

RESULT 5
US-09-747-408-1
; Sequence 1, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6

RESULT 6
US-09-747-408-10
; Sequence 10, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6

RESULT 7
US-10-728-028-1
; Sequence 1, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence

```

```
247 93.1 20 3 US-09-908-943A-25
248 27 93.1 20 5 US-10-801-487-25
249 27 93.1 20 5 US-10-801-938-25
250 27 93.1 20 5 US-10-801-509-25
251 27 93.1 20 5 US-10-801-486-25
252 27 93.1 20 5 US-10-801-493-25
253 27 93.1 24 5 US-10-728-246-5
254 27 93.1 24 5 US-10-728-246-6
255 27 93.1 26 3 US-09-792-079-11
256 27 93.1 26 4 US-10-159-279-11
257 27 93.1 28 3 US-09-867-847-4
258 27 93.1 28 3 US-09-865-294-66
259 27 93.1 28 3 US-09-792-079-5
260 27 93.1 28 4 US-10-159-279-5
261 27 93.1 28 4 US-10-363-082-2
262 27 93.1 28 4 US-10-433-385-7
263 27 93.1 28 4 US-10-390-472-4
264 27 93.1 28 4 US-10-741-205-36
265 27 93.1 28 4 US-10-416-262B-7
266 27 93.1 28 4 US-10-478-308-4
267 27 93.1 28 4 US-10-478-307-4
268 27 93.1 28 5 US-10-861-614-66
269 27 93.1 28 5 US-10-825-958-4
270 27 93.1 28 6 US-11-091-309-3
271 27 93.1 28 6 US-11-066-697-959
272 27 93.1 28 6 US-11-066-697-965
273 27 93.1 28 6 US-11-066-697-976
274 27 93.1 28 6 US-11-066-697-992
275 27 93.1 28 6 US-11-066-697-1003
276 27 93.1 30 4 US-09-861-847-1
277 27 93.1 30 4 US-10-301-488A-1
278 27 93.1 30 4 US-10-666-423-1
279 27 93.1 30 4 US-10-617-876-9
280 27 93.1 30 4 US-10-619-454-24
281 27 93.1 30 4 US-10-301-448-1
282 27 93.1 30 5 US-10-775-562-5
283 27 93.1 32 4 US-10-732-862A-99
284 27 93.1 32 3 US-09-930-915A-295
285 27 93.1 33 4 US-10-082-014-84
286 27 93.1 33 4 US-10-372-076-85
287 27 93.1 33 4 US-10-732-862A-98
288 27 93.1 33 4 US-10-806-006-295
289 27 93.1 33 4 US-10-677-074-85
290 27 93.1 33 4 US-10-805-913-295
291 27 93.1 35 3 US-09-867-847-3
292 27 93.1 35 3 US-09-972-475-16
293 27 93.1 35 4 US-10-463-729-16
294 27 93.1 35 5 US-10-825-958-3
295 27 93.1 35 6 US-11-066-697-979
296 27 93.1 35 6 US-11-066-697-1006
297 27 93.1 36 3 US-09-861-847-6
298 27 93.1 36 3 US-09-861-847-11
299 27 93.1 36 4 US-10-301-488A-6
300 27 93.1 36 4 US-10-301-488A-11

Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 6, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 66, Appl
Sequence 5, Appl
Sequence 2, Appl
Sequence 7, Appl
Sequence 4, Appl
Sequence 66, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 959, App
Sequence 965, App
Sequence 976, App
Sequence 992, App
Sequence 1003, Ap
Sequence 1, Appl
Sequence 1, Appl
Sequence 9, Appl
Sequence 24, Appl
Sequence 1, Appl
Sequence 5, Appl
Sequence 99, Appl
Sequence 295, App
Sequence 84, Appl
Sequence 85, Appl
Sequence 98, Appl
Sequence 295, App
Sequence 3, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 3, Appl
Sequence 979, App
Sequence 1006, Ap
Sequence 6, Appl
Sequence 11, Appl
Sequence 6, Appl
Sequence 11, Appl

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-11

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 2
US-09-867-847-19
; Sequence 19, Application US/09867847
; Patent No. US2002094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)_
; OTHER INFORMATION: AMIDATION
US-09-867-847-19

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 3
US-09-915-092-1
; Sequence 1, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
```

ALIGNMENTS

```
RESULT 1
US-09-867-847-11
; Sequence 11, Application US/09867847
; Patent No. US2002094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
```


101	27	93.1	9	4	US-10-619-454-25	Sequence 25, Appl	174	27	93.1	13	4	US-10-281-458-1	Sequence 1, Appl
102	27	93.1	9	4	US-10-619-454-28	Sequence 28, Appl	175	27	93.1	13	5	US-10-625-854-127	Sequence 127, App
103	27	93.1	9	4	US-10-619-454-57	Sequence 57, Appl	176	27	93.1	13	5	US-10-625-854-140	Sequence 140, App
104	27	93.1	9	4	US-10-619-454-157	Sequence 157, Appl	177	27	93.1	14	3	US-09-992-800-5	Sequence 5, Appl
105	27	93.1	10	3	US-09-867-847-29	Sequence 29, Appl	178	27	93.1	14	3	US-09-992-994-5	Sequence 5, Appl
106	27	93.1	10	3	US-09-915-092-19	Sequence 19, Appl	179	27	93.1	14	4	US-10-385-065-5	Sequence 5, Appl
107	27	93.1	10	5	US-10-889-999-20	Sequence 20, Appl	180	27	93.1	14	5	US-10-810-881A-114	Sequence 114, App
108	27	93.1	10	5	US-10-889-999-21	Sequence 21, Appl	181	27	93.1	14	5	US-10-505-313-2	Sequence 2, Appl
109	27	93.1	10	5	US-10-889-999-22	Sequence 22, Appl	182	27	93.1	14	5	US-10-625-854-115	Sequence 115, App
110	27	93.1	10	5	US-10-889-999-23	Sequence 23, Appl	183	27	93.1	14	5	US-10-625-854-128	Sequence 128, App
111	27	93.1	10	5	US-10-889-999-24	Sequence 24, Appl	184	27	93.1	14	5	US-10-625-854-141	Sequence 141, App
112	27	93.1	10	5	US-10-890-070-20	Sequence 20, Appl	185	27	93.1	14	6	US-11-063-350-5	Sequence 5, Appl
113	27	93.1	10	5	US-10-890-070-21	Sequence 21, Appl	186	27	93.1	15	3	US-09-972-475-14	Sequence 14, Appl
114	27	93.1	10	5	US-10-890-070-22	Sequence 22, Appl	187	27	93.1	15	3	US-09-996-357-9	Sequence 9, Appl
115	27	93.1	10	5	US-10-890-070-23	Sequence 23, Appl	188	27	93.1	15	4	US-10-235-483-56	Sequence 56, Appl
116	27	93.1	10	5	US-10-890-070-24	Sequence 24, Appl	189	27	93.1	15	4	US-10-235-483-57	Sequence 57, Appl
117	27	93.1	10	5	US-10-890-000-20	Sequence 20, Appl	190	27	93.1	15	4	US-10-235-483-58	Sequence 58, Appl
118	27	93.1	10	5	US-10-890-000-21	Sequence 21, Appl	191	27	93.1	15	4	US-10-235-483-60	Sequence 60, Appl
119	27	93.1	10	5	US-10-890-000-22	Sequence 22, Appl	192	27	93.1	15	4	US-10-235-483-61	Sequence 61, Appl
120	27	93.1	10	5	US-10-890-000-23	Sequence 23, Appl	193	27	93.1	15	4	US-10-235-483-63	Sequence 63, Appl
121	27	93.1	10	5	US-10-890-000-24	Sequence 24, Appl	194	27	93.1	15	4	US-10-235-483-65	Sequence 65, Appl
122	27	93.1	10	5	US-10-823-463-20	Sequence 20, Appl	195	27	93.1	15	4	US-10-463-729-14	Sequence 14, Appl
123	27	93.1	10	5	US-10-823-463-21	Sequence 21, Appl	196	27	93.1	15	5	US-10-625-854-103	Sequence 103, App
124	27	93.1	10	5	US-10-823-463-22	Sequence 22, Appl	197	27	93.1	15	5	US-10-625-854-116	Sequence 116, App
125	27	93.1	10	5	US-10-823-463-23	Sequence 23, Appl	198	27	93.1	15	5	US-10-625-854-129	Sequence 129, App
126	27	93.1	10	5	US-10-823-463-24	Sequence 24, Appl	199	27	93.1	15	5	US-10-625-854-142	Sequence 142, App
127	27	93.1	10	5	US-10-777-792-19	Sequence 19, Appl	200	27	93.1	16	5	US-10-625-854-91	Sequence 91, Appl
128	27	93.1	10	5	US-10-822-968-20	Sequence 20, Appl	201	27	93.1	16	5	US-10-625-854-104	Sequence 104, App
129	27	93.1	10	5	US-10-822-968-21	Sequence 21, Appl	202	27	93.1	16	5	US-10-625-854-117	Sequence 117, App
130	27	93.1	10	5	US-10-822-968-22	Sequence 22, Appl	203	27	93.1	16	5	US-10-625-854-130	Sequence 130, App
131	27	93.1	10	5	US-10-822-968-23	Sequence 23, Appl	204	27	93.1	16	5	US-10-625-854-143	Sequence 143, App
132	27	93.1	10	5	US-10-822-968-24	Sequence 24, Appl	205	27	93.1	17	3	US-09-992-800-3	Sequence 3, Appl
133	27	93.1	10	5	US-10-777-792-20	Sequence 20, Appl	206	27	93.1	17	3	US-09-992-994-3	Sequence 3, Appl
134	27	93.1	10	5	US-10-777-792-21	Sequence 21, Appl	207	27	93.1	17	3	US-09-998-491-8	Sequence 8, Appl
135	27	93.1	10	5	US-10-777-792-22	Sequence 22, Appl	208	27	93.1	17	4	US-10-385-065-3	Sequence 3, Appl
136	27	93.1	10	5	US-10-777-792-23	Sequence 23, Appl	209	27	93.1	17	4	US-10-451-367-26	Sequence 26, Appl
137	27	93.1	10	5	US-10-777-792-24	Sequence 24, Appl	210	27	93.1	17	4	US-10-475-281-8	Sequence 8, Appl
138	27	93.1	10	5	US-10-825-958-27	Sequence 27, Appl	211	27	93.1	17	4	US-10-810-919-3	Sequence 3, Appl
139	27	93.1	10	5	US-10-890-071-20	Sequence 20, Appl	212	27	93.1	17	5	US-10-684-346-24	Sequence 24, Appl
140	27	93.1	10	5	US-10-890-071-21	Sequence 21, Appl	213	27	93.1	17	5	US-10-997-078-46	Sequence 46, Appl
141	27	93.1	10	5	US-10-890-071-22	Sequence 22, Appl	214	27	93.1	17	5	US-10-997-700-19	Sequence 19, Appl
142	27	93.1	10	5	US-10-890-071-23	Sequence 23, Appl	215	27	93.1	17	6	US-11-063-350-3	Sequence 3, Appl
143	27	93.1	10	5	US-10-890-071-24	Sequence 24, Appl	216	27	93.1	17	6	US-11-066-697-950	Sequence 950, App
144	27	93.1	10	5	US-10-890-024-20	Sequence 20, Appl	217	27	93.1	17	6	US-11-066-697-983	Sequence 983, App
145	27	93.1	10	5	US-10-890-024-21	Sequence 21, Appl	218	27	93.1	19	3	US-09-825-242-5	Sequence 5, Appl
146	27	93.1	10	5	US-10-890-024-22	Sequence 22, Appl	219	27	93.1	19	4	US-10-429-216-5	Sequence 5, Appl
147	27	93.1	10	5	US-10-890-024-23	Sequence 23, Appl	220	27	93.1	19	4	US-10-816-022-5	Sequence 5, Appl
148	27	93.1	10	5	US-10-890-024-24	Sequence 24, Appl	221	27	93.1	19	4	US-10-816-529-5	Sequence 5, Appl
149	27	93.1	10	5	US-10-928-926-20	Sequence 20, Appl	222	27	93.1	19	4	US-10-815-353-5	Sequence 5, Appl
150	27	93.1	10	5	US-10-928-926-21	Sequence 21, Appl	223	27	93.1	19	4	US-10-815-391-5	Sequence 5, Appl
151	27	93.1	10	5	US-10-928-926-22	Sequence 22, Appl	224	27	93.1	19	5	US-10-828-548-5	Sequence 5, Appl
152	27	93.1	10	5	US-10-928-926-23	Sequence 23, Appl	225	27	93.1	19	5	US-10-816-380-5	Sequence 5, Appl
153	27	93.1	10	5	US-10-928-926-24	Sequence 24, Appl	226	27	93.1	19	5	US-10-889-999-75	Sequence 75, Appl
154	27	93.1	10	6	US-11-058-757-20	Sequence 20, Appl	227	27	93.1	19	5	US-10-890-070-75	Sequence 75, Appl
155	27	93.1	10	6	US-11-058-757-21	Sequence 21, Appl	228	27	93.1	19	5	US-10-890-000-75	Sequence 75, Appl
156	27	93.1	10	6	US-11-058-757-22	Sequence 22, Appl	229	27	93.1	19	5	US-10-788-666-5	Sequence 5, Appl
157	27	93.1	10	6	US-11-058-757-23	Sequence 23, Appl	230	27	93.1	19	5	US-10-923-471-5	Sequence 5, Appl
158	27	93.1	10	6	US-11-058-757-24	Sequence 24, Appl	231	27	93.1	19	5	US-10-823-463-75	Sequence 75, Appl
159	27	93.1	11	3	US-09-988-842-9	Sequence 9, Appl	232	27	93.1	19	5	US-10-923-469-5	Sequence 5, Appl
160	27	93.1	11	3	US-09-988-842-25	Sequence 25, Appl	233	27	93.1	19	5	US-10-933-559-5	Sequence 5, Appl
161	27	93.1	11	4	US-10-235-483-14	Sequence 14, Appl	234	27	93.1	19	5	US-10-815-404-5	Sequence 5, Appl
162	27	93.1	11	4	US-10-050-200-33	Sequence 33, Appl	235	27	93.1	19	5	US-10-934-609-5	Sequence 5, Appl
163	27	93.1	11	4	US-10-237-673-20	Sequence 20, Appl	236	27	93.1	19	5	US-10-923-474-5	Sequence 5, Appl
164	27	93.1	11	5	US-10-464-117-13	Sequence 13, Appl	237	27	93.1	19	5	US-10-884-892-5	Sequence 5, Appl
165	27	93.1	11	5	US-10-772-230-9	Sequence 9, Appl	238	27	93.1	19	5	US-10-822-968-75	Sequence 75, Appl
166	27	93.1	11	5	US-10-772-230-25	Sequence 25, Appl	239	27	93.1	19	5	US-10-777-792-75	Sequence 75, Appl
167	27	93.1	12	3	US-09-867-847-8	Sequence 8, Appl	240	27	93.1	19	5	US-10-890-071-75	Sequence 75, Appl
168	27	93.1	12	5	US-10-810-881A-115	Sequence 115, App	241	27	93.1	19	5	US-10-890-024-75	Sequence 75, Appl
169	27	93.1	12	5	US-10-810-881A-117	Sequence 117, App	242	27	93.1	19	5	US-10-934-819-5	Sequence 5, Appl
170	27	93.1	12	5	US-10-508-586-2	Sequence 2, Appl	243	27	93.1	19	5	US-10-923-267-5	Sequence 5, Appl
171	27	93.1	12	5	US-10-508-586-3	Sequence 3, Appl	244	27	93.1	19	5	US-10-928-926-75	Sequence 75, Appl
172	27	93.1	12	5	US-10-625-854-139	Sequence 139, App	245	27	93.1	19	6	US-11-058-757-75	Sequence 75, Appl
173	27	93.1	12	6	US-11-012-797A-33	Sequence 33, Appl	246	27	93.1	19	6	US-11-108-102-5	Sequence 5, Appl

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications_AA_Main:*

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*

3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*

4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	3	US-09-867-847-11
2	29	100.0	6	3	US-09-867-847-19
3	29	100.0	6	3	US-09-915-092-1
4	29	100.0	6	3	US-09-915-092-9
5	29	100.0	6	3	US-09-747-408-1
6	29	100.0	6	3	US-09-747-408-10
7	29	100.0	6	5	US-10-728-028-1
8	29	100.0	6	5	US-10-728-028-9
9	29	100.0	6	5	US-10-825-958-9
10	29	100.0	6	5	US-10-825-958-17
11	29	100.0	58	4	US-10-425-115-280164
12	29	100.0	90	4	US-10-424-599-165325
13	29	100.0	93	4	US-10-424-599-240310
14	29	100.0	99	5	US-10-450-763-56957
15	28	96.6	6	3	US-09-867-847-18
16	28	96.6	6	3	US-09-867-847-26
17	28	96.6	6	3	US-09-915-092-8
18	28	96.6	6	3	US-09-915-092-16
19	28	96.6	6	3	US-09-747-408-9
20	28	96.6	6	3	US-09-747-408-17
21	28	96.6	6	5	US-10-728-028-8
22	28	96.6	6	5	US-10-728-028-16
23	28	96.6	6	5	US-10-825-958-16
24	28	96.6	6	5	US-10-825-958-24
25	28	96.6	37	4	US-10-641-924-7
26	28	96.6	37	4	US-10-642-255-7
27	28	96.6	60	4	US-10-437-963-173619

28	96.6	87	4	US-10-437-963-133986	Sequence 133986,
28	96.6	109	4	US-10-437-963-105773	Sequence 105773,
28	96.6	135	4	US-10-437-963-141578	Sequence 141578,
28	96.6	175	4	US-10-437-963-122124	Sequence 122124,
28	96.6	186	5	US-10-481-032A-214	Sequence 214, App
28	96.6	186	5	US-10-481-032A-228	Sequence 228, App
28	96.6	188	4	US-10-437-963-172476	Sequence 172476,
28	96.6	198	4	US-10-437-963-172452	Sequence 172452,
28	96.6	416	6	US-10-055-475-14	Sequence 14, Appl
28	96.6	416	6	US-11-042-922-14	Sequence 14, Appl
28	96.6	514	4	US-10-055-475-13	Sequence 13, Appl
28	96.6	514	6	US-11-042-922-13	Sequence 13, Appl
28	96.6	564	6	US-11-097-143-12723	Sequence 12723, A
28	96.6	925	4	US-10-408-765A-2031	Sequence 2031, Ap
28	96.6	925	5	US-10-755-889-234	Sequence 234, App
28	96.6	925	5	US-10-370-715B-8	Sequence 8, Appli
28	96.6	925	5	US-10-631-467-680	Sequence 680, App
28	96.6	925	5	US-10-631-467-747	Sequence 747, App
28	96.6	1144	3	US-09-870-759-124	Sequence 124, App
28	96.6	1144	3	US-09-751-708A-124	Sequence 124, App
28	96.6	1144	4	US-10-428-817A-120	Sequence 120, App
28	96.6	1144	5	US-10-937-758A-101	Sequence 101, App
28	96.6	1144	5	US-10-631-467-1388	Sequence 1388, Ap
28	96.6	1144	5	US-10-631-467-1464	Sequence 1464, Ap
28	96.6	1443	6	US-11-097-143-32208	Sequence 32208, A
28	96.6	1640	4	US-10-437-963-109646	Sequence 109646,
27	93.1	6	3	US-09-867-847-7	Sequence 7, Appli
27	93.1	6	3	US-09-972-475-9	Sequence 9, Appli
27	93.1	6	3	US-09-915-092-10	Sequence 10, Appl
27	93.1	6	3	US-09-915-092-28	Sequence 28, Appl
27	93.1	6	3	US-09-956-625-25	Sequence 25, Appl
27	93.1	6	3	US-09-747-408-3	Sequence 3, Appli
27	93.1	6	3	US-09-747-408-11	Sequence 11, Appl
27	93.1	6	4	US-10-463-729-9	Sequence 9, Appli
27	93.1	6	5	US-10-728-028-10	Sequence 10, Appl
27	93.1	6	5	US-10-728-028-27	Sequence 27, Appl
27	93.1	6	5	US-10-728-028-28	Sequence 28, Appl
27	93.1	6	5	US-10-825-958-7	Sequence 7, Appli
27	93.1	6	5	US-10-825-958-18	Sequence 18, Appl
27	93.1	6	5	US-10-666-095-3	Sequence 3, Appli
27	93.1	7	3	US-09-867-847-12	Sequence 12, Appl
27	93.1	7	3	US-09-867-847-27	Sequence 27, Appl
27	93.1	7	3	US-09-867-847-28	Sequence 28, Appl
27	93.1	7	3	US-09-972-475-7	Sequence 7, Appli
27	93.1	7	3	US-09-915-092-2	Sequence 2, Appli
27	93.1	7	3	US-09-915-092-17	Sequence 17, Appl
27	93.1	7	3	US-09-915-092-18	Sequence 18, Appl
27	93.1	7	3	US-09-747-408-2	Sequence 2, Appli
27	93.1	7	3	US-09-747-408-18	Sequence 18, Appl
27	93.1	7	3	US-09-747-408-19	Sequence 19, Appl
27	93.1	7	4	US-10-463-729-7	Sequence 7, Appli
27	93.1	7	5	US-10-728-028-2	Sequence 2, Appli
27	93.1	7	5	US-10-728-028-17	Sequence 17, Appl
27	93.1	7	5	US-10-728-028-18	Sequence 18, Appl
27	93.1	7	5	US-10-825-958-10	Sequence 10, Appl
27	93.1	7	5	US-10-825-958-25	Sequence 25, Appl
27	93.1	7	5	US-10-825-958-26	Sequence 26, Appl
27	93.1	7	5	US-10-810-881A-128	Sequence 128, App
27	93.1	7	5	US-10-505-313-269	Sequence 269, App
27	93.1	8	3	US-09-850-061A-44	Sequence 44, Appl
27	93.1	8	3	US-09-972-475-5	Sequence 5, Appli
27	93.1	8	4	US-10-235-483-1	Sequence 1, Appli
27	93.1	8	4	US-10-463-729-5	Sequence 5, Appli
27	93.1	8	4	US-10-281-092-42	Sequence 42, Appl
27	93.1	8	4	US-10-721-774-44	Sequence 44, Appl
27	93.1	8	5	US-10-810-881A-125	Sequence 125, App
27	93.1	8	5	US-10-817-979-73	Sequence 73, Appl
27	93.1	9	3	US-09-867-847-9	Sequence 9, Appli
27	93.1	9	3	US-09-899-815-2	Sequence 2, Appli
27	93.1	9	3	US-09-747-408-20	Sequence 20, Appl
27	93.1	9	4	US-10-235-483-64	Sequence 64, Appl
27	93.1	9	4	US-10-619-454-3	Sequence 3, Appli

; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-46

Query Match 72.4%; Score 21; DB 7; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVPFA 6
|::||
Db 211 KLMYFA 216

RESULT 75
US-11-073-460-46
; Sequence 46, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-46

Query Match 72.4%; Score 21; DB 7; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVPFA 6
|::||
Db 211 KLMYFA 216

Search completed: December 29, 2005, 18:50:13
Job time : 6.29032 secs

```
RESULT 70
US-10-467-657-290
; Sequence 290, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 290
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-290

Query Match 72.4%; Score 21; DB 6; Length 221;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 41 LIFFA 45

RESULT 71
US-10-467-657-5750
; Sequence 5750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5750
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5750

Query Match 72.4%; Score 21; DB 6; Length 221;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 41 LIFFA 45

RESULT 72
US-10-467-657-6144
; Sequence 6144, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6144
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6144

Query Match 72.4%; Score 21; DB 6; Length 254;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 159 ILFFA 163

RESULT 73
US-10-632-150-46
; Sequence 46, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-46

Query Match 72.4%; Score 21; DB 6; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 211 KLMYFA 216

RESULT 74
US-11-073-457-46
; Sequence 46, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF-
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
```

```
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6144
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6144

Query Match 72.4%; Score 21; DB 6; Length 254;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 159 ILFFA 163

RESULT 73
US-10-632-150-46
; Sequence 46, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-46

Query Match 72.4%; Score 21; DB 6; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 211 KLMYFA 216

RESULT 74
US-11-073-457-46
; Sequence 46, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF-
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
```

; LENGTH: 182
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 ; OTHER INFORMATION: amino acid sequence
 US-10-793-626-2836

Query Match 72.4%; Score 21; DB 6; Length 182;
 Best Local Similarity 50.0%; Pred. No. 2.9e+02;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 | : |||
 Db 14 KVTFFS 19

RESULT 66
 US-10-467-657-3510
 ; Sequence 3510, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 3510
 ; LENGTH: 182
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-3510

Query Match 72.4%; Score 21; DB 6; Length 182;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
 | : |||
 Db 17 ILFFA 21

RESULT 67
 US-10-467-657-3436
 ; Sequence 3436, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 3436
 ; LENGTH: 190
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-3436

Query Match 72.4%; Score 21; DB 6; Length 190;
 Best Local Similarity 66.7%; Pred. No. 3e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 | : |||
 Db 46 KTVFFA 51

RESULT 68
 US-10-821-234-1372
 ; Sequence 1372, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: PLS_SEQ_genes Version 1.0
 ; SEQ ID NO 1372
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1372

Query Match 72.4%; Score 21; DB 6; Length 211;
 Best Local Similarity 66.7%; Pred. No. 3.4e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 | : |||
 Db 33 KTVFFA 38

RESULT 69
 US-10-467-657-8102
 ; Sequence 8102, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 8102
 ; LENGTH: 216
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-8102

Query Match 72.4%; Score 21; DB 6; Length 216;
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
 | : |||
 Db 18 LIFFA 22

US-10-467-657-5166
; Sequence 5166, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5166
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5166

Query Match 72.4%; Score 21; DB 6; Length 123;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
Db 29 ILFFA 33

RESULT 62
US-10-793-626-2374
; Sequence 2374, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2374
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2374

Query Match 72.4%; Score 21; DB 6; Length 134;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 7 KIIVF 11

RESULT 63
US-10-467-657-2420
; Sequence 2420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2420
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2420

Query Match 72.4%; Score 21; DB 6; Length 155;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
Db 18 MVFFA 22

RESULT 64
US-10-965-694-23
; Sequence 23, Application US/10965694
; Publication No. US20050271644A1
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Johannes
; APPLICANT: Muller-Reible, Clemens
; APPLICANT: Fregin, Andreas
; APPLICANT: Rost, Simone
; APPLICANT: Strom, Tim
; TITLE OF INVENTION: VITAMIN K EPOXID RECYCLING POLYPEPTIDE VKORC1, A THERAPEUTIC TARG
; FILE REFERENCE: MBP-025XX
; CURRENT APPLICATION NUMBER: US/10/965,694
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US 60/511,041
; PRIOR FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Fugu rubripes
US-10-965-694-23

Query Match 72.4%; Score 21; DB 6; Length 175;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
Db 91 IVFFA 95

RESULT 65
US-10-793-626-2836
; Sequence 2836, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2836

; SEQ ID NO 7886
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7886

Query Match 72.4%; Score 21; DB 6; Length 43;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 4; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 KIVFFA 6
:||||
Db 14 KVRFFA 19

RESULT 57

US-10-467-657-2216
; Sequence 2216, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2216
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2216

Query Match 72.4%; Score 21; DB 6; Length 52;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:||||
Db 42 RIVWFA 47

RESULT 58

US-10-467-657-5690
; Sequence 5690, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5690
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5690

Query Match 72.4%; Score 21; DB 6; Length 76;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
:||||
Db 23 QIVFF 27

RESULT 59

US-10-821-234-1703
; Sequence 1703, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt_SEQ_genes Version 1.0
; SEQ ID NO 1703
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1703

Query Match 72.4%; Score 21; DB 6; Length 91;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
:||||
Db 22 EIVFF 26

RESULT 60

US-10-793-626-430
; Sequence 430, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 430
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-430

Query Match 72.4%; Score 21; DB 6; Length 123;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:||||
Db 78 IVFFS 82

RESULT 61

; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7120
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7120

Query Match 75.9%; Score 22; DB 6; Length 601;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
:||||
Db 251 RIVFF 255

RESULT 53

US-10-821-234-1673
; Sequence 1673, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Grain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821a
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes Version 1.0
; SEQ ID NO 1673
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1673

Query Match 75.9%; Score 22; DB 6; Length 635;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
:||||
Db 259 KIVFF 263

RESULT 54

US-10-613-744-6
; Sequence 6, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347

; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-6

Query Match 75.9%; Score 22; DB 6; Length 858;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
:||||
Db 348 LVFFA 352

RESULT 55

US-10-873-528-2
; Sequence 2, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hanabro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2233
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-2

Query Match 75.9%; Score 22; DB 6; Length 2233;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
:||||
Db 1895 KVQFFA 1900

RESULT 56

US-10-467-657-7886
; Sequence 7886, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04


```

; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-678

Query Match      75.9%; Score 22; DB 6; Length 449;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 428 KIMFF 432

RESULT 49
US-11-082-389-198
; Sequence 198, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082.389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 198
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-198

Query Match      75.9%; Score 22; DB 7; Length 453;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 401 LVFFA 405

RESULT 50
US-11-210-316-22
; Sequence 22, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.

```

```

; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (102)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-22

Query Match      75.9%; Score 22; DB 7; Length 510;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 96 VIFFA 100

RESULT 51
US-11-210-316-26
; Sequence 26, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-210-316-26

Query Match      75.9%; Score 22; DB 7; Length 539;
Best Local Similarity 60.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 121 VIFFA 125

RESULT 52
US-10-467-657-7120
; Sequence 7120, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta

```

; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; PRIOR FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 572
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-572

Query Match 75.9%; Score 22; DB 7; Length 358;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
Db 61 KIVVFA 66

RESULT 46
US-11-055-822-836
; Sequence 836, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 836
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-836

Query Match 75.9%; Score 22; DB 7; Length 358;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
Db 61 KIVVFA 66

RESULT 47
US-11-194-246-308
; Sequence 308, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MEI
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592.US1 (MAR 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 432
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-308

Query Match 75.9%; Score 22; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|||
Db 4 KILFF 8

RESULT 48
US-10-467-657-678
; Sequence 678, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 678
; LENGTH: 449

Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|:|
Db 3 KIMFF 7

RESULT 42

US-10-793-626-2734
; Sequence 2734, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P034800S
; CURRENT APPLICATION NUMBER: US/10/793.626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2734
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2734

Query Match 75.9%; Score 22; DB 6; Length 330;

Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|:|
Db 3 KIMFF 7

RESULT 43

US-10-878-556A-19
; Sequence 19, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878.556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 19
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/cn03_human
; DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-19

Query Match 75.9%; Score 22; DB 6; Length 338;

Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|:|
Db 76 KLIFP 80

RESULT 44

US-10-131-826A-376
; Sequence 376, Application US/10131826A

; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: F3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131.826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-376

Query Match 75.9%; Score 22; DB 6; Length 344;

Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|:|
Db 279 KLIFP 283

RESULT 45

US-11-055-822-572
; Sequence 572, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

```
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838
```

```
Query Match 75.9%; Score 22; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 IVFFA 6
Db 156 LVFFA 160
```

```
RESULT 38
US-10-821-234-1322
; Sequence 1322, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1322
```

```
Query Match 75.9%; Score 22; DB 6; Length 233;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 IVFFA 6
Db 166 LVFFA 170
```

```
RESULT 39
US-10-467-657-432
; Sequence 432, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
```

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 432
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-432
```

```
Query Match 75.9%; Score 22; DB 6; Length 239;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
Db 128 KVVIFA 133
```

```
RESULT 40
US-10-793-626-2500
; Sequence 2500, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2500
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2500
```

```
Query Match 75.9%; Score 22; DB 6; Length 265;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
Db 230 KVVFWA 235
```

```
RESULT 41
US-10-793-626-2476
; Sequence 2476, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2476
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-2476
```

```
Query Match 75.9%; Score 22; DB 6; Length 330;
```

Best Local Similarity 60.0%; Pred. No. 1.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 3; Conservative 2;

Qy 2 IVFFA 6
:||||
Db 105 VIFFA 109

RESULT 34
US-10-467-657-6932
; Sequence 6932, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6932
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6932

Query Match 75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:||||
Db 19 LVFFA 23

RESULT 35
US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deanoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; PRIOR APPLICATION NUMBER: 2002-04-24
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match 75.9%; Score 22; DB 6; Length 215;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:||||
Db 166 LVFFA 170

RESULT 36
US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 568
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-568

Query Match 75.9%; Score 22; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:||||
Db 156 LVFFA 160

RESULT 37
US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia

QY 2 IVFFA 6
|:|
Db 371 IIVFA 375

RESULT 30

US-10-995-561-593
; Sequence 593, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 593
; LENGTH: 3623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-593

Query Match 79.3%; Score 23; DB 6; Length 3623;
Best Local Similarity 60.0%; Pred. No. 1.8e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 2;

QY 1 KIVFF 5
|:|
Db 2544 KIVFF 2548

RESULT 31

US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436

Query Match 75.9%; Score 22; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|
Db 36 KIVFF 40

RESULT 32

US-10-467-657-4746
; Sequence 4746, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:

; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4746
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4746

Query Match 75.9%; Score 22; DB 6; Length 98;
Best Local Similarity 80.0%; Pred. No. 98;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|
Db 62 KIVFF 66

RESULT 33

US-11-210-316-18
; Sequence 18, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (85)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (112)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-18

Query Match

75.9%; Score 22; DB 7; Length 167;

```
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2450
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2450

Query Match          79.3%; Score 23; DB 6; Length 311;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 296 VVFFA 300

RESULT 26
US-10-995-561-959
; Sequence 959, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 959
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-959

Query Match          79.3%; Score 23; DB 6; Length 481;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 275 KMVFFA 280

RESULT 27
US-11-080-991-104
; Sequence 104, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Velby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
```

```
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-104

Query Match          79.3%; Score 23; DB 7; Length 522;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 260 IIFFA 264

RESULT 28
US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930

Query Match          79.3%; Score 23; DB 6; Length 528;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 477 KLVFF 481

RESULT 29
US-10-467-657-2868
; Sequence 2868, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2868
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2868

Query Match          79.3%; Score 23; DB 6; Length 533;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

US-10-131-826A-230

Query Match 82.8%; Score 24; DB 6; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 557 IVFFA 561

RESULT 22

US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Lebat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PT_SEQ_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917

Query Match 82.8%; Score 24; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 579 KAVFFA 584

RESULT 23

US-11-098-674-1
; Sequence 1, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match 79.3%; Score 23; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5

Db 1 KLVFF 5

RESULT 24

US-10-131-826A-410
; Sequence 410, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 410
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-410

Query Match 79.3%; Score 23; DB 6; Length 229;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 118 KVIFF 122

RESULT 25

US-10-793-626-2450
; Sequence 2450, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:


```
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2120

Query Match      82.8%; Score 24; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      414 IVFFA 418

RESULT 19
US-10-689-742-13
; Sequence 13, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: McCoy, John M
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoys, Edward R
; APPLICANT: LaVallie, John A
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 13
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-13

Query Match      82.8%; Score 24; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      404 IVFFA 408

RESULT 20
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
```

```
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125

Query Match      82.8%; Score 24; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      531 KAVFFA 536

RESULT 21
US-10-131-826A-230
; Sequence 230, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131.826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 230
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo Sapien
```

```
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1056
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1056

Query Match      86.2%; Score 25; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFF 5
DB      7 KIVFF 11

RESULT 15
US-10-467-657-7892
; Sequence 7892, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7892
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7892

Query Match      82.8%; Score 24; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFF 5
DB      33 KIVFF 37

RESULT 16
US-10-467-657-2014
; Sequence 2014, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2120
; LENGTH: 426
```

```
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2014
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2014

Query Match      82.8%; Score 24; DB 6; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFA 6
DB      73 IVFFA 77

RESULT 17
US-10-467-657-9070
; Sequence 9070, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9070
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9070

Query Match      82.8%; Score 24; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFA 6
DB      264 IVFFA 268

RESULT 18
US-10-467-657-2120
; Sequence 2120, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2120
; LENGTH: 426
```

OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
OTHER INFORMATION: Alzheimer's disease amyloid protein

FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)..(17)
OTHER INFORMATION: signal peptide

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(40)

OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40
OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (18)..(687)

OTHER INFORMATION: soluble APP-alpha

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (18)..(671)

OTHER INFORMATION: soluble APP-beta

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (672)..(770)

OTHER INFORMATION: C99

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (672)..(713)

OTHER INFORMATION: beta-amyloid protein 42

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (672)..(711)

OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(770)

OTHER INFORMATION: C83

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(713)

OTHER INFORMATION: P3(42)

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(711)

OTHER INFORMATION: P3(40)

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (712)..(770)

OTHER INFORMATION: gamma-CTF(59)

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (714)..(770)

OTHER INFORMATION: gamma-CTF(57)

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (721)..(770)

OTHER INFORMATION: gamma-CTF(50)

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (740)..(770)

OTHER INFORMATION: C31

US-10-982-545-15

Query Match 93.1%; Score 27; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 687 KLVFFA 692

RESULT 12

US-10-789-273-38

Sequence 38, Application US/10789273
Publication No. US20050249725A1

GENERAL INFORMATION:
APPLICANT: Basi, Gurik

APPLICANT: Saldanha, Jose
APPLICANT: Vednock, Ted

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
TITLE OF INVENTION: BETA-AMYLOID PEPTIDE

FILE REFERENCE: ELN-002CP

CURRENT APPLICATION NUMBER: US/10789,273
CURRENT FILING DATE: 2004-02-27

PRIOR APPLICATION NUMBER: US/10/388,389
PRIOR FILING DATE: 2003-03-12

PRIOR APPLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06

PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 38
LENGTH: 770

TYPE: PRT
ORGANISM: Homo sapiens

US-10-789-273-38

Query Match 93.1%; Score 27; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 687 KLVFFA 692

RESULT 13

US-10-467-657-330

Sequence 330, Application US/10467657
Publication No. US20050260581A1

GENERAL INFORMATION:
APPLICANT: CHIRON SpA

APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia

APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04

SEQ ID NO 330
LENGTH: 269

TYPE: PRT
ORGANISM: Neisseria gonorrhoeae

US-10-467-657-330

Query Match 86.2%; Score 25; DB 6; Length 269;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|:|||||
Db 11 KIVFF 15

RESULT 14

US-10-793-626-1056

Sequence 1056, Application US/10793626
Publication No. US20050255478A1

GENERAL INFORMATION:
APPLICANT: Basi, Gurik

; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match 93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 8

US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/667,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 9

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 10

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 11

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 4

US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; FILE REFERENCE: PTO-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 5

US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match 93.1%; Score 27; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 6

US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; PRIOR FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match 93.1%; Score 27; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 7

US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24

245 20 69.0 692 7 US-11-103-957-29 Sequence 29, Appl
246 20 69.0 708 7 US-11-174-150-25 Sequence 25, Appl
247 20 69.0 710 7 US-11-078-189-18 Sequence 18, Appl
248 20 69.0 721 6 US-10-467-962B-49 Sequence 49, Appl
249 20 69.0 736 7 US-11-174-150-26 Sequence 26, Appl
250 20 69.0 736 7 US-11-078-189-9 Sequence 9, Appl
251 20 69.0 739 7 US-11-082-389-94 Sequence 94, Appl
252 20 69.0 739 7 US-11-078-189-12 Sequence 12, Appl
253 20 69.0 739 7 US-11-107-028-6 Sequence 6, Appl
254 20 69.0 741 6 US-10-467-657-6266 Sequence 6266, Ap
255 20 69.0 745 6 US-11-147-109-2 Sequence 2, Appl
256 20 69.0 748 6 US-10-821-234-1479 Sequence 1479, Ap
257 20 69.0 817 6 US-10-793-626-2948 Sequence 2948, Ap
258 20 69.0 852 6 US-10-467-657-5004 Sequence 5004, Ap
259 20 69.0 856 6 US-10-467-657-8534 Sequence 8534, Ap
260 20 69.0 874 6 US-10-510-386-28 Sequence 28, Appl
261 20 69.0 896 7 US-11-192-219-3 Sequence 3, Appl
262 20 69.0 898 7 US-11-166-730-3 Sequence 3, Appl
263 20 69.0 902 7 US-11-057-058-64 Sequence 64, Appl
264 20 69.0 916 6 US-10-467-657-4242 Sequence 4242, Ap
265 20 69.0 923 7 US-11-192-219-4 Sequence 4, Appl
266 20 69.0 989 6 US-10-821-234-975 Sequence 975, App
267 20 69.0 1013 7 US-11-103-957-9 Sequence 9, Appl
268 20 69.0 1047 6 US-10-510-386-200 Sequence 200, App
269 20 69.0 1165 7 US-11-192-219-2 Sequence 2, Appl
270 20 69.0 1167 6 US-10-601-368-18 Sequence 18, Appl
271 20 69.0 1217 7 US-11-074-176-252 Sequence 252, App
272 20 69.0 1730 7 US-11-192-967-4 Sequence 4, Appl
273 20 69.0 1730 7 US-11-193-715-4 Sequence 4, Appl
274 20 69.0 2844 6 US-10-770-726-45 Sequence 45, Appl
275 20 69.0 7968 7 US-11-186-731-5 Sequence 5, Appl
276 19 65.5 13 7 US-11-016-706-29 Sequence 29, Appl
277 19 65.5 27 7 US-11-157-930-14 Sequence 14, Appl
278 19 65.5 35 6 US-10-821-234-1704 Sequence 1704, Ap
279 19 65.5 43 7 US-11-075-400-28 Sequence 28, Appl
280 19 65.5 44 7 US-11-000-463-372 Sequence 372, App
281 19 65.5 46 6 US-10-467-657-9119 Sequence 9119, Ap
282 19 65.5 47 6 US-10-467-657-9186 Sequence 9186, Ap
283 19 65.5 57 6 US-10-467-657-5448 Sequence 5448, Ap
284 19 65.5 71 7 US-11-000-463-772 Sequence 772, App
285 19 65.5 80 6 US-10-986-501-200 Sequence 200, App
286 19 65.5 83 6 US-10-467-657-5366 Sequence 5366, Ap
287 19 65.5 86 6 US-10-467-657-3376 Sequence 3376, Ap
288 19 65.5 98 6 US-10-467-657-1377 Sequence 1377, App
289 19 65.5 100 7 US-11-123-896-137 Sequence 137, App
290 19 65.5 103 6 US-10-793-626-1708 Sequence 1708, Ap
291 19 65.5 103 6 US-10-793-626-2074 Sequence 2074, Ap
292 19 65.5 104 6 US-10-793-626-2512 Sequence 2512, Ap
293 19 65.5 106 7 US-11-064-174-50 Sequence 50, Appl
294 19 65.5 107 6 US-10-793-626-1586 Sequence 1586, Ap
295 19 65.5 107 6 US-10-467-657-1018 Sequence 1018, Ap
296 19 65.5 107 6 US-10-467-657-2102 Sequence 2102, App
297 19 65.5 107 7 US-11-000-463-300 Sequence 300, App
298 19 65.5 115 6 US-10-432-483-10 Sequence 10, Appl
299 19 65.5 117 6 US-10-467-657-2282 Sequence 2282, Ap
300 19 65.5 122 6 US-10-467-657-606 Sequence 606, App

ALIGNMENTS

RESULT 1
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US2005024972A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; PRIOR FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289

; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match 93.1%; Score 27; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 2

US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match 93.1%; Score 27; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 3

US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.

99	20	69.0	19	6	US-10-467-657-8712	Sequence 8712, Ap	172	20	69.0	325	6	US-10-454-437-142	Sequence 142, App
100	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	173	20	69.0	329	6	US-10-793-626-1942	Sequence 1942, Ap
101	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	174	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap
102	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	175	20	69.0	337	6	US-10-485-517-234	Sequence 234, App
103	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	176	20	69.0	342	6	US-11-082-389-214	Sequence 214, App
104	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	177	20	69.0	343	6	US-10-467-657-4824	Sequence 4824, Ap
105	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	178	20	69.0	343	6	US-10-467-657-7256	Sequence 7256, Ap
106	20	69.0	40	6	US-10-250-581-15	Sequence 18, Appl	179	20	69.0	343	6	US-10-467-657-7256	Sequence 7256, Ap
107	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	180	20	69.0	348	6	US-10-467-657-4840	Sequence 4840, Ap
108	20	69.0	42	6	US-10-250-581-18	Sequence 15, Appl	181	20	69.0	355	6	US-10-467-657-7996	Sequence 7996, Ap
109	20	69.0	42	6	US-10-250-581-16	Sequence 8811, Ap	182	20	69.0	355	6	US-10-995-561-636	Sequence 636, App
110	20	69.0	42	6	US-10-250-581-19	Sequence 16, Appl	183	20	69.0	355	6	US-10-454-437-102	Sequence 102, App
111	20	69.0	42	6	US-10-250-581-16	Sequence 19, Appl	184	20	69.0	357	6	US-10-467-657-2500	Sequence 102, App
112	20	69.0	42	6	US-10-250-581-19	Sequence 16, Appl	185	20	69.0	357	6	US-10-467-657-6648	Sequence 6648, Ap
113	20	69.0	54	6	US-10-467-657-4978	Sequence 19, Appl	186	20	69.0	362	6	US-10-995-561-637	Sequence 637, App
114	20	69.0	56	6	US-10-467-657-1050	Sequence 4378, Ap	187	20	69.0	389	7	US-11-018-018-2	Sequence 2, Appl
115	20	69.0	83	6	US-10-510-386-114	Sequence 1050, Ap	188	20	69.0	389	7	US-11-047-757-2	Sequence 2, Appl
116	20	69.0	95	6	US-10-467-657-2518	Sequence 114, App	189	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
117	20	69.0	102	6	US-10-793-626-2592	Sequence 2518, Ap	190	20	69.0	396	6	US-10-510-386-238	Sequence 238, App
118	20	69.0	105	6	US-10-467-657-3209	Sequence 2592, Ap	191	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appl
119	20	69.0	108	6	US-10-467-657-4266	Sequence 9209, Ap	192	20	69.0	399	7	US-11-018-018-3	Sequence 3, Appl
120	20	69.0	114	6	US-10-821-234-1140	Sequence 4266, Ap	193	20	69.0	406	6	US-10-467-657-7420	Sequence 7420, Ap
121	20	69.0	114	6	US-10-467-657-124	Sequence 1140, Ap	194	20	69.0	409	6	US-10-821-234-1425	Sequence 1425, Ap
122	20	69.0	114	6	US-10-467-657-1414	Sequence 1414, Ap	195	20	69.0	413	6	US-10-467-657-1858	Sequence 1858, Ap
123	20	69.0	114	6	US-10-467-657-3162	Sequence 1414, Ap	196	20	69.0	414	6	US-10-878-556A-1	Sequence 1, Appl
124	20	69.0	114	6	US-10-467-657-3754	Sequence 3754, Ap	197	20	69.0	418	6	US-10-467-657-5788	Sequence 5788, Ap
125	20	69.0	114	6	US-10-467-657-8674	Sequence 8674, Ap	198	20	69.0	432	7	US-11-113-424-186	Sequence 186, App
126	20	69.0	115	6	US-10-793-626-1554	Sequence 1554, Ap	199	20	69.0	436	6	US-10-467-657-7694	Sequence 7694, Ap
127	20	69.0	116	6	US-10-467-657-5514	Sequence 5514, Ap	200	20	69.0	436	6	US-11-082-389-256	Sequence 256, App
128	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	201	20	69.0	443	6	US-10-793-626-1860	Sequence 1860, Ap
129	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appl	202	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
130	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appl	203	20	69.0	445	6	US-10-873-528-30	Sequence 30, Appl
131	20	69.0	131	6	US-10-467-657-3308	Sequence 3308, Ap	204	20	69.0	448	6	US-10-763-712A-69	Sequence 69, Appl
132	20	69.0	137	6	US-10-821-234-1701	Sequence 1701, Ap	205	20	69.0	448	6	US-10-763-712A-112	Sequence 112, App
133	20	69.0	140	6	US-10-467-657-3486	Sequence 2486, Ap	206	20	69.0	449	6	US-10-821-234-1075	Sequence 1075, Ap
134	20	69.0	144	6	US-10-793-626-1640	Sequence 1640, Ap	207	20	69.0	450	6	US-10-467-657-7094	Sequence 7094, Ap
135	20	69.0	144	6	US-10-793-626-1958	Sequence 1958, Ap	208	20	69.0	450	6	US-10-467-657-8028	Sequence 8028, Ap
136	20	69.0	156	6	US-10-467-657-1280	Sequence 1280, Ap	209	20	69.0	450	6	US-10-763-712A-76	Sequence 76, Appl
137	20	69.0	179	6	US-10-467-657-2232	Sequence 2232, Ap	210	20	69.0	451	6	US-10-467-657-7104	Sequence 7104, Ap
138	20	69.0	182	6	US-10-980-388-89	Sequence 89, Appl	211	20	69.0	456	6	US-10-467-657-4150	Sequence 4150, Ap
139	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	212	20	69.0	466	7	US-11-102-240-104	Sequence 104, App
140	20	69.0	186	6	US-10-467-657-3918	Sequence 3918, Ap	213	20	69.0	470	7	US-11-186-284-123	Sequence 123, App
141	20	69.0	195	7	US-11-019-955-24	Sequence 24, Appl	214	20	69.0	471	6	US-10-995-561-901	Sequence 901, App
142	20	69.0	197	6	US-10-793-626-2856	Sequence 2856, Ap	215	20	69.0	477	6	US-10-431-826A-452	Sequence 452, App
143	20	69.0	200	6	US-10-793-626-394	Sequence 394, App	216	20	69.0	481	6	US-10-467-657-3124	Sequence 3124, Ap
144	20	69.0	200	6	US-10-793-626-1242	Sequence 1242, Ap	217	20	69.0	481	7	US-11-090-439-16	Sequence 16, Appl
145	20	69.0	204	6	US-10-980-388-102	Sequence 102, App	218	20	69.0	485	6	US-10-204-029-7	Sequence 7, Appl
146	20	69.0	210	6	US-10-467-657-6318	Sequence 6318, Ap	219	20	69.0	488	6	US-10-821-234-1654	Sequence 1654, Ap
147	20	69.0	214	6	US-10-508-263-108	Sequence 108, App	220	20	69.0	488	7	US-11-186-284-121	Sequence 121, App
148	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	221	20	69.0	489	6	US-10-467-657-7846	Sequence 7846, Ap
149	20	69.0	239	6	US-10-467-657-8743	Sequence 8743, Ap	222	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
150	20	69.0	241	7	US-11-019-955-27	Sequence 27, Appl	223	20	69.0	495	7	US-11-074-176-60	Sequence 60, Appl
151	20	69.0	250	7	US-11-082-389-216	Sequence 216, App	224	20	69.0	508	7	US-11-082-389-178	Sequence 178, App
152	20	69.0	257	7	US-11-102-240-94	Sequence 94, Appl	225	20	69.0	514	6	US-10-793-626-12	Sequence 12, Appl
153	20	69.0	266	6	US-10-995-561-544	Sequence 544, App	226	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
154	20	69.0	267	6	US-10-995-561-543	Sequence 543, App	227	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
155	20	69.0	268	7	US-11-019-955-28	Sequence 28, Appl	228	20	69.0	558	7	US-11-078-189-19	Sequence 19, Appl
156	20	69.0	271	6	US-10-793-626-1156	Sequence 1156, Ap	229	20	69.0	560	6	US-10-623-155-225	Sequence 225, App
157	20	69.0	272	6	US-10-467-657-2520	Sequence 2520, Ap	230	20	69.0	563	6	US-10-821-234-1067	Sequence 1067, Ap
158	20	69.0	276	6	US-10-873-730-134	Sequence 134, App	231	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
159	20	69.0	280	6	US-10-858-730-200	Sequence 200, App	232	20	69.0	585	6	US-10-967-457-18	Sequence 18, Appl
160	20	69.0	280	6	US-10-467-657-2130	Sequence 2130, Ap	233	20	69.0	585	6	US-10-939-890-500	Sequence 500, App
161	20	69.0	288	7	US-11-082-389-324	Sequence 324, App	234	20	69.0	585	7	US-11-078-663-18	Sequence 18, Appl
162	20	69.0	288	6	US-10-467-657-1272	Sequence 1272, Ap	235	20	69.0	585	7	US-11-078-914-18	Sequence 18, Appl
163	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appl	236	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
164	20	69.0	292	7	US-11-102-883-24	Sequence 24, Appl	237	20	69.0	626	6	US-10-467-657-6426	Sequence 6426, Ap
165	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	238	20	69.0	636	6	US-10-467-657-7618	Sequence 7618, Ap
166	20	69.0	299	6	US-10-467-657-2190	Sequence 2190, Ap	239	20	69.0	637	6	US-10-873-528-53	Sequence 53, Appl
167	20	69.0	312	7	US-11-055-822-16	Sequence 16, Appl	240	20	69.0	647	7	US-11-080-991-32	Sequence 32, Appl
168	20	69.0	316	7	US-11-082-389-62	Sequence 62, Appl	241	20	69.0	657	7	US-11-080-991-48	Sequence 48, Appl
169	20	69.0	321	6	US-10-467-657-2504	Sequence 2504, Ap	242	20	69.0	669	7	US-11-119-683-2	Sequence 2, Appl
170	20	69.0	324	6	US-10-467-657-7692	Sequence 7692, Ap	243	20	69.0	675	6	US-10-467-657-4004	Sequence 4004, Ap
171	20	69.0	324	6	US-10-467-657-8440	Sequence 8440, Ap	244	20	69.0	690	6	US-10-939-890-501	Sequence 501, App

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Published Applications AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US03_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	93.1	19	6	US-10-923-605-5
2	27	93.1	19	6	US-10-934-818-5
3	27	93.1	40	7	US-11-016-706-36
4	27	93.1	40	7	US-11-098-674-12
5	27	93.1	42	6	US-10-923-605-1
6	27	93.1	42	6	US-10-934-818-1
7	27	93.1	42	7	US-11-016-706-37
8	27	93.1	43	6	US-10-934-818-6
9	27	93.1	43	6	US-10-250-581-1
10	27	93.1	43	6	US-10-250-581-1
11	27	93.1	770	6	US-10-982-545-15
12	27	93.1	770	6	US-10-789-273-38
13	25	86.2	269	6	US-10-467-657-330
14	25	86.2	400	6	US-10-793-626-1056
15	24	82.8	50	6	US-10-467-657-7882
16	24	82.8	347	6	US-10-467-657-2014
17	24	82.8	402	6	US-10-467-657-9070
18	24	82.8	426	6	US-10-467-657-2120
19	24	82.8	524	6	US-10-689-742-13
20	24	82.8	660	7	US-11-186-284-125
21	24	82.8	677	6	US-10-131-826A-230
22	24	82.8	708	6	US-10-821-234-917
23	23	79.3	5	7	US-11-098-674-1
24	23	79.3	229	6	US-10-131-826A-410
25	23	79.3	311	6	US-10-793-626-2450
26	23	79.3	481	6	US-10-995-561-959
27	23	79.3	522	7	US-11-080-991-104
28	23	79.3	528	6	US-10-793-626-1930
29	23	79.3	533	6	US-10-467-657-2868
30	23	79.3	3623	6	US-10-995-561-593
31	22	75.9	47	6	US-10-467-657-5436
32	22	75.9	98	6	US-10-467-657-4746
33	22	75.9	167	7	US-11-210-316-18
34	22	75.9	211	6	US-10-467-657-6932
35	22	75.9	215	6	US-10-131-826A-4
36	22	75.9	228	6	US-10-467-657-568
37	22	75.9	228	6	US-10-467-657-4838
38	22	75.9	233	6	US-10-821-234-1322
39	22	75.9	239	6	US-10-467-657-432
40	22	75.9	265	6	US-10-793-626-2500
41	22	75.9	330	6	US-10-793-626-2476
42	22	75.9	330	6	US-10-793-626-2734
43	22	75.9	338	6	US-10-878-556A-19
44	22	75.9	344	6	US-10-131-826A-376
45	22	75.9	358	7	US-11-055-822-572
46	22	75.9	358	7	US-11-055-822-836
47	22	75.9	432	7	US-11-194-246-308
48	22	75.9	449	6	US-10-467-657-678
49	22	75.9	453	7	US-11-082-389-198
50	22	75.9	510	7	US-11-210-316-22
51	22	75.9	539	7	US-11-210-316-26
52	22	75.9	601	6	US-10-467-657-7120
53	22	75.9	635	6	US-10-821-234-1673
54	22	75.9	858	6	US-10-613-744-6
55	22	75.9	2233	6	US-10-873-528-2
56	21	72.4	43	6	US-10-467-657-7886
57	21	72.4	52	6	US-10-467-657-2216
58	21	72.4	76	6	US-10-467-657-5690
59	21	72.4	91	6	US-10-821-234-1703
60	21	72.4	123	6	US-10-793-626-430
61	21	72.4	123	6	US-10-467-657-5166
62	21	72.4	134	6	US-10-793-626-2374
63	21	72.4	155	6	US-10-467-657-2420
64	21	72.4	175	6	US-10-965-694-23
65	21	72.4	182	6	US-10-793-626-2836
66	21	72.4	182	6	US-10-467-657-3510
67	21	72.4	190	6	US-10-467-657-3436
68	21	72.4	211	6	US-10-821-234-1372
69	21	72.4	216	6	US-10-467-657-8102
70	21	72.4	221	6	US-10-467-657-230
71	21	72.4	221	6	US-10-467-657-5750
72	21	72.4	254	6	US-10-467-657-6144
73	21	72.4	272	6	US-10-632-150-46
74	21	72.4	272	7	US-11-073-457-46
75	21	72.4	272	7	US-11-073-460-46
76	21	72.4	278	6	US-10-957-569-45
77	21	72.4	370	6	US-10-821-234-1105
78	21	72.4	440	7	US-11-082-389-106
79	21	72.4	463	6	US-10-467-657-6352
80	21	72.4	463	6	US-10-467-657-7604
81	21	72.4	482	6	US-10-793-626-24
82	21	72.4	496	7	US-11-067-121-12
83	21	72.4	522	6	US-10-995-561-1030
84	21	72.4	525	7	US-11-082-389-350
85	21	72.4	569	7	US-11-082-389-104
86	21	72.4	582	7	US-11-090-439-58
87	21	72.4	592	6	US-10-467-657-4888
88	21	72.4	615	6	US-10-995-561-940
89	21	72.4	662	6	US-10-995-561-943
90	21	72.4	702	6	US-10-995-561-942
91	21	72.4	738	7	US-11-147-047-48
92	21	72.4	747	7	US-11-018-018-1
93	21	72.4	747	7	US-11-047-757-1
94	21	72.4	754	6	US-10-995-561-941
95	21	72.4	1061	7	US-11-000-463-347
96	21	72.4	1070	7	US-11-147-047-49
97	21	72.4	1091	7	US-11-000-463-348
98	21	72.4	3507	7	US-11-075-185-7

Sequence 959, App
Sequence 104, App
Sequence 1930, Ap
Sequence 2868, Ap
Sequence 593, App
Sequence 5436, Ap
Sequence 4746, Ap
Sequence 18, Appl
Sequence 6932, Ap
Sequence 4, Appl
Sequence 568, App
Sequence 4838, Ap
Sequence 1322, Ap
Sequence 432, App
Sequence 2500, Ap
Sequence 2476, Ap
Sequence 2734, Ap
Sequence 19, Appl
Sequence 376, App
Sequence 572, App
Sequence 836, App
Sequence 308, App
Sequence 678, App
Sequence 198, App
Sequence 22, Appl
Sequence 26, Appl
Sequence 1720, Ap
Sequence 1673, Ap
Sequence 6, Appl
Sequence 2, Appl
Sequence 7886, Ap
Sequence 2216, Ap
Sequence 5690, Ap
Sequence 1703, Ap
Sequence 430, App
Sequence 5166, Ap
Sequence 2374, Ap
Sequence 2420, Ap
Sequence 23, Appl
Sequence 2836, Ap
Sequence 3510, Ap
Sequence 3436, Ap
Sequence 1372, Ap
Sequence 8102, Ap
Sequence 290, App
Sequence 5750, Ap
Sequence 6144, Ap
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 45, Appl
Sequence 1105, Ap
Sequence 106, App
Sequence 6352, Ap
Sequence 7604, Ap
Sequence 24, Appl
Sequence 12, Appl
Sequence 1030, Ap
Sequence 350, App
Sequence 104, App
Sequence 58, Appl
Sequence 4888, Ap
Sequence 940, App
Sequence 943, App
Sequence 942, App
Sequence 48, Appl
Sequence 1, Appl
Sequence 941, App
Sequence 347, App
Sequence 49, Appl
Sequence 348, App
Sequence 7, Appl


```

OX  NCBI_TaxID=7200;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  TISSUE=Salivary gland;
RX  PubMed=15371479; DOI=10.1242/jeb.01185;
RA  Valenzuela J.G., Garfield M., Rowton B.D., Pham V.M.;
RT  "Identification of the most abundant secreted proteins from the
RT  salivary glands of the sand fly Lutzomyia longipalpis, vector of
RT  Leishmania chagasi.";
RL  J. Exp. Biol. 207:3717-3729(2004).
DR  EMBL; AY445935; AAS05318.1; -; mRNA.
DR  InterPro: IPR003534; Royaljelly.
DR  Pfam; PF03022; MRJP; 1.
SQ  SEQUENCE 399 AA; 45277 MW; F4E19F115794AAE8 CRC64;

Query Match      93.1%; Score 27; DB 2; Length 399;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches  4; Conservative  2; Mismatches  0; Indels  0; Gaps  0;

QY      1 KIVFFA 6
       |:|
Db      305 KVIFFA 310

Search completed: December 29, 2005, 17:46:50
Job time : 92.1936 secs

```

THIS PAGE BLANK (USPTO)

RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontseki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayateu M., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayaashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kachon H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayaashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK076505; BAC36369.1; -; mRNA.
 DR HSSP; P08592; 1NMJ.
 DR SMR; Q8BPC7; 74-183.
 DR MGI; MGI:88059; App.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 DR GO; GO:0016020; C:membrane; TAS.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0030198; F:extracellular matrix organization and bioge. .; IGI.
 DR InterPro; IPR008155; A4 APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00320; A4 INTRA; 1.
 FT NON TER 1
 SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 384;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 301 KLVFFA 306
 |:|||||
 301 KLVFFA 306
 RESULT 74
 Q4NSU7_THEDA PRELIMINARY; PRT; 391 AA.
 ID Q4NSU7;
 AC Q4NSU7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=rp02_0195;
 OS Theileria parva.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
 OC Theileria.
 OX NCBI_TaxID=5875;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Muguga;
 RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
 RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
 RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J.,
 RA Jiang L., Lynn J., Weaver B., Shoabi A., Wasawo D., Crabtree J.,
 RA Wortman J.R., Haas B., Anguilo S.V., Creasy T.H., Lu C., Sun B.,
 RA Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,
 RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
 RA Venter J.C., Fraser C.M., Nene V.;
 RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
 RT lymphocytes.";
 RL Science 309:134-137(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Muguga;
 RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
 RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
 RA Ralph S.A., Mann D.J., Xiong Z., Shallow S.J., Weidman J., Jiang L.,
 RA Lynn J., Weaver B., Shoabi A., Wasawo D., Crabtree J., Wortman J.R.,
 RA Haas B., Anguilo S., Creasy T.H., Lu C., Suh B., Silva J.C.,
 RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
 RA Fraser C.M., Nene V.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAGK01000002; EAK32476.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 391 AA; 44445 MW; 129227F0ABAF933C CRC64;
 Query Match 93.1%; Score 27; DB 2; Length 391;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIVFFA 6
 Db 130 KLVFFA 135
 |:|||||
 130 KLVFFA 135
 RESULT 75
 Q5WPU9_LUTLO PRELIMINARY; PRT; 399 AA.
 ID Q5WPU9_LUTLO
 AC Q5WPU9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE 43.2 kDa salivary protein.
 GN ORFNames=LJM11_Clu9;
 OS Lutzomyia longipalpis (Sand fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
 OC Psychodidae; Lutzomyia; Lutzomyia.

```

DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1_1
SQ SEQUENCE 357 AA; 40962 MW; 07D9BEFF6C5B2D8 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 357;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 274 KLVFFA 279
|:|||||

RESULT 71
QBPL1 XANAC PRELIMINARY; PRT; 366 AA.
AC Q8PPL1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein XAC0675.
GN OrderedLocusNames=XAC0675;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
Almeida N.F., Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergro F.,
Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
El-borhy H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C.,
Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,
Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
DR ENBL; AE011696; AM35564.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 366 AA; 40845 MW; 6EF65B2BEC8844 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 366;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 340 KLVFFA 345
|:|||||

RESULT 72
O67225 AQAE PRELIMINARY; PRT; 380 AA.
ID O67225
AC O67225
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hydrogenase expression/formation protein HypD.

```

```

GN Name=hypD; OrderedLocusNames=AQ_1157;
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
DR EMBL; AE000726; AAC07185.1; -; Genomic_DNA.
DR PIR; F70399; F70399.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PIRSF; PIRSF005622; Hydrn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 380;
Best Local Similarity 66.7%; Pred. No. 6.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 141 KVIFFA 146
|:|||||

RESULT 73
QBPC7 MOUSE PRELIMINARY; PRT; 384 AA.
ID QBPC7_MOUSE PRELIMINARY;
AC Q8BPC7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
DE library, clone:483432I09 product:amyloid beta (A4) protein, full
DE insert sequence. (Fragment).
DE Name=App;
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glasi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

```

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Bevan M., Robben J., Grymonprez B., Volckaert G., Bancroft I.,
 RA Mewes H.W., Rudd S., Schoof H., Mayer K.F.X.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Robben J., Grymonprez B., Volckaert G., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL079349; CAB53090.1; -; Genomic DNA.
 DR EMBL; AL161535; CAB78332.1; -; Genomic DNA.
 DR PIR; H85138; H85138. GILT.
 DR InterPro; IPR004911; GILT.
 DR InterPro; IPR000834; Peptidase_M14.
 DR Pfam; PF03227; GILT; 1.
 DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 231 AA; 26025 MW; 734109A78E942295 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 231;
 Best Local Similarity 83.3%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 12 KLVFFA 17

RESULT 68
 Q9XGY6 SIMCH PRELIMINARY; PRT; 352 AA.
 AC Q9XGY6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Wax synthase
 OS Simmondsia chinensis (Jojoba).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Simmondsiaceae; Simmondsia.
 OX NCBI_TaxID=3999;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20177844; PubMed=10712527; DOI=10.1104/pp.122.3.645;
 RA Lardizabal K.D., Metz J.G., Sakamoto T., Hutton W.C., Pollard M.R.,
 RA Lasser M.W.;
 RT "Purification of a jojoba embryo wax synthase, cloning of its cDNA and
 RT production of high levels of wax in seeds of transgenic Arabidopsis.";
 RL Plant Physiol. 122:645-655 (2000).
 DR EMBL; AF149919; AAD38041.1; -; mRNA.
 DR PIR; T48903; T48903.
 DR InterPro; IPR004299; MBOAT_fam.
 DR Pfam; PF03062; MBOAT; 1.
 SQ SEQUENCE 352 AA; 40156 MW; F91D6BD896003629 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 352;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 135 KLVFFA 140

RESULT 69
 Q8U460 PYRFU PRELIMINARY; PRT; 357 AA.
 AC Q8U460;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein PF0234.
 GN OrderedLocustNames=PF0234;
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE010148; AAL80358.1; -; Genomic DNA.
 DR InterPro; IPR008553; DUF835.
 DR Pfam; PF05763; DUF835; 1.
 DR Complete proteome; Hypothetical protein.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 357 AA; 39940 MW; 9EEFE2540FC8D65 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 357;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 197 KLVFFA 202

RESULT 70
 Q8UUI8 BRARE PRELIMINARY; PRT; 357 AA.
 AC Q8UUI8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative membrane protein (Fragment).
 GN Nameaappa;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole embryo;
 RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
 RA Musa A., Lehrach H., Russo V.E.A.;
 RT "Distinct expression patterns of two zebrafish homologues of the human
 RT APP gene during embryonic development.";
 RL Dev. Genes Evol. 211:563-567 (2001).
 DR EMBL; AJ315637; CAC85734.1; -; mRNA.
 DR HSP; Q16019; IHZ3.
 DR SMR; Q8UUI8; 62-170.
 DR ZFIN; ZDB-GENE-000616-13; appa.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR008155; A4_APP.

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehama J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK052448; BAC34997.1; -; mRNA.
DR HSSP; P08592; INMJ.
DR MGI; MGI:88059; App.
DR GO; GO:0016021; C:integral to membrane; IDA.
DR GO; GO:0016020; C:membrane; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IGI.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PRO0203; AMYLOIDA4.
DR PRINTS; PRO0204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0EF5 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 218;
Best Local Similarity 83.3%; Pred. NO. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
|:|||||
Db 135 KLVFFA 140
|:|||||
RESULT 66
Q9SV79 ARATH
ID Q8VY56_ARATH PRELIMINARY; PRT; 229 AA.
AC Q8VY56;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At4g12870.
GN Name=At4g12870;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072432; AAL62424.1; -; mRNA.
DR InterPro; IPR004911; GILT.
DR Pfam; PF03227; GILT; 1.
KW Hypothetical protein.
SQ SEQUENCE 229 AA; 25707 MW; BF3DD2587EAA82D6 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. NO. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
|:|||||
Db 9 KLVFFA 14
|:|||||
RESULT 67
Q9SV79 ARATH
ID Q9SV79_ARATH PRELIMINARY; PRT; 231 AA.
AC Q9SV79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At4g12900.
GN Name=At4g12900; Synonyms=AT4g12900;

DE Hypothetical protein.
GN OrderedLocusNames=RS6777;
OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=1117;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303 (2003).
DR EMBL; BX294144; CAD75000.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 137 AA; 15530 MW; 5DC133B06CC5FC0 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 137;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 85 KLVFFA 90

RESULT 63
Q9ST29 ARATH PRELIMINARY; PRT; 152 AA.
AC Q9ST29;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein T20K18.220 (Hypothetical protein AT4g12870).
GN Name=T20K18.220; Synonyms=AT4g12870;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
RA Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
RA Lemcke K., Mayer K.F.X.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049640; CAB41004.1; -; Genomic DNA.
DR EMBL; AL161535; CAB78329.1; -; Genomic DNA.
DR PIR; T06645; T06645.
DR InterPro; IPR004911; GILT.
DR Pfam; PF03227; GILT; 1.
KW Hypothetical protein.
SQ SEQUENCE 152 AA; 17095 MW; ED47CEAE7607B131 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 152;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 9 KLVFFA 14

RESULT 64
Q6AKE9 DESPS PRELIMINARY; PRT; 203 AA.
AC Q6AKE9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Related to McbG protein.
GN OrderedLocusNames=DP2447;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=LSV54 / DSM 12343;
RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
RT from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902 (2004).
DR EMBL; CR522870; CAG37176.1; -; Genomic DNA.
DR InterPro; IPR001646; 5peptide_repeat.
DR Pfam; PF00805; Pentapeptide; 3.
KW Complete proteome.
SQ SEQUENCE 203 AA; 23270 MW; 2EA1CD022861292D CRC64;

Query Match 93.1%; Score 27; DB 2; Length 203;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 52 KLVFFA 57

RESULT 65
Q8BPV5 MOUSE PRELIMINARY; PRT; 218 AA.
AC Q8BPV5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
DE library, clone:D430025B14 product:amyloid beta (A4) protein, full
DE insert sequence. (Fragment).
GN Name=App;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.,
RA Carninci P., Hayashizaki Y.,
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90089-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 peptide in dog, polar bear and five other mammals by cross-species
 polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC - FUNCTION: Functional neuronal receptor which couples to
 intracellular signaling pathway through the GTP-binding protein
 G(O) (By similarity).
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - SIMILARITY: Belongs to the APP family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 DR EMBL; X56124; CAA39589.1; -; mRNA.
 DR EMBL; X56126; CAA39591.1; -; mRNA.
 DR HSSP; P08592; INMJ.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083:SP6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Transmembrane.
 FT CHAIN <1 6
 FT CHAIN 7 >59
 FT CHAIN 7 48
 FT CHAIN 7 46
 FT CHAIN 47 >59
 FT CHAIN 49 >59
 FT CHAIN 49 >59
 FT TOPO_DOM <1 34
 FT TRANSMEM 35 58
 FT TOPO_DOM 59 >59
 FT NON_TER 1 1
 FT NON_TER 59 59
 SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;
 Query Match 93.1%; Score 27; DB 1; Length 59;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 Db 22 KLVFFA 27
 RESULT 60
 O35463 CRIGR PRELIMINARY; PRT; 79 AA.
 AC O35463
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alzheimer's amyloid beta protein (Fragment).
 GN Name-beta APP;
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Cricetinae; Cricetulus.
 OX NCBI_TaxID=10029;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sambamurti K., Pinnix I., Gandhi S.;
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF030413; AAB86608.1; -; mRNA.
 DR HSSP; P08592; INMJ.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 FT NON_TER 1 79
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;
 Query Match 93.1%; Score 27; DB 2; Length 79;
 Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 Db 36 KLVFFA 41
 RESULT 61
 Q8JH58 CHESE PRELIMINARY; PRT; 113 AA.
 ID Q8JH58
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Amyloid beta protein (Fragment).
 OS Chelydra serpentina serpentina (common snapping turtle).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
 OX NCBI_TaxID=134619;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21876906; PubMed=11882478;
 RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
 RT "Octylphenol (OP) alters the expression of members of the amyloid
 protein family in the hypothalamus of the snapping turtle, Chelydra
 serpentina serpentina.";
 RL Environ. Health Perspect. 110:269-275 (2002).
 DR EMBL; AF541917; AAN04908.1; -; mRNA.
 DR HSSP; Q16019; 11YT.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;
 Query Match 93.1%; Score 27; DB 2; Length 113;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 Db 30 KLVFFA 35
 RESULT 62
 Q7UPR1 RHOB PRELIMINARY; PRT; 137 AA.
 ID Q7UPR1
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).

Name=APP;
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
[1]
NCBI_TaxID=9986;
[1]
NUCLEOTIDE SEQUENCE.
TISSUE=Brain;
MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F; Johnston E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
Brain Res. Mol. Brain Res. 10:299-305(1991).
-!- FUNCTION: Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G(O) (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the APP family.
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; X56129; CAA39594.1; -; mRNA.
HSP; P08592; INMJ.
InterPro; IPR008155; A4 APP.
InterPro; IPR001255; Beta-APP.
PANTHER; PTHR10083:SF6; Beta-APP; 1.
Pfam; PF03494; Beta-APP; 1.
PRINTS; PR00204; BETAAMYLOID.
PROSITE; PS00319; A4 EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Amyloid; Transmembrane.
CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 93.1%; Score 27; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 21 KLVFFA 26

RESULT 58
A4_SHEEP
ID A4_SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).

fragment 57)] (Fragment).

Name=APP;
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
[1]
NUCLEOTIDE SEQUENCE.
TISSUE=Heart;
MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F; Johnston E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";
Brain Res. Mol. Brain Res. 10:299-305(1991).
-!- FUNCTION: Functional neuronal receptor which couples to intracellular signaling pathway through the GTP-binding protein G(O) (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Belongs to the APP family.
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

EMBL; X56130; CAA39595.1; -; mRNA.
HSP; P08592; INMJ.
InterPro; IPR008155; A4 APP.
InterPro; IPR001255; Beta-APP.
PANTHER; PTHR10083:SF6; Beta-APP; 1.
Pfam; PF03494; Beta-APP; 1.
PRINTS; PR00204; BETAAMYLOID.
PROSITE; PS00319; A4 EXTRA; PARTIAL.
PROSITE; PS00320; A4_INTRA; PARTIAL.
Amyloid; Transmembrane.
CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

Query Match 93.1%; Score 27; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 21 KLVFFA 26

RESULT 59
A4_BOVIN
ID A4_BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42); Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal fragment 57)] (Fragment).

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
 DE C-terminal fragment 59); Gamma-CTF(59) (Gamma-secretase C-terminal
 DE fragment 57)] (Fragment).
 DE Name=APP;
 OS Ursus maritimus (Polar bear) (Thalarchos maritimus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
 OC Ursus.
 OX NCBI_TaxID=29073;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=156157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; X56128; CAA39593.1; -; mRNA.
 DR PIR; B60045; B60045.
 DR HSP; P08592; INMW.
 DR InterPro; IPR008155; A4_APP.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Transmembrane.
 FT CHAIN <1 5 Soluble APP-beta (By similarity).
 FT CHAIN 6 >57 CTF-alpha (By similarity).
 FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
 FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
 FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
 FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
 FT TOPO_DOM <1 33 Extracellular (Potential).
 FT TRANSMEM 34 57 Potential.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6172 MW; 84209D88BA82DFA CRC64;
 Query Match 93.1%; Score 27; DB 1; Length 57;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 |:|:|
 DB 21 KLVFFA 26
 RESULT 56
 A4 CANFA STANDARD; PRT; 58 AA.
 ID A4 CANFA
 AC Q28280;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
 DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
 DE fragment 57)] (Fragment).
 GN Name=APP;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=92017079; PubMed=156157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC EMBL; X56125; CAA39590.1; -; mRNA.
 DR HSP; P08592; INMW.
 DR Ensembl; ENSCAFG00000008557; Canis familiaris.
 DR InterPro; IPR008155; A4_APP.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Transmembrane.
 FT CHAIN <1 6 Soluble APP-beta (By similarity).
 FT CHAIN 7 >58 CTF-alpha (By similarity).
 FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
 FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
 FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
 FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
 FT TOPO_DOM <1 34 Extracellular (Potential).
 FT TRANSMEM 35 58 Potential.
 FT NON_TER 1 1
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
 Query Match 93.1%; Score 27; DB 1; Length 58;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLVFFA 6
 |:|:|
 DB 22 KLVFFA 27
 RESULT 57
 A4 RABIT STANDARD; PRT; 58 AA.
 ID A4 RABIT
 AC Q28748;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);

DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Amyloid beta protein (Fragment).
 OS Grampus griseus (Risso's dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Odontoceti; Delphinidae; Grampus.
 NCBI_TaxID=83653;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sarasa M.;
 RT "The molecular machinery of Alzheimer's disease in the dolphin.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY926589; AAX81918.1; -, mRNA.
 FT NON_TER 1 1
 FT NON_TER 42 42
 SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

 Query Match 93.1%; Score 27; DB 2; Length 42;
 Best Local Similarity 83.3%; Pred. No. 92;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 KIVFFA 6
 Db 16 KLVFFA 21

 RESULT 52
 ID Q56JJ7 TURTR PRELIMINARY; PRT; 42 AA.
 AC Q56JJ7;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE Amyloid beta protein (Fragment).
 OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
 OC Odontoceti; Delphinidae; Tursiops.
 NCBI_TaxID=9739;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gallego C., Sarasa M.;
 RT "The molecular machinery of Alzheimer's disease in the dolphin.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY926588; AAX81917.1; -, mRNA.
 FT NON_TER 1 1
 FT NON_TER 42 42
 SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

 Query Match 93.1%; Score 27; DB 2; Length 42;
 Best Local Similarity 83.3%; Pred. No. 92;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 KIVFFA 6
 Db 16 KLVFFA 21

 RESULT 53
 ID Q7M088 CAVPO PRELIMINARY; PRT; 42 AA.
 AC Q7M088;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Beta-amyloid protein (Fragment).
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 OC Hystricognathi; Caviidae; Cavia.
 NCBI_TaxID=10141;
 RN [1]

RP PROTEIN SEQUENCE.
 RX MEDLINE=3290653; PubMed=7685598;
 RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
 RA Kamiya H., Ohno M.;
 RT "Receptor-mediated specific biological activity of a beta-amyloid
 RT protein fragment for NK-1 substance P receptors.";
 RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
 DR PIR; P0512; P0512.
 DR HSP; Q16019; I1YT.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 FT NON_TER 1 1
 FT NON_TER 42 42
 SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

 Query Match 93.1%; Score 27; DB 2; Length 42;
 Best Local Similarity 83.3%; Pred. No. 92;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 KIVFFA 6
 Db 16 KLVFFA 21

 RESULT 54
 ID Q8WZ99 HUMAN PRELIMINARY; PRT; 52 AA.
 AC Q8WZ99;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE Amyloid protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15203367; DOI=10.1136/jnnp.2003.010611;
 RA Wakutani Y., Watanabe K., Adachi Y., Wada-Isoe K., Urakami K.,
 RA Ninomiya H., Saido TC., Hashimoto T., Iwatsubo T., Nakashima K.;
 RT "Novel amyloid precursor protein gene missense mutation (D678N) in
 RT probable familial Alzheimer's disease.";
 RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).
 DR EMBL; AB066441; BAB71958.2; -, mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 FT NON_TER 1 1
 FT NON_TER 52 52
 SQ SEQUENCE 52 AA; 5597 MW; 3F0E8E9EC18011AD CRC64;

 Query Match 93.1%; Score 27; DB 2; Length 52;
 Best Local Similarity 83.3%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 KIVFFA 6
 Db 16 KLVFFA 21

 RESULT 55
 ID A4 URSWA STANDARD; PRT; 57 AA.
 AC Q29149;
 DT 01-NOV-1997 (Rel. 35, Created)

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Stapleton J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Carlson M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AEO03589; AAS64635.1; -; Genomic_DNA.
DR InterPro: IPR011990; TPR-like_helical.
DR InterPro: IPR001680; WD40.
DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1503 AA; 167957 MW; A0DDDF3532590486 CRC64;
Query Match 96.6%; Score 28; DB 2; Length 1503;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
DB 1264 KLIFFA 1269
RESULT 49
ID Q8A6R7_BACTN PRELIMINARY; PRT; 1676 AA.
AC Q8A6R7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Conserved protein, with weak HamHI domain.
GN OrderedLocusNames=Bt1809;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_Taxid=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL: AB016933; AAO76916.1; -; Genomic_DNA.
DR InterPro: IPR002048; EF-hand.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1676 AA; 193673 MW; 28065878C0F6C961 CRC64;
Query Match 96.6%; Score 28; DB 2; Length 1676;
Best Local Similarity 83.3%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
DB 1656 KLIFFA 1661
RESULT 50
Q9UC33 HUMAN
ID Q9UC33 HUMAN PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Beta-amyloid peptide (Fragment).
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_Taxid=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids.";
RL Nature 359:325-327(1992).
DR HSSP: Q16019; 1BA4.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0005488; F:binding; IEA.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PRO0204; BETAAMYLOID.
DR PROSITE: PS00204; BETAAMYLOID.
SQ SEQUENCE 33 AA; 3674 MW; B1DEFE2F4167ABD0 CRC64;
Query Match 93.1%; Score 27; DB 2; Length 33;
Best Local Similarity 83.3%; Pred. No. 74;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
DB 16 KLVFFA 21
RESULT 51
ID Q56JU6_GRAGR PRELIMINARY; PRT; 42 AA.
AC Q56JU6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hopkins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003589; AAF51483.1; -; Genomic_DNA.
DR FlyBase; FBgn0031262; Oeeg3.
DR GO; GO:0005488; F-binding, IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1443 AA; 161316 MW; A8C5997678040B88 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1443;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1204 KIIFFA 1209

RESULT 47
Q5BI64 DROME PRELIMINARY; PRT; 1458 AA.
AC Q5BI64;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE LP14662p.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT021360; AAX33508.1; -; mRNA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1458 AA; 163133 MW; 2D704C8970E541EC CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1458;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1219 KIIFFA 1224

RESULT 48
Q7KTZ4 DROME PRELIMINARY; PRT; 1503 AA.
AC Q7KTZ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG11838-PB, isoform B.
GN Name=Oeeg3; ORFNames=CG11838;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gdycayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foerster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

```

RESULT 44
Q68K27 CHLRE
ID Q68K27_CHLRE PRELIMINARY; PRT; 1384 AA.
AC Q68K27;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Intraflagellar transport particle protein 140.
GN Name=IFT140;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Walker B.L., Hou Y., Dentler W.L., Witman G.B., Pazour G.J.;
RT "Intraflagellar transport protein IFT140."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY686103; AAT95430.1; -; mRNA.
DR GO; GO:0019861; C:flagellum; IEA.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 5.
DR TIGRPfam; TIGR00756; PPR; 2.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Flagellum.
SQ SEQUENCE 1384 AA; 154603 MW; 5D3E70C8440DABCD CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1384;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
Db 1154 KIIFPA 1159

RESULT 45
Q7QEF0 ANOQA
ID Q7QEF0_ANOQA PRELIMINARY; PRT; 1408 AA.
AC Q7QEF0;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ENSANGP0000001545 (Fragment).
GN ORFNames=ENSANG0000001308;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL "Anopheles gambiae re-annotation."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; ARA0100847; EAA06955.1; -; Genomic_DNA.
DR GO; GO:0005488; P:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.

```

```

FT NON_TER 1408 1408
SQ SEQUENCE 1408 AA; 157382 MW; FF63317DAB976DB2 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1408;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
Db 1212 KIIFPA 1217

RESULT 46
Q9VPR0 DROME
ID Q9VPR0_DROME PRELIMINARY; PRT; 1443 AA.
AC Q9VPR0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 26, Last annotation update)
DE CG11838-PA, isoform A.
GN Name=Oseg3; ORFNames=CG11838;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Fabros B., Deicher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gortell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swiras R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

```

```

RESULT 42
QBR410_MOUSE
ID QBR410_MOUSE PRELIMINARY; PRT; 1145 AA.
AC QBR410;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ICR;
RA Hagiwara K., Endo Y., Xin H., Takahashi M., Huguin, Nukiwa T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY090567; AAM11887.1; -; mRNA.
DR HSSP; P29477; 1DWV.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005829; C:cytosol; ISS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042803; P:protein homodimerization activity; IDA.
DR GO; GO:0024742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0001542; P:ovulation (sensu Mammalia); IMP.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. .; ISS.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxred FAD/NAD(P).
DR Pfam; PF00667; FAD binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130685 MW; DAD5AAPF53680B005 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1145;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 515 KIVFFA 520

RESULT 43
Q6P6A0_MOUSE
ID Q6P6A0_MOUSE PRELIMINARY; PRT; 1145 AA.
AC Q6P6A0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Nos2 protein.

```

```

GN OS
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.F., Heif F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062378; AAH62378.1; -; mRNA.
DR HSSP; P29477; 1WKG.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0042803; P:protein homodimerization activity; IDA.
DR GO; GO:0042742; P:defense response to bacteria; IMP.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006801; P:superoxide metabolism; IMP.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin like.
DR InterPro; IPR008254; Flav nitox synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxred FAD/NAD(P).
DR Pfam; PF00667; FAD binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD binding_1; 1.
DR Pfam; PF02898; NO synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130671 MW; C26E09F536923295 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1145;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 515 KIVFFA 520

```


pterins.";

RT Biochemistry 39:4608-4621(2000).

RL [12]

RR X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF TRP-457 MUTANTS.

RD MEDLINE=21526413; PubMed=11669619; DOI=10.1021/bi011183k;

RE Aoyagi M., Arvai A.S., Ghosh S., Stuehr D.J., Tainer J.A.,

RF Getzoff E.D.;

RA "Structures of tetrahydrobiopterin binding-site mutants of inducible

RR nitric oxide synthase oxygenase dimer and implicated roles of

RT Trp457.";

RL Biochemistry 40:12826-12832(2001).

RR [13]

RR X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.

RD MEDLINE=22325496; PubMed=12437348; DOI=10.1021/bi026313j;

RE Rosenfeld R.J., Garcin E.D., Panda K., Andersson G., Aberg A.,

RF Wallace A.V., Morris G.M., Olson A.J., Stuehr D.J., Tainer J.A.,

RA Getzoff E.D.;

RR "Conformational changes in nitric oxide synthases induced by

RT chlorzoxazone and nitroindazoles: crystallographic and computational

RT analyses of inhibitor potency.";

RL Biochemistry 41:13915-13925(2002).

RR [14]

RR X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 77-495.

RD MEDLINE=22351711; PubMed=12464241; DOI=10.1016/S0003-9861(02)00555-6;

RE Fedorov R., Ghosh D.K., Schlichting I.;

RF "Crystal structures of cyanide complexes of P450cam and the oxygenase

RR domain of inducible nitric oxide synthase - structural models of the

RT short-lived oxygen complexes.";

RL Arch. Biochem. Biophys. 409:25-31(2003).

CC -1- FUNCTION: Produces nitric oxide (NO) which is a messenger molecule

CC with diverse functions throughout the body. In macrophages, NO

CC mediates tumoricidal and bactericidal actions.

CC -1- CATALYTIC ACTIVITY: L-arginine + n NADPH + m O(2) = citrulline +

CC nitric oxide + n NADP(+).

CC -1- COFACTOR: Heme.

CC -1- COFACTOR: FAD. Binds 1 mole of FAD.

CC -1- COFACTOR: FMN. Binds 1 mole of FMN.

CC -1- COFACTOR: Tetrahydrobiopterin (BH4). May stabilize the dimeric

CC form of the enzyme.

CC -1- ENZYME REGULATION: Not stimulated by calcium/calmodulin. Aspirin

CC inhibits expression and function of this enzyme and effects may be

CC exerted at the level of translational/posttranslational

CC modification and directly on the catalytic activity.

CC -1- SUBUNIT: Homodimer. Binds SLC9A3R1 (By similarity).

CC -1- TISSUE SPECIFICITY: Macrophages.

CC -1- INDUCTION: By treatment with endotoxins or cytokines.

CC -1- SIMILARITY: Belongs to the NOS family.

CC -1- SIMILARITY: Contains 1 flavodoxin-like domain.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

DR EMBL; M87039; AAA39315.1; -; mRNA.

DR EMBL; M92549; -; NOT ANNOTATED CDS; mRNA.

DR EMBL; M84373; AAA39834.1; -; mRNA.

DR EMBL; U43428; AAC52356.1; -; mRNA.

DR EMBL; AF065919; AAC17914.1; -; mRNA.

DR EMBL; AF065920; AAC17915.1; -; mRNA.

DR EMBL; AF065921; AAC17916.2; -; mRNA.

DR EMBL; AF065922; AAC17917.2; -; mRNA.

DR EMBL; AF065923; AAC17918.2; -; mRNA.

DR F01; A43271; A43271.

DR PDB; 1DD7; X-ray; A=114-498.

DR PDB; 1DF1; X-ray; A/B=77-499.

DR PDB; 1DWV; X-ray; A/B=77-496.

DR PDB; 1DWW; X-ray; A/B=77-496.

DR PDB; 1DWX; X-ray; A/B=77-496.

DR PDB; 1JWJ; X-ray; A/B=66-498.

DR PDB; 1JWK; X-ray; A/B=66-498.

DR PDB; 1M8D; X-ray; A/B=65-498.

AC O9GLV6;
 DT 01-MAR-2001 (TRENBLrel. 16, Created)
 DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE RNA helicase.
 GN Name=RHIV-1;
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
 OC Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20261798; PubMed=10799277; DOI=10.1006/mpat.1999.0349;
 RA Zhang X., Wang C., Schook L.B., Hawken R.J., Rutherford M.S.;
 RT "An RNA helicase, RHIV -1, induced by porcine reproductive and
 RT respiratory syndrome virus (PRRSV) is mapped on porcine chromosome
 RT 10q13.";
 RL Microb. Pathog. 28:267-278(2000).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AF181119; AAG09428.1; -; mRNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004386; F:helicase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR011545; DEAD/DEAF_N.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELIC; 1.
 KW Helicase, Hydrolase, Nuclear protein; Repeat.
 SQ SEQUENCE 940 AA; 107584 MW; 118CA910B0AF7821 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 940;
 Best Local Similarity 83.3%; Pred. No. 7.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 290 KIVFFA 295
 RESULT 40
 ID NOS2 MOUSE STANDARD; PRT; 1144 AA.
 AC P29477; O70515; O70516;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
 DE (Inducible NOS) (iNOS) (Macrophage NOS) (MAC-NOS).
 GN Name=Nos2; Synonyms=Inos1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92229444; PubMed=1373522;
 RA Xie Q.-W., Cho H.-J., Calaycay J.J., Munford R.A., Swiderek K.M.,
 RA Lee T.-D., Ding A., Troso T., Nathan C.;
 RT "Cloning and characterization of inducible nitric oxide synthase from
 RT mouse macrophages.";
 RL Science 256:225-228(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92357701; PubMed=1379716;
 RA Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;
 RT "Cloned and expressed macrophage nitric oxide synthase contrasts with
 RT the brain enzyme.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
 RN [3]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92210618; PubMed=1372907;
 RA Lyons C.R., Orloff G.J., Cunningham J.M.;
 RT "Molecular cloning and functional expression of an inducible nitric
 RT oxide synthase from a murine macrophage cell line.";
 RL J. Biol. Chem. 267:6370-6374(1992).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96088781; PubMed=7503239;
 RA Kone B.C., Schweibel J., Turner P., Mohaupt M.G., Cangro C.B.;
 RT "Role of NF-kappa B in the regulation of inducible nitric oxide
 RT synthase in an MTL cell line.";
 RL Am. J. Physiol. 269:F718-F729(1995).
 RN [5]
 RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-211; LEU-967 AND PHE-968.
 RX STRAIN=B10.S/J, BALB/cBYJ, DBA/2J, NOD/LtJ, and SJL/J; TISSUE=Spleen;
 RC MEDLINE=99370037; PubMed=10438970;
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
 RA Blankenhorn E.P.;
 RT "Sequence polymorphisms in the chemokines Sca1 (TCA-3), Sca2
 RT (monocyte chemoattractant protein (MCP)-1), and Sca12 (MCP-5) are
 RT candidates for eae7, a locus controlling susceptibility to monophasic
 RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
 RL J. Immunol. 163:2262-2266(1999).
 RN [6]
 RP EFFECT OF ASPIRIN.
 RC TISSUE=Macrophage;
 RX MEDLINE=95372392; PubMed=7544010;
 RA Anin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,
 RA Weismann G., Abramson S.B.;
 RT "The mode of action of aspirin-like drugs: effect on inducible nitric
 RT oxide synthase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.
 RX MEDLINE=97477482; PubMed=9334294; DOI=10.1126/science.278.5337.425;
 RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Ghosh D.K., Getzoff E.D.,
 RA Stuehr D.J., Tainer J.A.;
 RT "The structure of nitric oxide synthase oxygenase domain and inhibitor
 RT complexes.";
 RL Science 278:425-431(1997).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
 RX MEDLINE=98182450; PubMed=9516116; DOI=10.1126/science.279.5359.2121;
 RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,
 RA Tainer J.A.;
 RT "Structure of nitric oxide synthase oxygenase dimer with pterin and
 RT substrate.";
 RL Science 279:2121-2126(1998).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
 RX MEDLINE=20031637; PubMed=10562538; DOI=10.1093/emboj/18.22.6260;
 RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,
 RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;
 RT "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin
 RT hook and pterin-binding segment in dimerization and
 RT tetrahydrobiopterin interaction.";
 RL EMBO J. 18:6260-6270(1999).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.
 RX MEDLINE=20031638; PubMed=10562539; DOI=10.1093/emboj/18.22.6271;
 RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,
 RA Tainer J.A., Stuehr D.J., Getzoff E.D.;
 RT "N-terminal domain swapping and metal ion binding in nitric oxide
 RT synthase dimerization.";
 RL EMBO J. 18:6271-6281(1999).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
 RX MEDLINE=20233702; PubMed=10769116; DOI=10.1021/bi992409a;
 RA Crane B.R., Arvai A.S., Ghosh S., Getzoff E.D., Stuehr D.J.,
 RA Tainer J.A.;
 RT "Structures of the N(omega)-hydroxy-L-arginine complex of inducible
 RT nitric oxide synthase oxygenase dimer with active and inactive

```

O95786 HUMAN
ID O95786 HUMAN PRELIMINARY; PRT; 925 AA.
AC O95786;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Name=DDX58; Synonyms=RIG-I;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sun Y.W.;
RT "RIG-I, a human homolog gene of RNA helicase, is induced by retinoic
acid during the differentiation of acute promyelocytic leukemia
cell.";
RL Thesis (1997), Shanghai Institute of Hematology, Rui-Jin Hospital,
Shanghai Second Medical University.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Yi-Wu S.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038963; AAD19826.1; -; mRNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR HGNC; HGNC:19102; DDX58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0001661; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR Helicase.
SQ SEQUENCE 925 AA; 106613 MW; 5922B4F3DD0F00D4 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 292 KVVFFA 297
|:|||||

RESULT 37
Q5VYTL HUMAN
ID Q5VYTL HUMAN PRELIMINARY; PRT; 925 AA.
AC Q5VYTL;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE OTHUMP00000021185.
GN Names=RP11-334P12.2; ORFNames=RP11-334P12.2-001;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doggett S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

```

```

RA Sehra H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AL353671; CAH71251.1; -; Genomic DNA.
DR EMBL; AL161783; CAH72600.1; -; Genomic DNA.
DR EMBL; AL161783; CAH71251.1; JOINED; Genomic DNA.
DR EMBL; AL353671; CAH72600.1; JOINED; Genomic DNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR Helicase; Hydrolase; Nuclear protein.
KW Helicase; 925 AA; 106600 MW; BF0D501C395BAE25 CRC64;
SQ SEQUENCE 925 AA; 106600 MW; BF0D501C395BAE25 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 292 KVVFFA 297
|:|||||

RESULT 38
Q6Q899 MOUSE
ID Q6Q899 MOUSE PRELIMINARY; PRT; 926 AA.
AC Q6Q899;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DEAD/H box polypeptide RIG-I.
GN Name=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wei J.; Gu J.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY553221; AAS59532.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR006935; ResIII.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF04851; ResIII; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR Helicase.
SQ SEQUENCE 926 AA; 105877 MW; 632462010107698E CRC64;

Query Match 96.6%; Score 28; DB 2; Length 926;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 293 KVVFFA 298
|:|||||

RESULT 39
Q9GLV6 FIG
ID Q9GLV6 FIG PRELIMINARY; PRT; 940 AA.

```

QY 1 KIVFFA 6
DB 564 KIVFFA 569

RESULT 35
Q9GQ82 DROME
ID Q9GQ82_DROME PRELIMINARY; PRT; 785 AA.
AC Q9GQ82;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Aspartyl beta-hydroxylase variant 1 (CG8421-PA, isoform A).
GN Name=Aph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
RA Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
RA O'Neill K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
RA Friedman P.A.;
RT "Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved
RT isoform of Asph missing the catalytic domain share exons with
RT junctin.";
RL J. Biol. Chem. 275:39543-39554(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.R., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brattier P.,
RA Burtis K.C., Buesan D.A., Butler H., Cadiieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.B., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laspo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.M., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kimms I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacle J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF289493; AAG40806.1; -; mRNA.
DR EMBL; AB003808; AAM70947.1; -; Genomic DNA.
DR Ensembl; CG8421; Drosophila melanogaster.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
DR GO; GO:0030376; C:integral to endoplasmic reticulum membrane; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004597; F:peptide-aspartate beta-dioxygenase activity; IEA.
DR GO; GO:0018193; P:peptide-amino acid modification; IEA.
DR InterPro; IPR007803; Asp Arg Hydrol.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR011990; TPR-like helical.
DR Pfam; PF05118; Asp Arg Hydrol; 1.
DR PROSITE; PS0293; TPR_REGION; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 785 AA; 89843 MW; 30ABDFCD6836F7F1 CRC64;

Query Match 96.6% Score 28; DB 2; Length 785;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;

*Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

Db 53 KIVFFA 58

RESULT 36

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RL melanogaster euchromatic genome sequence.";
 RN Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Priese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective.";
 RN Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 RP NUCLEOTIDE SEQUENCE.
 RX Berkeley Drosophila Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- INTERACTION;
 CC O46085:IG:63B12.5; NExp=1; IntAct=EBI-123244, EBI-151469;
 DR EMBL; AS003808; AAF58064.2; -; Genomic_DNA.
 DR Ensembl; CG8421; Drosophila melanogaster.
 DR FlyBase; FBgn0034075; CG8421.
 DR FlyBase; FBgn0034075; CG8421.
 SQ SEQUENCE 556 AA; 63144 MW; B420980CBDC6357A CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 556;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 53 KIIFFA 58
 RESULT 33
 QSHYEL HUMAN
 ID QSHYEL1 HUMAN PRELIMINARY; PRT; 703 AA.
 AC QSHYEL1
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein DKF2p686N19181 (Fragment).
 GN Name=DKF2p686N19181;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa;
 OC Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skin endothel;

RG The German cDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Meves H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 RN EMBL; BX647917; CAI46068.1; -; mRNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004386; F:Helicase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR011545; DEAD/DEAH N.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICc; 1.
 KW Hypothetical protein.
 FT NON TER 703
 SQ SEQUENCE 703 AA; 80308 MW; 3CF7500F4F955586 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 703;
 Best Local Similarity 83.3%; Pred. No. 6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFEA 6
 DB 247 KVVFFA 252
 RESULT 34
 QGAG25 LEIXX
 ID QGAG25 LEIXX PRELIMINARY; PRT; 721 AA.
 AC QGAG25;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE ATP-dependent RNA helicase.
 GN OrderedLocustNames=LXX07490;
 OS Leifsonia xylis (subsp. xylis).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococcineae; Microbacteriaceae; Leifsonia.
 OX NCBI_TaxID=59736;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CTCB07;
 RX PubMed=15305603;
 RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
 RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
 RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
 RA Takita M.A., da Silva A.C.R., Furian L.R., Carraro D.M., Camarotte G.,
 RA Almeida N.F., Jr., Carrier H., Coutinho L.L., El-Dorri H.A.,
 RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
 RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
 RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
 RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
 RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;
 RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
 RT xylis subsp. xylis.";
 RL Mol. Plant Microbe Interact. 17:827-836(2004).
 DR EMBL; AE016822; BAF88670.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004386; F:Helicase activity; IEA.
 DR InterPro; IPR011545; DEAD/DEAH N.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDC; 1.
 DR SMART; SM00490; HELICc; 1.
 KW Complete proteome; DNA-binding; Helicase; Hydrolase.
 SQ SEQUENCE 721 AA; 78860 MW; 73F5D2A8435BADE3 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 721;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
RESULT 30
O59243_PYRHO
ID O59243_PYRHO PRELIMINARY; PRT; 447 AA.
AC O59243;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PH1606.
GN OrderedLocusNames=PH1606;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Savada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hoshizawa A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Rushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:53-76(1998).
DR EMBL; BA000001; BAA30718.1; -; Genomic_DNA.
DR PIR; F71039; F71039.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005355; F:glucose transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000803; Gluc_transporter.
DR PRINTS; PR00172; GLUCRNSPORT.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 447 AA; 51173 MW; 509F45A302D3B059 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 447;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIVFFA 6
DB 207 KIIFFA 212

RESULT 31
O95S93_DROME
ID O95S93_DROME PRELIMINARY; PRT; 556 AA.
AC O95S93;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GM052229p.
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RC Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY060905; AAL28453.1; -; mRNA.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
SQ SEQUENCE 556 AA; 63089 MW; 95D82EAC57D11FE8 CRC64;
```

```
Query Match 96.6%; Score 28; DB 2; Length 556;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIVFFA 6
DB 53 KIIFFA 58

RESULT 32
O9V719_DROME
ID O9V719_DROME PRELIMINARY; PRT; 556 AA.
AC O9V719;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8421-PD, isoform D (CG8421-pe, isoform e).
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
```

OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=21085660; PubMed=11127851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner T., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690 (2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayashizaki Y., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Konno H., Akiyama J., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada K.,
 RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kaehiwa K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Osawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanganaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Oheato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL: AK078287; BAC37205.1; -; mRNA.
 DR Ensembl: ENSMUSG0000040296; Mus musculus.
 DR MGI: MGI:2442858; Ddx58.
 DR GO: GO:0005524; F:ATP binding; IEA.
 DR GO: GO:0004386; F:helicase activity; IEA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR Pfam: PF00270; DEAD; 1.
 DR SMART: SM00487; DEXDC; 1.
 KW Helicase; Hypothetical protein; Nuclear protein.
 SQ SEQUENCE 410 AA; 46841 MW; ECC9E3D2D2BC5FE0 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 410;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 293 KVVFFA 298
 ID 1:|||||
 RESULT 29
 Q9PHV5 CAMJF
 ID Q9PHV5 CAMJF PRELIMINARY; PRT; 442 AA.
 AC Q9PHV5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative integral membrane protein.
 GN OrderedLocustNames=Cj0560;
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCTC 11168;
 RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
 RA Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
 RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrell B.G.;
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668 (2000).
 DR EMBL: AL139075; CAB75196.1; -; Genomic_DNA.
 DR FIR; H81402; H81402.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0015297; F:antipporter activity; IEA.
 DR GO: GO:0015238; F:drug transporter activity; IEA.
 DR GO: GO:0006855; P:multidrug transport; IEA.
 DR InterPro: IPR002114; HPR_SerP_S.
 DR InterPro: IPR002528; MatE.
 DR Pfam: PF01554; MatE; 1.
 DR TIGRFAMs: TIGR00797; matE; 1.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 442 AA; 49452 MW; 38EA04E7AB1A8F3E CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 442;
 Best Local Similarity 83.3%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 313 KVVFFA 318
 ID 1:|||||

```

DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane;
SQ SEQUENCE 387 AA; 41104 MW; DC7CD48C609FBA3 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|||||
Db 184 KVVFFA 189

RESULT 26
Q81SK9 BACAN
ID Q81SK9_BACAN PRELIMINARY; PRT; 387 AA.
AC Q81SK9_Q610U3; Q6KUP8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Germination protein GerN.
GN OrderedLocNames=Ba1639, BAS1521, GBA1639;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.B., Tettelin S., Fouts D.E., Eseen J.A., Gill S.R.,
RA Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri I.H., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomas B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.P., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics."
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN-Sterne;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne."
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017029; AAP25572.1; --; Genomic DNA.
DR EMBL; AE017334; AAT30749.1; --; Genomic DNA.
DR EMBL; AE017225; AAT53839.1; --; Genomic DNA.
DR TIGR; BA1639; --.
DR TIGR; GBA1639; --.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.

DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 40932 MW; D59FA08A283BCA3 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|||||
Db 184 KVVFFA 189

RESULT 27
Q6L2B4 PICTO
ID Q6L2B4_PICTO PRELIMINARY; PRT; 410 AA.
AC Q6L2B4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lipopolysaccharide N-acetylglucosaminyltransferase.
GN OrderedLocNames=PT0303;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
RA Schepers B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AE017261; AAT42888.1; --; Genomic DNA.
DR GO; GO:0016757; F:transferase activity; transferring glycosyl. --; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
DR InterPro; IPR001296; Glyco_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 410 AA; 48120 MW; C192F0152E66E9B0 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 410;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|||||
Db 235 KIIFFA 240

RESULT 28
Q8CS13 MOUSE
ID Q8CS13_MOUSE PRELIMINARY; PRT; 410 AA.
AC Q8CS13;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:6430573D20 product:hypothetical DEAD/DEAH box
DE helicase containing protein, full insert sequence.
GN Name=Bdx38;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.

```



```

OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax."
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA001000008; EAL15336.1; -; Genomic DNA.
SQ SEQUENCE 387 AA; 41122 MW; 15CC136E79B12C38 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 184 KVVFFA 189

RESULT 23
Q63DD4_BACCZ
ID Q63DD4_BACCZ PRELIMINARY; PRT; 387 AA.
AC Q63DD4;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18770.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRfams; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41090 MW; DBA5991FDD63F33 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 184 KVVFFA 189

RESULT 24
Q6HKU6_BACHK
ID Q6HKU6_BACHK PRELIMINARY; PRT; 387 AA.
AC Q6HKU6;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Na+/H+ exchanger family protein.
GN Name=gerN; OrderedLocusNames=BT9727_1493;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=97-27;
RC Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017355; AAT63168.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRfams; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41076 MW; DFECAD90985F951 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 184 KVVFFA 189

RESULT 25
Q73AP3_BACCI
ID Q73AP3_BACCI PRELIMINARY; PRT; 387 AA.
AC Q73AP3;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE Germination protein gerN.
GN OrderedLocusNames=BCCE1729;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXOI."
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017269; AA940658.1; -; Genomic DNA.
DR TIGR; BCE1729; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.

```


RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser M.D., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Friese E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S.J., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT *melanogaster* euchromatid genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Friese E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celinker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatid:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celinker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.N., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RX Berkeley *Drosophila* Genome Project;
RA Celinker S., Carlson J., Wan K., Pfeiffer B., Friese E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "*Drosophila melanogaster* release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RX FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
RA Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
RA O'Neil K.T., Pocht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
RA Friedman P.A.;

RT "Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved
RT isoform of Asph missing the catalytic domain share exons with
RT junction.";
RL J. Biol. Chem. 275:39543-39554(2000).
DR EMBL; AF003908; AAF58063.2; -; Genomic_DNA.
DR EMBL; AF289494; AAG40807.1; -; mRNA.
DR Ensembl; CG8421; *Drosophila melanogaster*.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
SQ SEQUENCE 382 AA; 43287 MW; 60E5C03AEBFC6E8B CRC64;

Query Match 96.6%; Score 28; DB 2; Length 382;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|||
Db 53 KIIFFA 58

RESULT 21

Q9K110_BACCE
ID Q9K110_BACCE PRELIMINARY; PRT; 387 AA.
AC Q9K110;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GerN.
GN Name=gerN;
OS *Bacillus cereus*.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*;
OC *Bacillus cereus* group.
OX NCBI_TaxID=1396;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=ATCC10876;
RC MEDLINE=20576148; PubMed=11133940; DOI=10.1128/JB.183.2.476-482.2001;
RA Thackray P.D., Behravan J., Southworth T.W., Moir A.;
RT "GerN, an antiporter homologue important in germination of *Bacillus*
RT *cereus* endospores.";
RL J. Bacteriol. 183:476-482(2001).
DR EMBL; AF246294; AAF91326.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; P:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41093 MW; 40DE45B71B715D01 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|||
Db 184 KIVFFA 189

RESULT 22

Q4WT39_BACCE
ID Q4WT39_BACCE PRELIMINARY; PRT; 387 AA.
AC Q4WT39;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Na+/H+ antiporter
GN ORFNames=BCE_G3241_1647;

```

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=306264;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RM3195;
RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
RA Nelson K.E.;
RT "Major structural and novel potential virulence mechanisms from the
RT genomes of multiple Campylobacter species.";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AFJ01000002; EAL53713.1; -; Genomic DNA.
SQ SEQUENCE 362 AA; 40365 MW; 1580A8B12D60CAED CRC64;

Query Match 96.6%; Score 28; DB 2; Length 362;
Best Local Similarity 83.3%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KIVFFA 6
Db 132 KIVFFA 137

RESULT 18
Q6D7U3 ERWCT
ID Q6D7U3_ERWCT PRELIMINARY; PRT; 372 AA.
AC Q6D7U3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hydrogenase isoenzymes formation protein.
GN Name=hypD; OrderedLocusNames=ECA1232;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmon G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004).
DR EMBL; BX950851; CAG74142.1; -; Genomic DNA.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PRSF; PRSF005622; Hydrn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
SQ Complete proteome.
QY SEQUENCE 372 AA; 41130 MW; A001A18AC015E620 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 372;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 139 KIVFFA 144

```

```

RESULT 19
Q7M9N5_WOLSU
ID Q7M9N5_WOLSU PRELIMINARY; PRT; 373 AA.
AC Q7M9N5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE HYDROGENASE PROTEIN.
GN Name=hypD; OrderedLocusNames=WS0793;
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSMZ 1740;
RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695 (2003).
DR EMBL; BX571659; CAE09906.1; -; Genomic DNA.
DR InterPro; IPR002780; HypD.
DR Pfam; PF01924; HypD; 1.
DR PRSF; PRSF005622; Hydrn_mat_hypD; 1.
DR TIGRFAMs; TIGR00075; hypD; 1.
KW Complete proteome.
SQ SEQUENCE 373 AA; 41793 MW; 3B7815EDB25790A6 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 373;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 138 KIVFFA 143

RESULT 20
Q9V7J0_DROME
ID Q9V7J0_DROME PRELIMINARY; PRT; 382 AA.
AC Q9V7J0; Q9G081;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE C8421-PB, isoform B (Aspartyl beta-hydroxylase variant 2).
GN Name=Asph; ORFNames=C8421;
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=107311132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

```

RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Mateu Y., Nikaide I., Pesole G., Quackenbush J.,
RA Sakai L.M., Stauber P., Suzuki R., Tomita M., Wegner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX STRAIN=C57BL/6J; TISSUE=Heart;
RA The RIKEN Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20499374; PubMed=11041159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipette sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Heart;
RX STRAIN=C57BL/6J; TISSUE=Heart;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Nunazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2001) to the ENBL/GenBank/DBJ databases.
RN

DR EMBL; AK052871; BAC35183.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR Pfam; PF00270; DEAD; 1.
DR SMART; SM00487; DEXdc; 1.
KW Helicase, Hypothetical protein.
FT NON TER 231 231
SQ SEQUENCE 231 AA; 1D191607390D7FBB CRC64;

Query Match 96.6%; Score 28; DB 2; Length 231;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 145 KIVFFA 150
|:|:|:|
|:|:|:|

RESULT 16
Q61C67 CAEBR
ID Q61C67 CAEBR PRELIMINARY; PRT; 315 AA.
AC Q61C67;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG13055 (Fragment).
GN Name=CBG13055;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodirinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C. briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; CAAC01000061; CAB67532.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00262; G PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Hypothetical protein; Receptor;
KW Transducer; Transmembrane.
FT NON TER 1 1
FT NON TER 315 315
SQ SEQUENCE 315 AA; 579B590D01874512 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 315;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 117 KIVFFA 122
|:|:|:|
|:|:|:|

RESULT 17
Q4HSJ7 CAMUP
ID Q4HSJ7 CAMUP PRELIMINARY; PRT; 362 AA.
AC Q4HSJ7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hydrogenase expression/formation protein HypD.
GN Name=HypD; ORFNames=CUP0294;
OS Campylobacter upsaliensis RM3195.

DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE 19 kDa globulin precursor (Alpha-globulin).
 OS Oryza sativa (Rice)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
 RC STRAIN=cv. Japonica / Nipponbare; TISSUE=Endosperm;
 RX MEDLINE=92119226; PubMed=8501968;
 RA Shorosh B.S., Wen L., Zen K.C., Huang J.K., Pan J.S., Hermodson M.A.,
 RA Tanaka K., Muthukrishnan S., Reeck G.R.;
 RT "A novel cereal storage protein: molecular genetics of the 19 kDa
 RT globulin of rice.";
 RL Plant Mol. Biol. 18:151-154 (1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 5-186.
 RC STRAIN=cv. Japonica / Lemont; TISSUE=Endosperm;
 RX MEDLINE=93277591; PubMed=8503935;
 RA Krishnan H.B., Pueppke S.G.;
 RT "Nucleotide sequence of an abundant rice seed globulin: homology with
 RT the high molecular weight glutelins of wheat, rye and triticale.";
 RL Biochem. Biophys. Res. Commun. 193:460-466 (1993).
 CC 1- FUNCTION: Seed storage protein.
 CC 1- SIMILARITY: Belongs to the 2S seed storage albumins family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; X63990; CAA45400.1; -; mRNA.
 DR EMBL; Li2252; AAN72362.1; ALT_INIT; mRNA.
 DR PIR; S20024; WNR219.
 DR HSP; P24565; 1PNE.
 DR Gramene; P29835; -
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001419; Glutenin.
 DR PANTHER; PTHR14054; Glutenin; 1.
 DR Pfam; PF00234; Tryp alpha amyl; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 DR Direct protein sequencing; Seed storage protein; Signal;
 KW Storage protein.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 186 19 kDa globulin.
 SQ SEQUENCE 186 AA; 21050 MW; 9E09BA74CB0B6810 CRC64;
 Query Match 96.6%; Score 28; DB 1; Length 186;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 4 KVVFFA 9
 RESULT 14
 P93414 ORYSA
 ID P93414 ORYSA PRELIMINARY; PRT; 186 AA.
 AC P93414;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE 26 kDa globulin (Alpha-globulin).
 GN Name=P010D04.16; Synonyms=OJ1057_B02.5;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Endosperm;
 RX MEDLINE=96235139; PubMed=8666249; DOI=10.1016/0378-1119(95)00887-X;
 RA Nakase M., Hotta H., Adachi T., Aoki N., Nakamura R., Masumura T.,
 RA Tanaka K., Matsuda T.;
 RT "Cloning of the rice seed alpha-globulin-encoding gene: sequence
 RT similarity of the 5'-flanking region to those of the genes encoding
 RT wheat high molecular-weight glutenin and barley D hordein.";
 RL Gene 170:223-226 (1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RT "Oryza sativa BAC OJ1057 B02 genomic sequence.";
 RT Submitted (AUG-2004) to The EMBL/GenBank/DBJ databases.
 DR EMBL; D50643; BAA09308.1; -; Genomic DNA.
 DR EMBL; AC130605; AAT44292.1; -; Genomic DNA.
 DR EMBL; AC113332; AAT93857.1; -; Genomic DNA.
 DR PIR; JC4784; JC4784.
 DR HSP; P24565; 1PNE.
 DR Gramene; P93414; -
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001419; Glutenin.
 DR Pfam; PF00234; Tryp alpha amyl; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 186 AA; 21055 MW; AE2B8F1107C8BC94 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 186;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 4 KVVFFA 9
 RESULT 15
 Q8C6Y8 MOUSE
 ID Q8C6Y8 MOUSE PRELIMINARY; PRT; 231 AA.
 AC Q8C6Y8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
 DE library, clone:D83015B12 product:hypothetical DEAD/DEAH box helicase
 DE containing protein, full insert sequence. (Fragment).
 GN Name=Ddx58;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

```

FT NON TER 1 1
SQ SEQUENCE 1265 AA; 143403 MW; C9C157ABE90FF928 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1265;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1081 KIVFFA 1086

RESULT 10
Q5F3M1_CHICK PRELIMINARY; PRT; 1412 AA.
AC Q5F3M1;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein.
GN ORFNames=RCJNB04.13m2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Plachy J., Carninci P., Hayaishizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851629; CAH65263.1; -; mRNA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40. 2.
DR SMART; SM00320; WD40. 4.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein.
SQ SEQUENCE 1412 AA; 158448 MW; FA0050885B274747 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 1412;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1225 KIVFFA 1230

RESULT 11
Q4LBQ8_SODGL PRELIMINARY; PRT; 88 AA.
AC Q4LBQ8;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE CheY protein.
GN Name=cheY;
OS Sodalis glossinidius.
OC Plasmodium pSG4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PLASMID=pSG4;
RA Darby A.C., Lagnel J., Matthew C.Z., Bourtsis K., Maudlin I.,
RA Welburn S.C.;
RT "Extrachromosomal DNA of the symbiont Sodalis glossinidius.";

```

```

RL J. Bacteriol. 187:5003-5007(2005).
DR EMBL; AJ868439; CAI59440.1; -; Genomic DNA.
DR EMBL; AJ868438; CAI59427.1; -; Genomic DNA.
KW Plasmid.
SQ SEQUENCE 88 AA; 10177 MW; F4168F2A56B8D0AC CRC64;

Query Match 96.6%; Score 28; DB 2; Length 88;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 42 KIIFFA 47

RESULT 12
Q9RQ09_BACTN PRELIMINARY; PRT; 183 AA.
AC Q9RQ09; O7C422;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE RNA polymerase sigma factor SigZ-like protein (RNA polymerase ECF-type
DE sigma factor).
GN Name=sigZ; OrderedLocusNames=BT1278;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroidales; Bacteroidaceae;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482;
RX MEDLINE=99380605; PubMed=10449780; DOI=10.1073/pnas.96.17.9833;
RA Hooper L.V., Xu J., Falk P.G., Midtvedt T., Gordon J.I.;
RT "A molecular sensor that allows a gut commensal to control its
RT nutrient foundation in a competitive ecosystem.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9833-9838(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550859; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AF137263; AAF01488.1; -; Genomic DNA.
DR EMBL; AE016931; AAO76385.1; -; Genomic DNA.
DR GO; GO:0016987; F:sigma factor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR007627; Sigma70_r2.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF04542; Sigma70_r2; 1.
KW Complete proteome; DNA-binding; DNA-directed RNA polymerase;
KW Nucleotidyltransferase; Sigma factor; Transcription;
KW Transcription regulation; Transferase.
SQ SEQUENCE 183 AA; 22042 MW; 6B24DABC99BEC643 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 183;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 172 KIIFFA 177

RESULT 13
GL19_ORYSA
ID GL19_ORYSA STANDARD; PRT; 186 AA.
AC P29835;
DT 01-APR-1993 (Rel. 25, Created)

```

```

ID Q6RUU2_MOUSE PRELIMINARY; PRT; 663 AA.
AC Q6RUU2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Brathwaite M., Waelitz P., Dudekula D., Nagaraja R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY491413; RAS21643.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 663 AA; 77192 MW; CEB02E3BED356F1C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
DB 433 KIVFFPA 438

RESULT 7
Q83IB2_TROW8 PRELIMINARY; PRT; 690 AA.
AC Q83IB2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative helicase regulator.
GN OrderedLocNames=TW130;
OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=218496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bentley S.D., Maiwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
Dover L.G., Norbertczak H.T., Beara G.S., Quail M.A., Harris D.E.,
von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
Barrell B.G., Parkhill J., Rellman D.A.;
RL "Sequencing and analysis of the genome of the Whipple's disease
bacterium Tropheryma whipplei.";
RL Lancet 361:637-644(2003).
DR EMBL; BX251410; CAD66810.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome.
SQ SEQUENCE 690 AA; 76266 MW; CD3633B94B669E32 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
DB 526 KIVFFPA 531

```

```

RESULT 8
Q83GW3_TROWT PRELIMINARY; PRT; 698 AA.
AC Q83GW3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA helicase.
GN OrderedLocNames=TW118;
OS Tropheryma whipplei (strain Twist) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcales; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=203267;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Twist;
RX MEDLINE=22784088; PubMed=12902375;
RA Raoult D., Ogata H., Audic S., Robert C., Suhr K., Drancourt M.,
Claverie J.-M.;
RL "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a
reduced genome.";
RL Genome Res. 13:1800-1809(2003).
DR EMBL; AE016850; AA04215.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF00176; SNF2_N; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome; Helicase.
SQ SEQUENCE 698 AA; 77193 MW; 6D104BF533CDDE72 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
DB 534 KIVFFPA 539

RESULT 9
Q6ZQ91_MOUSE PRELIMINARY; PRT; 1265 AA.
ID Q6ZQ91_MOUSE PRELIMINARY;
AC Q6ZQ91;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE KIAA0590 protein (Fragment).
GN Name=KIAA0590;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
Saga Y., Nagase T., Ohara O., Koga H.;
RL "Prediction of the coding sequences of mouse homologues of KIAA gene:
iii. the complete nucleotide sequences of 500 mouse KIAA-homologous
cDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries.";
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129167; BAC97977.1; -; mRNA.

```

Q4TRF8;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Membrane protein.
 GN ORFNames=ELI0568;
 OS Erythrocyte litoralis HTCC2594.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
 OC Sphingomonadaceae; Erythrobacter.
 OX NCBI_TaxID=314225;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HTCC2594;
 RA Giovannoni S.J., Cho J.-C., Ferreira S., Johnson J., Kravitz S.,
 RA Halpern A., Remington K., Beeson K., Tran B., Rogers Y.-H.,
 RA Friedman R., Venter J.C.;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAGG0100001; EAL76762.1; -; Genomic DNA.
 SQ SEQUENCE 450 AA; 50280 MW; 077F448E75ADF977 CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 116 KIVFFA 121
 RESULT 4
 ID Q4S4T5_TETNG PRELIMINARY; PRT; 464 AA.
 AC Q4S4T5;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Chromosome 2 SCAFI4738, whole genome shotgun sequence.
 DE (Fragment).
 GN ORFNames=GSTENG00024047001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bounneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Craud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chappie C., McKernan K.J., McRwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.;
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
 RT the early vertebrate proto-karyotype.";
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAG01014738; CAG04347.1; -; Genomic DNA.

FT NON TER 464 464
 SQ SEQUENCE 464 AA; 53213 MW; 0F9FF81DB193CE5C CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 464;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 304 KIVFFA 309
 RESULT 5
 ID Q91VU5_MOUSE PRELIMINARY; PRT; 606 AA.
 AC Q91VU5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Wdtd2 protein.
 GN Name=AI661311; Synonyms=Wdtd2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RC MEDLINS=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129; TISSUE=Mammary tumor. Brcal-/fl;
 RC NIH MGC Project;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC009019; AAH09019.1; -; mRNA.
 DR Ensembl; ENSMUSG0000024169; Mus musculus.
 DR MGI; MGI:2146906; AI661311.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR011990; TPR-like_helical.
 SQ SEQUENCE 606 AA; 70992 MW; 4BB6057E07ADA16C CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 606;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 376 KIVFFA 381
 RESULT 6
 ID Q6RUU2_MOUSE

251 25 86.2 26 2 Q4XGPI_PLACH
252 25 86.2 46 2 Q4YT9_PLABE
253 25 86.2 47 2 Q8EXM4_LEPIN
254 25 86.2 46 2 Q8QGY9_FUGRU
255 25 86.2 49 2 Q4XA79_PLACH
256 25 86.2 51 2 Q7RF81_PLAYO
257 25 86.2 51 2 Q4YGS7_PLABE
258 25 86.2 55 2 Q82VG8_NITEU
259 25 86.2 59 2 Q4XGP8_PLABE
260 25 86.2 62 1 Y078_HELPU
261 25 86.2 62 1 Y085_HELPU
262 25 86.2 63 2 Q64S36_BACFR
263 25 86.2 72 2 Q4HSS4_CAMUP
264 25 86.2 77 2 Q5K6Q9_CRAGI
265 25 86.2 79 2 Q5WJL8_BACSK
266 25 86.2 81 1 MORAD_ECOLI
267 25 86.2 81 2 Q9APF7_9BACT
268 25 86.2 81 2 Q57RF2_SALCH
269 25 86.2 81 2 Q65TTO_MANSM
270 25 86.2 81 2 Q7N6P4_PHOLL
271 25 86.2 81 2 Q8D897_VIBVU
272 25 86.2 81 2 Q9KT78_VIBCH
273 25 86.2 81 2 Q83S38_SHIFL
274 25 86.2 81 2 Q7MM72_VIBVU
275 25 86.2 81 2 Q8X807_ECO57
276 25 86.2 83 2 Q8CLV3_YERPE
277 25 86.2 83 2 Q5PG40_SALPA
278 25 86.2 83 2 Q8Z886_SALTI
279 25 86.2 83 2 Q8ZQQ0_SALMON
280 25 86.2 85 2 Q87MY3_VIBPA
281 25 86.2 108 1 Y3403_METJA
282 25 86.2 109 2 Q6VYX4_ORYSA
283 25 86.2 111 2 Q9A126_ECOLI
284 25 86.2 116 2 Q49347_MYCGE
285 25 86.2 121 2 Q4V8R3_BRARE
286 25 86.2 128 2 Q6DUB9_PSEFL
287 25 86.2 130 1 Y613_PASMU
288 25 86.2 132 2 Q6BXU4_DEBHA
289 25 86.2 131 2 Q9LIH4_ARATH
290 25 86.2 135 2 Q5LGT9_BACFN
291 25 86.2 141 2 Q67684_AQUAE
292 25 86.2 141 2 Q64XP1_BACFR
293 25 86.2 143 1 COFI_YEAST
294 25 86.2 143 2 Q6BWX4_DEBHA
295 25 86.2 143 2 Q6CQ22_KLUJA
296 25 86.2 143 2 Q6FV81_CANGA
297 25 86.2 143 2 Q9HF97_ZYGRO
298 25 86.2 143 2 Q759P0_ASHGO
299 25 86.2 143 2 Q8EMC6_OCEIH
300 25 86.2 143 2 Q8EMC6_OCEIH

ALIGNMENTS

RESULT 1
Q73N39_TREEDE PRELIMINARY; PRT; 164 AA.
AC Q73N39;
DT 05-JUL-2004 (TREMREL. 27, Created)
DT 05-JUL-2004 (TREMREL. 27, Last sequence update)
DE Membrane protein, putative.
GN OrderedLocusNames=TDE1317;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35405 / DSM 14222;
RX PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,

RA Selengut J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregorgis E., Geer K., Tsegaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstock G.M., Norris S.J., Fraser C.M., Paulsen I.T.,
RT "Comparison of the genome of the oral pathogen Treponema denticola
with other spirochete genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651 (2004).
DR EMBL; AE017250; AAS11834.1; -, Genomic_DNA.
DR TIGR; TDE1317; -.
KW Complete proteome.
SQ SEQUENCE 164 AA; 18968 MW; 27E92778DDA9117C CRC64;
Query Match 100.0%; Score 29; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 50 KIVFFA 55
RESULT 2
Q81FH5_BACCR PRELIMINARY; PRT; 387 AA.
AC Q81FH5;
DT 01-JUN-2003 (TREMREL. 24, Created)
DT 01-JUN-2003 (TREMREL. 24, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Na+/H+ antiporter NnpA (inosine-dependent germination).
GN OrderedLocusNames=BC1612;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapatal V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fongstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
RL Nature 423:87-91 (2003).
DR EMBL; AE017003; AAP08591.1; -, Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGR; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41037 MW; 907C03E6B8A150B4A CRC64;
Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 184 KIVFFA 189
RESULT 3
Q4TRF8_9SPHN PRELIMINARY; PRT; 450 AA.
ID Q4TRF8_9SPHN

105	27	93.1	714	2	Q56JK4 CANFA	Q56jk4	canis faml	178	26	89.7	248	2	Q813W8 PLAF7	Q813w8	plasmodium
106	27	93.1	733	2	Q8P6Q5_RAT	Q8p6q5	rattus norv	179	26	89.7	253	2	Q9KL60_VIBCH	Q9kl60	vibrio chol
107	27	93.1	737	1	A4_FUGRU	Q9P279	fugu rubrip	180	26	89.7	270	2	Q7MW75_FORGI	Q7mw75	porphyron
108	27	93.1	738	1	Q6NUZ1_BARE	Q6nu21	brachydanio	181	26	89.7	279	2	Q4ILF1_GIBBE2	Q4ilf1	gibberella
109	27	93.1	738	2	Q90W28_BARE	Q90w28	brachydanio	182	26	89.7	281	2	Q51Z31_MAGGR	Q51z31	magnaporthe
110	27	93.1	747	2	Q91963_9PIPI	Q91963	xenopus. ap	183	26	89.7	281	2	Q4XSI1_PLACH	Q4xsi1	plasmodium
111	27	93.1	749	2	Q56JK2_SNECO	Q56jk2	stenella co	184	26	89.7	284	2	Q4ZX22_PSESY	Q4zx22	pseudomonas
112	27	93.1	749	2	Q6NRR1_XENLA	Q6nrr1	xenopus lao	185	26	89.7	292	2	Q4WK19_ASFFU	Q4wk19	aspergillus
113	27	93.1	750	2	Q6DJB6_XENTR	Q6djb6	xenopus tre	186	26	89.7	300	2	Q9XU61_CABEL	Q9xu61	caenorhabdi
114	27	93.1	751	1	A4_SAISC	Q95241	s amyloid b	187	26	89.7	301	2	Q5B613_EMEMI	Q5b613	aspergillus
115	27	93.1	751	2	Q6GSCO_HUMAN	Q6gsc0	homo sapien	188	26	89.7	306	2	Q68RL2_9HEMI	Q68rl2	glycaspis b
116	27	93.1	751	2	Q6RH28_CANFA	Q6rh28	canis faml	189	26	89.7	312	2	Q9Z2U4_9CAEN	Q9z2u4	littorina s
117	27	93.1	751	2	Q56JK5_CANFA	Q56jk5	canis faml	190	26	89.7	321	1	Y189_RICPR	Q9zdx5	rickettsia
118	27	93.1	751	2	Q4R4R8_MACFA	Q4r4r8	macaca fasc	191	26	89.7	333	2	Q6TG00_HELZE	Q6tg00	heilotichis z
119	27	93.1	751	2	Q9DGJ7_CHICK	Q9dgj7	gallus gall	192	26	89.7	336	1	RSMC_BUCAP	Q8k915	buchnera ap
120	27	93.1	754	2	Q4RY33_TETNG	Q4ry33	tetradon n	193	26	89.7	337	2	Q54NZ2_DICDI	Q54nz2	dictyosteli
121	27	93.1	759	2	Q4S0J4_TETNG	Q4s0j4	tetradon n	194	26	89.7	347	2	Q87PM3_VIBPA	Q87pm3	vibrio para
122	27	93.1	760	2	Q55HW1_CRYNE	Q55hw1	cryptococcu	195	26	89.7	349	2	Q9XU59_CABEL	Q9xu59	caenorhabdi
123	27	93.1	770	1	A4_CAVPO	Q60495	c amyloid b	196	26	89.7	352	2	Q8YUK9_ANASP	Q8yuk9	anabaena sp
124	27	93.1	770	1	A4_HUMAN	P50677	h amyloid b	197	26	89.7	360	2	Q7NMZ9_GLOVI	Q7nmz9	gloeobacter
125	27	93.1	770	1	A4_MACFA	P53601	m amyloid b	198	26	89.7	366	2	Q8DIZ5_SYNEL	Q8diz5	synechococc
126	27	93.1	770	1	A4_MOUSE	P12023	p amyloid b	199	26	89.7	380	2	Q7VJC1_HELHP	Q7vjc1	helicobacte
127	27	93.1	770	1	A4_PANTR	Q51s80	p amyloid b	200	26	89.7	382	2	Q9KDE2_BACHD	Q9kde2	bacillus ha
128	27	93.1	770	1	A4_PIG	P79307	s amyloid b	201	26	89.7	390	2	Q5WLG1_BACSK	Q5wlg1	bacillus cl
129	27	93.1	770	1	A4_RAT	P08592	r amyloid b	202	26	89.7	391	2	Q8A2G6_BACTN	Q8a2g6	bacteroides
130	27	93.1	770	2	Q6RH30_CANFA	Q6rh30	canis faml	203	26	89.7	400	2	Q7PXH6_ANOGA	Q7pxh6	anopheles g
131	27	93.1	770	2	Q56JRK_CANFA	Q56jk6	canis faml	204	26	89.7	402	2	Q7DIT8_ECOLI	Q7dit8	escherichia
132	27	93.1	770	2	Q53ZT3_MOUSE	Q53zt3	mus musculu	205	26	89.7	402	2	Q9ZB96_ECO57	Q9zb96	escherichia
133	27	93.1	770	2	Q547B7_RAT	Q547b7	rattus norv	206	26	89.7	402	2	Q83PP1_SHIFL	Q83pp1	shigella fl
134	27	93.1	780	1	A4_TETFL	Q73683	tetradon f	207	26	89.7	405	1	SVY_BORBU	SVY	borrelia bu
135	27	93.1	955	2	Q6R2Z2_9POTV	Q80r22	calla lily	208	26	89.7	405	1	Q661P9_BORGA	Q661p9	borrelia ga
136	27	93.1	962	2	QANTK2_9BELT	Qantk2	anaeromyxob	209	26	89.7	421	2	Q9LH60_ARATH	Q9lh60	arabidopsis
137	27	93.1	1016	2	Q59912_9POTV	Q59912	zuccchini ye	210	26	89.7	468	2	Q61GJ7_CABER	Q61gj7	caenorhabdi
138	27	93.1	1056	2	Q6FKH6_CANGA	Q6fkhe6	cardida gla	211	26	89.7	472	2	Q4WEZ5_ASFFU	Q4wez5	aspergillus
139	27	93.1	1655	2	Q4Q5Q4_LEIMA	Q4q5q4	leishmania	212	26	89.7	479	2	Q9QDL5_9POTV	Q9qdl5	sarcophilus
140	27	93.1	1916	2	Q8OKU4_9POTV	Q8oku4	zuccchini ye	213	26	89.7	479	2	Q4F979_9POTV	Q4f979	eustrephus
141	27	93.1	3080	1	POLG_ZYMCV	P18479	z genome po	214	26	89.7	480	2	Q4N8N8_THEFA	Q4n8n8	theileria p
142	27	93.1	3080	2	Q6WN47_9POTV	Q6wn47	zuccchini ye	215	26	89.7	496	2	Q5K4D0_9POTV	Q5k4d0	dasheen mos
143	27	93.1	3080	2	Q6WN48_9POTV	Q6wn48	zuccchini ye	216	26	89.7	502	2	Q5LIS5_GEOKA	Q5lis5	geobacillus
144	27	93.1	3080	2	Q6WN49_9POTV	Q6wn49	zuccchini ye	217	26	89.7	522	2	Q4XPM5_PLACH	Q4xpm5	plasmodium
145	27	93.1	3080	2	Q6Y2U7_9POTV	Q6y2u7	zuccchini ye	218	26	89.7	524	2	Q912R1_9POTV	Q912r1	dasheen mos
146	27	93.1	3080	2	Q7T908_9POTV	Q7t908	zuccchini ye	219	26	89.7	539	2	Q9Q999_9POTV	Q9q999	dasheen mos
147	27	93.1	3080	2	Q7T914_9POTV	Q7t914	zuccchini ye	220	26	89.7	557	2	Q4UGZ4_THEAN	Q4ugz4	theileria a
148	27	93.1	3083	1	POLG_ZYMVS	Q36979	z genome po	221	26	89.7	598	2	Q644G8_9SALA	Q644g8	gyrinophilu
149	27	93.1	3105	2	Q70XR2_9POTV	Q70xr2	soybean mos	222	26	89.7	604	2	Q645F2_9SALA	Q645f2	stereochilu
150	26	89.7	40	2	Q91FF3_IRV6	Q91ff3	chilo iride	223	26	89.7	607	2	Q8SJI9_URSAM	Q8sj19	ursus ameri
151	26	89.7	66	2	Q728F0_DESVH	Q728f0	desulfovibr	224	26	89.7	607	2	Q644P6_9SALA	Q644p6	thorius n.
152	26	89.7	74	1	Y131_MYCGE	P47377	mycoplasma	225	26	89.7	611	2	Q6ZLV9_9TELE	Q6zlv9	ophisurus m
153	26	89.7	81	2	Q6D3D0_ERWCT	Q6d3d0	erwinia car	226	26	89.7	613	2	Q4ZG30_9TELE	Q4zgs0	scieropages
154	26	89.7	89	2	Q83VF2_LACLC	Q83vf2	lactococcus	227	26	89.7	620	2	Q29198_ARCFU	Q29198	archaeoglob
155	26	89.7	105	2	Q64CV5_9ARCH	Q64cv5	uncultured	228	26	89.7	624	2	Q6FBJ6_AC1AD	Q6fjb6	acinetobact
156	26	89.7	109	2	Q9X292_THEMEA	Q9x292	thermotoga	229	26	89.7	626	2	Q8RM01_AC1AD	Q8rm01	acinetobact
157	26	89.7	145	2	Q5USA9_9PEZI	Q5usa9	monacrospor	230	26	89.7	685	1	MDL1_CANAL	P97998	candida alb
158	26	89.7	156	2	Q8DN20_STRPN	Q8dn20	streptococc	231	26	89.7	685	2	Q5A951_CANAL	Q5a951	candida alb
159	26	89.7	156	2	Q7N992_STRPN	Q7n992	streptococc	232	26	89.7	726	2	Q4Y7D6_PLACH	Q4y7d6	plasmodium
160	26	89.7	160	2	Q81Y15_BACAN	Q81y15	bacillus an	233	26	89.7	738	2	Q5A445_CANAL	Q5a445	candida alb
161	26	89.7	190	2	Q92WB8_RHIME	Q92wb8	rhizobium m	234	26	89.7	743	2	Q6BM34_DEBHA	Q6bm34	debaromyce
162	26	89.7	194	2	Q97G46_CLOAB	Q97g46	clostridium	235	26	89.7	771	2	Q4SD14_TETNG	Q4sd14	tetradon n
163	26	89.7	196	2	Q6HVS9_BACAN	Q6hvs9	bacillus an	236	26	89.7	774	2	Q64777_ARATH	Q64777	arabidopsis
164	26	89.7	202	2	Q7P578_FUSNV	Q7p578	fusobacteri	237	26	89.7	787	2	Q4XMD0_PLACH	Q4xmd0	plasmodium
165	26	89.7	202	2	Q8RE19_FUSNN	Q8re19	fusobacteri	238	26	89.7	804	2	Q64770_ARATH	Q64770	arabidopsis
166	26	89.7	218	2	Q5CYB3_CRIPV	Q5cyb3	cryptospori	239	26	89.7	881	2	Q6BM22_DEBHA	Q6bm22	debaromyce
167	26	89.7	218	2	Q5CIV9_CRYHO	Q5civ9	cryptospori	240	26	89.7	911	2	Q6MUF5_MYCMS	Q6muf5	mycophasma
168	26	89.7	220	2	Q52T74_PEMVM	Q52t74	peanut mott	241	26	89.7	957	2	Q7T3T7_OREMO	Q7t3t7	oreochromis
169	26	89.7	230	2	Q7RDM9_PLAYO	Q7rdm9	plasmodium	242	26	89.7	969	2	Q71953_9POTV	Q71953	dasheen mos
170	26	89.7	231	2	Q637W5_BACZ	Q637w5	bacillus ce	243	26	89.7	973	2	Q9VTH1_DROME	Q9vth1	drosophila
171	26	89.7	241	2	Q4XAZ2_PLACH	Q4xaz2	plasmodium	244	26	89.7	1094	2	Q4Q4Z7_LEIMA	Q4q4z7	leishmania
172	26	89.7	241	2	Q4MXQ0_BACCE	Q4mxq0	bacillus ce	245	26	89.7	1119	2	Q9LM79_ARATH	Q9lm79	arabidopsis
173	26	89.7	241	2	Q638P6_BACZ	Q638p6	bacillus ce	246	26	89.7	1273	2	Q9LM82_ARATH	Q9lm82	arabidopsis
174	26	89.7	241	2	Q6HG76_BACHK	Q6hg76	bacillus th	247	26	89.7	3099	1	POLG_PEMVM	POLG	p genome po
175	26	89.7	241	2	Q734P7_BACCR	Q734p7	bacillus ce	248	26	89.7	3191	2	Q912R2_9POTV	Q912r2	dasheen mos
176	26	89.7	241	2	Q81B59_BACCR	Q81b59	bacillus ce	249	26	89.7	3381	2	Q81DK4_PLAF7	Q81dk4	plasmodium
177	26	89.7	241	2	Q81N30_BACAN	Q81n30	bacillus an	250	26	89.7	86.2	20	Q8CYA3_STRR6	Q8cya3	streptococc

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KIVPFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	164	2	Q73N39 TREDE
2	29	100.0	387	2	Q81FH5_BACCR
3	29	100.0	450	2	Q4TFP8_9SPHN
4	29	100.0	464	2	Q4S4T5_TETNG
5	29	100.0	606	2	Q91VU5_MOUSE
6	29	100.0	663	2	Q6RUU2_MOUSE
7	29	100.0	690	2	Q831B2_TROW8
8	29	100.0	698	2	Q83GW3_TROWT
9	29	100.0	1265	2	Q6ZQ91_MOUSE
10	29	100.0	1412	2	Q5F3M1_CHICK
11	28	96.6	88	2	Q4LBQ8_SODGL
12	28	96.6	183	2	Q9RQ09_BACTEROIDES
13	28	96.6	186	1	QL19_ORYSA
14	28	96.6	186	2	P93414_ORYSA
15	28	96.6	231	2	Q8CV8_MOUSE
16	28	96.6	315	2	Q61C67_CAERB
17	28	96.6	362	2	Q4HSJ7_CAMUP
18	28	96.6	372	2	Q6D7U3_ERWCT
19	28	96.6	373	2	Q7M9N5_WOLSU
20	28	96.6	382	2	Q9V7J0_DROME
21	28	96.6	387	2	Q9K110_BACCE
22	28	96.6	387	2	Q4MT39_BACCC
23	28	96.6	387	2	Q63DD4_BACCC
24	28	96.6	387	2	Q6HKU6_BACHK
25	28	96.6	387	2	Q73AP3_BACCC1
26	28	96.6	387	2	Q81SK9_BACAN
27	28	96.6	410	2	Q6L2B4_PICTO
28	28	96.6	410	2	Q8C513_MOUSE
29	28	96.6	442	2	Q9PHV5_CAMJE
30	28	96.6	447	2	Q59243_PYROCC
31	28	96.6	556	2	Q95893_DROSOPHILA

Q9V7I9	DROSOPHILA	556	2	Q9V7I9	DROME
Q5HYE1	HOMO SAPIEN	703	2	Q5HYE1	HUMAN
Q6AG25	LEIFSONIA X	721	2	Q6AG25	LEIXX
Q9GQ82	DROSOPHILA	785	2	Q9GQ82	DROME
Q95786	HOMO SAPIEN	925	2	Q95786	HUMAN
Q5VYU1	HOMO SAPIEN	925	2	Q5VYU1	HUMAN
Q6G899	MUS MUSCULUS	926	2	Q6G899	MOUSE
Q9GLV6	SUS SCROFA	940	2	Q9GLV6	PIG
P29477	MUS MUSCULUS	1144	1	NOS2	MOUSE
Q8X410	MUS MUSCULUS	1144	2	Q8X410	MOUSE
Q6P6A0	MUS MUSCULUS	1145	2	Q6P6A0	MOUSE
Q68K27	CHILAMYDOMON	1384	2	Q68K27	CHLRE
Q7QEF0	ANOPHELES G	1408	2	Q7QEF0	ANOXA
Q5B164	DROSOPHILA	1458	2	Q5B164	DROME
Q7KT24	DROSOPHILA	1503	2	Q7KT24	DROME
Q8A6R7	BACTERIOIDES	1676	2	Q8A6R7	BACTN
Q9UC33	HOMO SAPIEN	33	2	Q9UC33	HUMAN
Q5EJJ6	GRAMPUS GRI	42	2	Q5EJJ6	GRAGR
Q5GJJ7	TURSIOPS TR	42	2	Q5GJJ7	TURTR
Q7M088	CAVIA PORCE	42	2	Q7M088	CAVPO
Q8WZ99	HOMO SAPIEN	52	2	Q8WZ99	HUMAN
Q29149	U ALZHEIMER	57	1	A4	URSMA
Q28280	C ALZHEIMER	58	1	A4	CANFA
Q28748	O ALZHEIMER	58	1	A4	RABIT
Q28053	B ALZHEIMER	58	1	A4	SHEEP
Q35463	CRICETULUS	59	1	A4	BOVIN
Q81H58	CHELYDRA SE	79	2	Q81H58	CHESE
Q7UPR1	RHODOPIRELL	113	2	Q7UPR1	RHOBA
Q98TZ9	ARABIDOPSIS	137	2	Q98TZ9	ARATH
Q6AKE9	DESPTALE	152	2	Q6AKE9	DESPT
Q8BPV5	MOUSE	203	2	Q8BPV5	MOUSE
Q8VY56	ARATH	218	2	Q8VY56	ARATH
Q8SV79	ARABIDOPSIS	229	2	Q8SV79	ARATH
Q9XGY6	SIMMONDSIA	231	2	Q9XGY6	SIMCH
Q8U460	PYROCOCUS	352	2	Q8U460	PYRCH
Q8UUI8	BRARE	357	2	Q8UUI8	BRARE
Q8PPL1	XANTHOMAS	366	2	Q8PPL1	XANAC
Q67225	AQUIFEX AEO	380	2	Q67225	AQUAE
Q8BPC7	MUS MUSCULUS	384	2	Q8BPC7	MOUSE
Q4NSU7	THELERIA P	391	2	Q4NSU7	THEPA
Q5WPU9	LEUTOMYIA L	399	2	Q5WPU9	LEUTLO
Q5L117	GEOKA	403	2	Q5L117	GEOKA
Q4UY55	XANCP	404	2	Q4UY55	XANCP
Q8P597	XANTHOMAS	404	2	Q8P597	XANCP
Q9M1Q8	ARABIDOPSIS	428	2	Q9M1Q8	ARATH
Q89329	ZUCCHINI YE	461	2	Q89329	9POTV
Q7T910	ZUCCHINI YE	470	2	Q7T910	9POTV
Q8UUS0	BRARE	472	2	Q8UUS0	BRARE
Q52NV6	9POTV	488	2	Q52NV6	9POTV
Q7T911	ZUCCHINI YE	490	2	Q7T911	9POTV
Q7T912	ZUCCHINI YE	490	2	Q7T912	9POTV
Q5K4D4	SOYBEAN MOS	493	2	Q5K4D4	9POTV
Q5G4D5	XANCP	493	2	Q5G4D5	XANCP
Q5GVS5	XANTHOMAS	508	2	Q5GVS5	XANCP
Q93296	CHICK	534	2	Q93296	CHICK
Q9V1A1	CHICK	569	2	Q9V1A1	CHICK
Q919B7	BRARE	612	2	Q919B7	BRARE
Q50Z85	ENTH1	615	2	Q50Z85	ENTH1
Q4WBU2	ASPFLU	623	2	Q4WBU2	ASPFLU
Q5B2V4	EMENI	630	2	Q5B2V4	EMENI
Q7Z2T1	BRARE	638	2	Q7Z2T1	BRARE
Q98SG0	XENLA	678	2	Q98SG0	XENLA
Q5R477	PONPY	693	2	Q5R477	PONPY
Q6RH29	CANFA	695	2	Q6RH29	CANFA
Q56JK3	CANIS FAMIL	695	2	Q56JK3	CANFA
Q6GR78	MUSE	695	2	Q6GR78	MUSE
Q9DGJ8	CHICK	695	2	Q9DGJ8	CHICK
Q98SF9	XENLA	695	2	Q98SF9	XENLA
Q7ZXQ0	XENLA	695	2	Q7ZXQ0	XENLA

THIS PAGE BLANK (USPTO)

R.She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: H90318
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <KUR>
A;Cross-references: UNIPROT:Q97XW2; UNIPARC:UPI0000064436; GB:AE006641; NID:gl3814829; E
C;Genetics:
A;Gene: glpK-1

Query Match 86.2%; Score 25; DB 2; Length 294;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|:|
Db 184 KVVYFA 189

RESULT 75
D64240
methionyl-tRNA formyltransferase (EC 2.1.2.9) homolog - Mycoplasma genitalium
C;Species: Mycoplasma genitalium
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C;Accession: D64240
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: D64240
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-311 <TIGR>
A;Cross-references: UNIPROT:P47605; UNIPARC:UPI000012AAEE; GB:U39721; GB:I43967; NID:gl
A;Experimental source: strain G-37
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: methionyl-tRNA formyltransferase; phosphoribosylglycinamide formyltransfe
C;Keywords: protein biosynthesis; transferase

Query Match 86.2%; Score 25; DB 2; Length 311;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 3 KIVFF 7

Search completed: December 29, 2005, 17:49:02
Job time : 19.9677 secs

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Frazer, C.M.; Moxon, E.R.; Rappuoli, R.; Vella, P.; et al.
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: AB1000; MUID:20175755; PMID:10710307

A;Accession: AB1056
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-262 <TET>
 A;Cross-references: UNIPROT:Q9JVB3; UNIPARC:UPI00000C4774; GB:AE002517; GB:AE002098; NID:10710307
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB1663

Query Match 86.2%; Score 25; DB 2; Length 262;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
 Db 4 KIVFF 8

RESULT 70
 AB1820

conserved hypothetical protein NMA1921 [imported] - *Neisseria meningitidis* (strain Z2491)
 C;Species: *Neisseria meningitidis*
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C;Accession: AB1820

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Kles, S.R.; Morel, P.; et al.
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A;Reference number: AB1775; MUID:20222556; PMID:10761919

A;Accession: AB1820
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-269 <PAR>
 A;Cross-references: UNIPROT:Q9JTB4; UNIPARC:UPI00000C4CCE; GB:AL162757; GB:AL157959; NID:10761919
 A;Experimental source: serogroup A, strain Z2491
 C;Genetics:
 A;Gene: NMA1921

Query Match 86.2%; Score 25; DB 2; Length 269;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
 Db 11 KIVFF 15

RESULT 71
 S05343

NAD ADP-ribosyltransferase (EC 2.4.2.30) - *Rhodospirillum rubrum*
 C;Species: *Rhodospirillum rubrum*
 C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
 C;Accession: S05343; J05335

R;Fitzmaurice, W.P.; Saari, L.L.; Lowery, R.G.; Ludden, P.W.; Roberts, G.P.
 Mol. Gen. Genet. 218, 340-347, 1989
 A;Title: Genes coding for the reversible ADP-ribosylation system of dinitrogenase reductase in *Rhodospirillum rubrum*.
 A;Reference number: J04446; MUID:89384461; PMID:2506427

A;Accession: S05343
 A;Molecule type: DNA
 A;Residues: 1-276 <FIT>

A;Cross-references: UNIPROT:P14299; UNIPARC:UPI0000129874; EMBL:X16187; NID:G46389; PIDN:10761919
 A;Note: part of this sequence, including the amino end of the mature protein, was confirmed by sequencing.
 C;Genetics:
 A;Gene: drat

A;Start codon: TTG
 C;Superfamily: Azospirillum NAD-nitrogenase ADP-D-ribosyltransferase
 C;Keywords: Glycosyltransferase; NAD; pentosyltransferase

Query Match 86.2%; Score 25; DB 2; Length 276;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
 Db 243 KIVFF 247

RESULT 72
 AI2038

carboxyphosphoenolpyruvate phosphonmutase [imported] - *Nostoc* sp. (strain PCC 7120)
 C;Species: *Nostoc* sp. PCC 7120
 A;Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C;Accession: AI2038

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; et al.
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Anabaena* sp. strain PCC 7120.
 A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AI2038
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-287 <KUR>

A;Cross-references: UNIPROT:Q8YVW0; UNIPARC:UPI00000CE22D; GB:BA000019; PIDN:BA073562.1;
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: all1863

C;Superfamily: carboxyphosphoenolpyruvate phosphonmutase
 Query Match 86.2%; Score 25; DB 2; Length 287;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
 Db 228 KIVFF 232

RESULT 73
 D69355

hypothetical protein AF0844 - *Archaeoglobus fulgidus*
 C;Species: *Archaeoglobus fulgidus*
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: D69355

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; et al.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon *Archaeoglobus fulgidus*.
 A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: D69355
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-293 <KLE>

A;Cross-references: UNIPROT:O29414; UNIPARC:UPI0000056F64; GB:AE001046; GB:AE000782; NID:9389475
 Query Match 86.2%; Score 25; DB 2; Length 293;
 Best Local Similarity 66.7%; Pred. No. 1.8e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 6
 Db 140 KIVFF 145

RESULT 74
 H90318

glycerol kinase (glpK-1) [imported] - *Sulfolobus solfataricus*
 C;Species: *Sulfolobus solfataricus*
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: H90318

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KIVFF 5
Db	208 KIVFF 212
RESULT 65	
C64666	
glutamine transport protein glnQ - Helicobacter pylori (strain 26695)	
C:Species: Helicobacter pylori	
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004	
C:Accession: C64666	
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;	
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne	
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Matthey, L.	
Nature 388, 539-547, 1997	
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.	
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.	
A:Reference number: A64520; MUID:97394467; PMID:9252185	
A:Accession: C64666	
A>Status: nucleic acid sequence not shown; translation not shown	
A:Molecule type: DNA	
A:Residues: 1-248 <TOM>	
A:Cross-references: UNIPROT:Q25785; UNIPARC:UPI0000D31A1; GB:AE000623; GB:AE000511; NID	
A:Experimental source: strain 26695	
C:Genetics:	
A:Gene: glnQ; HPI171	
C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology	
C:Keywords: ATP; glutamine transport; nucleotide binding; P-loop	
F:20-215/Domain: ATP-binding cassette homology <ABC>	
F:37-44/Region: nucleotide-binding motif A (P-loop)	
F:160-164/Region: nucleotide-binding motif B	
Query Match 86.2%; Score 25; DB 2; Length 248;	
Best Local Similarity 100.0%; Pred. No. 1.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KIVFF 5
Db	208 KIVFF 212
RESULT 66	
T28170	
hypothetical protein ORF9 - Melanoplus sanguinipes entomopoxvirus (strain Tuscon)	
C:Species: Melanoplus sanguinipes entomopoxvirus	
A:Variety: strain Tuscon	
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004	
C:Accession: T28170	
R:Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.	
J. Virol. 73, 533-552, 1999	
A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.	
A:Reference number: Z20484; MUID:99102612; PMID:9847359	
A:Accession: T28170	
A>Status: preliminary; translated from GB/EMBL/DBJ	
A:Molecule type: DNA	
A:Residues: 1-254 <AFO>	
A:Cross-references: UNIPROT:Q9YW83; UNIPARC:UPI00000F390B; EMBL:AF063866; NID:94049647;	
A:Experimental source: strain Tuscon	
C:Genetics:	
A:Note: MSV009	
Query Match 86.2%; Score 25; DB 2; Length 254;	
Best Local Similarity 100.0%; Pred. No. 1.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KIVFF 5
Db	95 KIVFF 99
RESULT 67	

AC1561	
conserved hypothetical protein homolog lin1028 [imported] - Listeria innocua (strain Cl)	
C:Species: Listeria innocua	
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	
C:Accession: AC1561	
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker	
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.	
D.; Jones, L.M.; Karst, U.	
Science 294, 849-852, 2001	
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M	
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,	
A:Title: Comparative genomics of Listeria species.	
A:Reference number: AB1077; MUID:21537279; PMID:11679669	
A:Accession: AC1561	
A>Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-256 <GLA>	
A:Cross-references: UNIPROT:Q92C23; UNIPARC:UPI00000CC42D; GB:AL592022; PIDN:CAC96259.1.	
A:Experimental source: strain Clfp11262	
C:Genetics:	
A:Gene: lin1028	
Query Match 86.2%; Score 25; DB 2; Length 256;	
Best Local Similarity 100.0%; Pred. No. 1.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KIVFF 5
Db	3 KIVFF 7
RESULT 68	
AE1203	
conserved hypothetical proteins homolog lmo1029 [imported] - Listeria monocytogenes (st	
C:Species: Listeria monocytogenes	
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004	
C:Accession: AE1203	
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke	
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.	
D.; Jones, L.M.; Karst, U.	
Science 294, 849-852, 2001	
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; M	
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland	
A:Title: Comparative genomics of Listeria species.	
A:Reference number: AB1077; MUID:21537279; PMID:11679669	
A:Accession: AE1203	
A>Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-256 <GLA>	
A:Cross-references: UNIPROT:Q8Y888; UNIPARC:UPI0000055436; GB:NC_003210; PIDN:CAC99107.	
A:Experimental source: strain EGD-e	
C:Genetics:	
A:Gene: lmo1029	
Query Match 86.2%; Score 25; DB 2; Length 256;	
Best Local Similarity 100.0%; Pred. No. 1.6e+02;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 KIVFF 5
Db	3 KIVFF 7
RESULT 69	
AB1056	
conserved hypothetical protein NMB1663 [imported] - Neisseria meningitidis (strain MC58	
C:Species: Neisseria meningitidis	
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004	
C:Accession: AB1056	
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.	
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.	
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.	
Science 287, 1809-1815, 2000	

Db 185 KIAFFA 190
|||
|||

RESULT 60
A75004
hypothetical protein PAB1033 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: A75004
R:anonymous, Genoscope
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: A75004
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-219 <KAW>
A:Cross-references: UNIPROT:Q9UYE1; UNIPARC:UPI000006347D; GB:AJ248288; GB:AL096836; NID
C:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1033

Query Match 86.2%; Score 25; DB 2; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|||
|||

Db 109 KIVFF 113

RESULT 61
G72322
glutaredoxin-related protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: G72322
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: G72322
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-221 <ARN>
A:Cross-references: UNIPROT:Q9WZX2; UNIPARC:UPI00000D396F; GB:AE001753; GB:AE000512; NID
C:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0868

Query Match 86.2%; Score 25; DB 2; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|||
|||

Db 25 KIVFF 29

RESULT 62
T47768
hypothetical protein F24I3.160 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T47768
R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A:Reference number: 224475
A:Accession: T47768
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-222 <NTA>
A:Cross-references: UNIPROT:Q9M1J2; UNIPARC:UPI000000C63B; EMBL:AL138655
A:Experimental source: cultivar Columbia; BAC clone F24I3
C:Genetics:
A:Map position: 3
A:Introns: 84/3; 143/3; 181/3
A:Note: F24I3.160
C:Superfamily: DNA-directed RNA polymerase, RPBS subunit

Query Match 86.2%; Score 25; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|||
|||

Db 86 KIVFF 90

RESULT 63
A90260
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: A90260
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.;
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: A90260
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-225 <KUR>
A:Cross-references: UNIPROT:Q97Z59; UNIPARC:UPI0000064342; GB:AE006641; NID:G13814264; P
C:Genetics:
A:Gene: SS01074

Query Match 86.2%; Score 25; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|||
|||

Db 4 KIVFF 8

RESULT 64
F71849
amino acid ABC transporter, ATP-binding protein - Helicobacter pylori (strain J99)
C:Species: Helicobacter pylori
A:Variety: strain J99
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: F71849
R:Aim, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: F71849
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <ARN>
A:Cross-references: UNIPROT:Q9ZK44; UNIPARC:UPI00000D36EE; GB:AE001537; GB:AE001439; NID
C:Experimental source: strain J99
C:Genetics:
A:Gene: jhp1098
C:Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
F;20-215/Domain: ATP-binding cassette homology <ABC>

Query Match 86.2%; Score 25; DB 2; Length 248;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

A;Molecule type: DNA
A;Residues: 1-143 <WED>
A;Cross-references: UNIPARC:UPI0000110C55; EMBL:273155; NID:g1360250; PIDN:CAA97502.1; P
A;Note: experimental source strain S288C
R;Wedler, H.; Wambutt, R.
submitted to the EMBL Data Library, January 1995
A;Description: Sequence of a 37 kb DNA fragment from chromosome XII of *Saccharomyces cerevisiae*
A;Reference number: S50950
A;Accession: S50970
A;Molecule type: DNA
A;Residues: 'MGKKFIRSGENVKFLCS', 6-143 <WEW>
A;Cross-references: UNIPARC:UPI0000069A87; EMBL:247973; NID:g642313; PIDN:CAA88007.1; P
A;Comment: Cofilin reversibly regulates actin polymerization and depolymerization in a p
C;Genetics:
A;Gene: SGD:COF1; MIPS:YLL050C
A;Cross-references: SGD:S0003973; MIPS:YLL050C
A;Map position: 12L
A;Introns: 5/2
C;Superfamily: cofilin
C;Keywords: actin binding
F;88-118/Region: actin binding #status predicted

Query Match 86.2%; Score 25; DB 1; Length 143;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFP 5
|:|:|:
82 KIVFFP 86

Db

RESULT 57
B90157
hypothetical protein SSO0168 [imported] - *Sulfolobus solfataricus*
C;Species: *Sulfolobus solfataricus*
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
A;Accession: B90157
R;She, Q.; Singh, R. K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M. J.; Chan-
Jong, I.; Jeffries, A. C.; Kozera, C. J.; Medina, N.; Peng, X.; Thi-Ngoc, H. P.; Redder, H
arrett, R. A.; Ragan, M. A.; Sensen, C. W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: *Sulfolobus solfataricus* complete genome.
A;Reference number: A99139
A;Accession: B90157
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-193 <KUR>
A;Cross-references: UNIPROT:Q980V9; UNIPARC:UPI00000641A8; GB:AE006641; NID:g13813299; P
C;Genetics:
A;Gene: SSO0168

Query Match 86.2%; Score 25; DB 2; Length 193;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFP 6
|:|:|:
117 KIVFFP 122

Db

RESULT 58
B81256
phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / phosphoribosyl-ATP diphosphatase (EC 3
C;Species: *Campylobacter jejuni*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81256
R;Parkhill, J.; Wren, B. W.; Mungall, K.; Ketley, J. M.; Churcher, C.; Basham, D.; Chillin
C. W.; Quail, M.; Rajandream, M. A.; Rutherford, K. M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: B81256
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-207 <PAR>
A;Cross-references: UNIPROT:Q9PW71; UNIPARC:UPI000012C76D; GB:AL139079; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: hisI; Cj1604
C;Superfamily: hisI bifunctional enzyme; hisI bifunctional enzyme homology; hisI protein
C;Keywords: hydrolase

Query Match 86.2%; Score 25; DB 2; Length 207;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFP 6
|:|:|:
51 KIVFFP 56

Db

RESULT 59
A35617
HDEL receptor ERD2 - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: 26K endoplasmic reticulum retention receptor; ER lumen protein-retain
C;Species: *Saccharomyces cerevisiae*
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A;Accession: A35617; S45774; S50290; S42504
R;Semenza, J. C.; Hardwick, K. G.; Dean, N.; Pelham, H. R. B.
Cell 61, 1349-1357, 1990
A;Title: ERD2, a yeast gene required for the receptor-mediated retrieval of luminal ER f
A;Reference number: A35617; MUID:90304893; PMID:2194670
A;Accession: A35617
A;Molecule type: DNA
A;Residues: 1-219 <SEM>
A;Cross-references: UNIPROT:P18414; UNIPARC:UPI000012A121; GB:M34777; NID:g171466; PIDN
R;Goffeau, A.; Jonniaux, J. L.; Purnelle, B.; Skala, J.; de Wergifosse, P.; van Dyck, L.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45745
A;Accession: S45774
A;Molecule type: DNA
A;Residues: 1-219 <GOF>
A;Cross-references: UNIPARC:UPI000012A121; EMBL:Z35801; NID:g536054; PIDN:CAA84860.1; P
R;de Wergifosse, P.; Jacques, B.; Jonniaux, J. L.; Purnelle, B.; Skala, J.; Goffeau, A.
Yeast 10, 1489-1496, 1994
A;Title: The sequence of a 22.4 kb DNA fragment from the left arm of yeast chromosome I
NA-binding protein.
A;Reference number: S50284; MUID:95176707; PMID:7871888
A;Accession: S50290
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 64-219 <DEF>
A;Cross-references: UNIPARC:UPI0000168A10; EMBL:X78214; NID:g463261; PIDN:CAA55054.1; P
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
C;Genetics:
A;Gene: SGD:ERD2; MIPS:YBL040C
A;Cross-references: SGD:S0000136; MIPS:YBL040C
A;Map position: 2L
A;Introns: 8/1
C;Function:
A;Description: achieves retention of proteins specific to the lumen of the endoplasmic
usually KDEL in animal cells and HDEL in budding yeasts
C;Superfamily: KDEL receptor
C;Keywords: Golgi apparatus; protein trafficking; sorting signal recognition; transmembr
F;4-20/Domain: transmembrane #status predicted <TM1>
F;38-54/Domain: transmembrane #status predicted <TM2>
F;61-82/Domain: transmembrane #status predicted <TM3>
F;99-115/Domain: transmembrane #status predicted <TM4>
F;122-138/Domain: transmembrane #status predicted <TM5>
F;186-202/Domain: transmembrane #status predicted <TM6>

Query Match 86.2%; Score 25; DB 1; Length 219;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFP 6

A:Gene: moaD

A:Map position: 17.7 min
 C:Complex: heterodimer with D chain (PIR:S31883) [validated, MUID:93293873]
 C:Function:
 A:Description: required for the addition of the Mo-binding dithiolene group to a molybdo
 C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein
 C:Keywords: heterodimer; molybdopterin biosynthesis
 F:81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 86.2%; Score 25; DB 2; Length 81;
 Best Local Similarity 66.7%; Pred. No. 56;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|
 Db 3 KVLFFA 8

RESULT 53

AC0598
 molybdopterin converting factor, chain 1 [imported] - Salmonella enterica subsp. enteric
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 16-Aug-2004
 C:Accession: AC0598
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connerston, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AC0598
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-83 <PAR>
 A:Cross-references: UNIPARC:UPI000005A0EA; GB:AL513382; PIDN:CAD05253.1; PID:g16502022;
 C:Genetics:
 A:Gene: STY0839
 C:Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 86.2%; Score 25; DB 2; Length 83;
 Best Local Similarity 66.7%; Pred. No. 57;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|
 Db 5 KVLFFA 10

RESULT 54

C64516
 hypothetical protein MJEC503 - Methanococcus jannaschii plasmid pURB801
 C:Species: Methanococcus jannaschii
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C:Accession: C64516
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
 Reisch, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
 rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: C64516
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-108 <BUL>
 A:Cross-references: UNIPROT:Q60302; UNIPARC:UPI000013C25B; GB:L77119; NID:g1500688; TIGR
 C:Genetics:
 A:Map position: ECSREV5174-4848
 A:Genome: plasmid
 A:Note: this stable 16-kilobase pair plasmid is also designated ECS (small extrachromoso
 C:Superfamily: uncharacterized conserved protein

Query Match 86.2%; Score 25; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 73;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|
 Db 2 KIVFYA 7

RESULT 55

B70457
 gliding motility protein MglA - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: B70457
 R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
 V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: B70457
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-141 <AQF>
 A:Cross-references: UNIPROT:O67684; UNIPARC:UPI000005670A; GB:AE000757; GB:AE000657; NID
 A:Experimental source: strain VFS
 C:Genetics:
 A:Gene: mglA2
 C:Superfamily: gliding motility protein

Query Match 86.2%; Score 25; DB 1; Length 141;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
 |:|:|
 Db 4 KIVFF 8

RESULT 56

A44397
 cofillin - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein L0595; protein YLL050C
 C:Species: Saccharomyces cerevisiae
 C:Date: 31-Dec-1993 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C:Accession: A44397; B44397; JN0529; S64802; S50970; S31309; S36087
 R:Moore, A.L.; Janney, P.A.; Louie, K.A.; Drubin, D.G.
 J. Cell Biol. 120, 421-435, 1993
 A:Title: Cofilin is an essential component of the yeast cortical cytoskeleton.
 A:Reference number: A44397; MUID:93132073; PMID:8421056
 A:Accession: A44397
 A:Molecule type: DNA
 A:Residues: 1-143 <MOO>
 A:Cross-references: UNIPROT:Q03048; UNIPARC:UPI0000110C55; EMBL:Z14971; NID:g3563; PIDN:
 A:Note: sequence extracted from NCBI backbone (NCBIN:122683, NCBI:P:122684)
 A:Accession: B44397
 A:Molecule type: protein
 A:Residues: 43-56; 83-96, 'X', 98; 106-129, 'DS', 132-141 <MO2>
 A:Cross-references: UNIPARC:UPI0000173E79; UNIPARC:UPI0000173E7A; UNIPARC:UPI0000173E7B
 A:Note: sequence extracted from NCBI backbone
 R:Ida, K.; Moriyama, K.; Matsumoto, S.; Kawasaki, H.; Nishida, E.; Yahara, I.
 Gene 124, 115-120, 1993
 A:Title: Isolation of a yeast essential gene, COF1, that encodes a homologue of mammalian
 A:Reference number: JN0529; MUID:93178959; PMID:8440472
 A:Accession: JN0529
 A:Molecule type: DNA
 A:Residues: 1-143 <IID>
 A:Cross-references: UNIPARC:UPI0000110C55; GB:DL3230; NID:g287599; PIDN:BAA02514.1; PID:
 R:Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
 submitted to the Protein Sequence Database, May 1996
 A:Reference number: S64792
 A:Accession: S64802

A;Cross-references: UNIPARC:UPI0000139223; GB:AE001447; GB:AE001439; NID:G4154583; PIDN:
A;Experimental source: strain J99
C;Genetics:
A;Gene: HP0085; jhp0078

Query Match 86.2%; Score 25; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KIVFF 5
|||||
Db 16 KIVFF 20

RESULT 49
F90736
molybdopterin biosynthesis protein D chain [imported] - Escherichia coli (strain O157:H7
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 16-Aug-2004
C;Accession: F90736
R;Hayashi, T.; Makino, K.; Onishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F90736
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-81 <HAY>
A;Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000D09BF; PIDN:BA834285.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0862
C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 86.2%; Score 25; DB 2; Length 81;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|::|||
Db 3 KVLFFA 8

RESULT 50
A82251
molybdenum cofactor biosynthesis protein D VC1027 [imported] - Vibrio cholerae (strain N
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 16-Aug-2004
C;Accession: A82251
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82251
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-81 <HEI>
A;Cross-references: UNIPROT:Q9K778; UNIPARC:UPI00000C2E5B; GB:AE004184; GB:AE003852; NID
A;Experimental source: serogroup O1, strain N16961, biotype El Tor
C;Genetics:
A;Gene: VC1027
A;Map position: 1
C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein
F;81/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 86.2%; Score 25; DB 2; Length 81;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db |::|||
3 KVLFFA 8

RESULT 51
G85586
molybdopterin biosynthesis [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: G85586
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouais, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85586
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-81 <STO>
A;Cross-references: UNIPROT:Q8X807; UNIPARC:UPI00000D09BF; GB:AE005174; NID:G12513773; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: moad
C;Superfamily: Molybdopterin biosynthesis sulfur carrier protein

Query Match 86.2%; Score 25; DB 2; Length 81;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|::|||
Db 3 KVLFFA 8

RESULT 52
H64814
molybdopterin biosynthesis protein D chain [validated] - Escherichia coli (strain K-12)
N;Alternate names: moAD protein; molybdopterin-converting factor 10K chain; molybdopterin
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;Accession: H64814; S35001; A46585; S31882
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64814
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-81 <BLAY>
A;Cross-references: UNIPROT:P30748; UNIPARC:UPI00001116DF; GB:AE0000181; GB:U000096; NID:
A;Experimental source: strain K-12, substrain MG1655
R;Rivers, S.L.; McInairn, E.; Blasco, F.; Giordano, G.; Boxer, D.H.
Mol. Microbiol. 8, 1071-1081, 1993
A;Title: Molecular genetic analysis of the moa operon of Escherichia coli K-12 required
A;Reference number: S34998; MUID:93368423; PMID:8361352
A;Accession: S35001
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-44, 'R', 46-81 <RIV>
A;Cross-references: UNIPARC:UPI000016F2FD; EMBL:X70420; NID:G42007; PIDN:CAA49864.1; PI
A;Experimental source: strain K12
R;Pitterle, D.M.; Rajagopalan, K.V.
J. Biol. Chem. 268, 13499-13505, 1993
A;Title: The biosynthesis of molybdopterin in Escherichia coli. Purification and charac
A;Reference number: A46585; MUID:93293873; PMID:8514782
A;Accession: A46585
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8, 'E', 10-15 <PIT>
A;Cross-references: UNIPARC:UPI0000178EC3
A;Note: sequence extracted from NCBI backbone (NCBIP:134491)
C;Genetics:

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: P9639
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-774 <STO>
A:Cross-references: UNIPROT:O64777; UNIPARC:UPI00000A26B1; GB:AE005173; NID:g3056587; PI
C:Genetics:
A:Gene: T1P9.8
A:Map position: 1
C:Superfamily: S-locus receptor-like kinase SRK; protein kinase homology; S-locus-specific

Query Match 89.7%; Score 26; DB 2; Length 774;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:|||||
Db 5 RIVFFA 10

RESULT 45
A86340
protein F2D10.24 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: A86340
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A86340
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1119 <STO>
A:Cross-references: UNIPROT:Q9LM79; UNIPARC:UPI00000A3B0B; GB:AE005172; NID:g8886947; PI
C:Genetics:
A:Gene: F2D10.24
A:Map position: 1

Query Match 89.7%; Score 26; DB 2; Length 1119;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:|||||
Db 1045 KILFFA 1050

RESULT 46
JU0330
hypothetical protein, 2.4K (lytA 5' region) - Streptococcus pneumoniae
C:Species: Streptococcus pneumoniae
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JU0330
R:Diaz, E.; Garcia, J.L.
Gene 90, 157-162, 1990
A>Title: Characterization of the transcription unit encoding the major pneumococcal auto
A:Reference number: JU0329; MUID:90337339; PMID:1974230
A:Accession: JU0330
A:Molecule type: DNA

A:Residues: 1-20 <DIP>
A:Cross-references: UNIPROT:Q8CYA3; UNIPARC:UPI00000E477A
A:Experimental source: strain M31
C:Genetics:
A:Start codon: GTG

Query Match 86.2%; Score 25; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
:|||||
Db 14 KIVFF 18

RESULT 47
A99091
hypothetical protein spr1755 [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A99091
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burtgett, S.; DeHoff, B.S.; E e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.; A>Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: A99091
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <KUR>
A:Cross-references: UNIPROT:Q8CYA3; UNIPARC:UPI00000E477A; GB:AE007317; PIDN:AAL00558.1
C:Genetics:
A:Gene: spr1755

Query Match 86.2%; Score 25; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
:|||||
Db 14 KIVFF 18

RESULT 48
E64530
hypothetical protein (HP0085, jhp0078) - Helicobacter pylori
C:Species: Helicobacter pylori
A:Variety: strains J99, 26695
C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: E64530; A71976
R:Tomb, J.P.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen ne, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A>Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: E64530
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62 <TON>
A:Cross-references: UNIPROT:O24912; UNIPARC:UPI0000139223; GB:AE000530; GB:AE000511; NID
A:Experimental source: strain 26695
R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A:Reference number: A71800; MUID:99120557; PMID:9923682
A:Accession: A71976
A:Molecule type: DNA
A:Residues: 1-62 <ARN>

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH1271

C;Superfamily: yceG protein

Query Match 89.7%; Score 26; DB 2; Length 382;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

|||||

Db 25 KIVFFS 30

RESULT 40

E86038

Probable LPS biosynthesis enzyme waal [imported] - Escherichia coli (strain O157:H7, sub

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: E86038

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: E86038

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-402 <STO>

A;Cross-references: UNIPROT:Q92IT8; UNIPARC:UPI00000D00DF; GB:AE005174; NID:gl2518378; F

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: waal

Query Match 89.7%; Score 26; DB 2; Length 402;

Best Local Similarity 83.3%; Pred. No. 1.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

|||||

Db 126 KIVFFS 131

RESULT 41

D91191

lipid A-core surface polymer ligase [imported] - Escherichia coli (strain O157:H7, sub

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: D91191

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: D91191

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-402 <HAY>

A;Cross-references: UNIPROT:Q92IT8; UNIPARC:UPI00000D00DF; GB:BA000007; PIDN:BA037923.1;

A;Experimental source: strain O157:H7, substrain RIMD 0509952

C;Genetics:

A;Gene: ECs4500

Query Match 89.7%; Score 26; DB 2; Length 402;

Best Local Similarity 83.3%; Pred. No. 1.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

|||||

Db 126 KIVFFS 131

RESULT 42

A70146

tyrosine-tRNA ligase (EC 6.1.1.1) tyrS - Lyme disease spirochete

N;Alternate names: tyrosyl-tRNA synthetase

C;Species: Borrelia burgdorferi (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C;Accession: A70146

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White

son, D.; Peterson, J.; Kurlavag, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: A70146

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-405 <KLB>

A;Cross-references: UNIPROT:O51343; UNIPARC:UPI000005745B; GB:AE001142; GB:AE000783; NID

A;Experimental source: strain B31

C;Superfamily: tyrosine-tRNA ligase

C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 89.7%; Score 26; DB 2; Length 405;

Best Local Similarity 83.3%; Pred. No. 1.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

|||||

Db 31 KIVFFA 36

RESULT 43

H69382

ABC transporter, ATP-binding protein homolog - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004

C;Accession: H69382

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodeso

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F

; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: H69382

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-620 <KLB>

A;Cross-references: UNIPROT:O29198; UNIPARC:UPI0000056E80; GB:AE001029; GB:AE000782; NI

C;Keywords: ATP; nucleotide binding; P-loop

F;428-612/Domain: ATP-binding cassette homology <ABC>

F;445-452/Region: nucleotide-binding motif A (P-loop)

Query Match 89.7%; Score 26; DB 2; Length 620;

Best Local Similarity 83.3%; Pred. No. 2.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6

|||||

Db 59 KILFFA 64

RESULT 44

F96639

protein TIF9.8 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004

C;Accession: F96639

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

RESULT 30
A95895
probable permease protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasmid
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: A95895
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhxwester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:1148131
A:Accession: A95895
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <KUR>
A:Cross-references: UNIPROT:Q92WB8; UNIPARC:UPI00000CB514; GB:AL591985; PIDN:CAC48825.1
A:Experimental source: strain 1021, megaplasmid pSymB
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: Smb20443
A:Genome: plasmid

Query Match 89.7%; Score 26; DB 2; Length 190;
Best Local Similarity 83.3%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 116 RIVFFA 121

RESULT 31
B97211
uncharacterized conserved membrane protein CAC2524 [imported] - Clostridium acetobutylic
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97211
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: B97211
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-194 <KUR>
A:Cross-references: UNIPROT:Q97G46; UNIPARC:UPI00000CA55C; GB:AE001437; PIDN:AAK80477.1
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2524

Query Match 89.7%; Score 26; DB 2; Length 194;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 165 KILFFA 170

RESULT 32
T32514
hypothetical protein C44B12.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004

C:Accession: T32514
R:Tin-Wollam, A.
A:Description: The sequence of C. elegans cosmid C44B12.
A:Reference number: Z21183
A:Accession: T32514
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-247 <TIN>
A:Cross-references: UNIPROT:O44145; UNIPARC:UPI00001793B3; EMBL:AF036692; PIDN:AAB88324.
A:Experimental source: strain Bristol N2; clone C44B12
C:Genetics:
A:Gene: CESP:C44B12.1
A:Map position: 4
A:Introns: 28/3; 82/1; 164/1; 192/1
Query Match 89.7%; Score 26; DB 2; Length 247;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 224 KIVFFS 229

RESULT 33
D82405
transcription regulator LuxR family VCA0888 [imported] - Vibrio cholerae (strain N16961
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
A:Accession: D82405
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.;
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82405
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-253 <HEI>
A:Cross-references: UNIPROT:Q9KL60; UNIPARC:UPI00000C36AA; GB:AE004416; GB:AE003853; NI
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0888
A:Map position: 2

Query Match 89.7%; Score 26; DB 2; Length 253;
Best Local Similarity 83.3%; Pred. No. 93;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 51 KIVFFS 56

RESULT 34
T31855
hypothetical protein C02E7.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
A:Accession: T31855
R:Fulton, B.; Wohldmann, P.
submitted to the EMBL Data Library, June 1998
A:Description: the sequence of C. elegans cosmid C02E7.
A:Reference number: Z21093
A:Accession: T31855
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-277 <FUL>
A:Cross-references: UNIPARC:UPI000017B71A; EMBL:AF016446; PIDN:AA24170.1; GSPDB:GN0002
A:Experimental source: strain Bristol N2; clone C02E7
C:Genetics:

A;Accession: S30236
 A;Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A;Residues: 1-1016 <WUM>
 A;Cross-references: UNIPROT:Q05912; UNIPARC:UPI00000ECC69; EMBL:X68509; NID:G288233; PID
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992
 C;Superfamily: tobacco etch virus genome polyprotein
 C;Keywords: coat protein; genome-linked protein; nucleotidyltransferase; phosphoprotein;
 P;9-61/Product: VPg protein #status predicted <VPG>
 P;62-494/Product: nuclear inclusion protein a #status predicted <NIA>
 P;495-1010/Product: RNA-directed RNA polymerase #status predicted <POL>
 P;1011-1016/Product: coat protein (fragment) #status predicted <COP>
 P;125/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted

Query Match 93.1%; Score 27; DB 2; Length 1016;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 837 KLVFFA 842

RESULT 26
 E64214
 Hypothetical protein homolog MG131 - Mycoplasma genitalium
 C;Species: Mycoplasma genitalium
 C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: E64214
 R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
 M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
 C.A.; Venter, J.C.
 Science 270, 397-403, 1995
 A;Title: The minimal gene complement of Mycoplasma genitalium.
 A;Reference number: A64200; MUID:96026346; PMID:7569993
 A;Accession: E64214
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A;Residues: 1-74 <TIGR>
 A;Cross-references: UNIPROT:P47377; UNIPARC:UPI000013931D; GB:U39691; GB:L43967; NID:g10
 A;Experimental source: strain G-37
 C;Genetics:
 A;Genetic code: SGC3

Query Match 89.7%; Score 26; DB 2; Length 74;
 Best Local Similarity 83.3%; Pred. No. 30;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 34 KLVFFA 39

RESULT 27
 B72213
 conserved hypothetical protein - Thermotoga maritima (strain MSBB)
 C;Species: Thermotoga maritima
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: B72213
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A;Reference number: A72200; MUID:99287316; PMID:10360571
 A;Accession: B72213
 A;Status: preliminary
 A:Molecule type: DNA
 A;Residues: 1-109 <ARN>
 A;Cross-references: UNIPROT:Q9X292; UNIPARC:UPI00000C120B; GB:AE001815; GB:AE000512; NID
 A;Experimental source: strain MSBB
 C;Genetics:
 A;Gene: TM1771

C;Superfamily: Bacillus subtilis conserved hypothetical protein yqhY

Query Match 89.7%; Score 26; DB 2; Length 109;
 Best Local Similarity 83.3%; Pred. No. 43;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 19 KLVFFA 24

RESULT 28
 H95252
 PTS system, IIB component [imported] - Streptococcus pneumoniae (strain TIGR4)
 C;Species: Streptococcus pneumoniae
 C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C;Accession: H95252
 R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A;Reference number: A95000; MUID:21357209; PMID:11463916
 A;Accession: H95252
 A;Status: preliminary
 A:Molecule type: DNA
 A;Residues: 1-156 <KUR>
 A;Cross-references: UNIPROT:Q97N92; UNIPARC:UPI0000051B4E; GB:AE005672; PIDN:AAK76217.1;
 A;Experimental source: strain TIGR4
 C;Genetics:
 A;Gene: SP2163
 C;Superfamily: phosphotransferase system mannose-specific enzyme II, factor III

Query Match 89.7%; Score 26; DB 2; Length 156;
 Best Local Similarity 83.3%; Pred. No. 59;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 56 KIVFFS 61

RESULT 29
 F98117
 Hypothetical protein PTS-EII [imported] - Streptococcus pneumoniae (strain R6)
 C;Species: Streptococcus pneumoniae
 C;Date: 22-Oct-2001 #sequence_revision 23-Oct-2001 #text_change 09-Jul-2004
 C;Accession: F98117
 R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 y, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A;Reference number: A97872; MUID:21429245; PMID:11544234
 A;Accession: F98117
 A;Status: preliminary
 A:Molecule type: DNA
 A;Residues: 1-156 <KUR>
 A;Cross-references: UNIPROT:Q8DN20; UNIPARC:UPI00000E3754; GB:AE007317; PIDN:AAL00771.1;
 C;Genetics:
 A;Gene: PTS-EII

Query Match 89.7%; Score 26; DB 2; Length 156;
 Best Local Similarity 83.3%; Pred. No. 59;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 56 KIVFFS 61

R;Murrell, J.; Farlow, M.; Ghetti, B.; Benson, M.D.
Science 254, 97-99, 1991
A;Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A;Reference number: I9562; MUID:92022553; PMID:1925564
A;Accession: 159562
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 689-716, 'F', 718-737 <MUR>
A;Cross-references: UNIPARC:UPI000017FEA; GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:
R;Kamino, K.; Orr, H.T.; Payami, H.; Wajisman, E.M.; Alonso, M.E.; Pullet, S.M.; Anderson,
arakis, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A;Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A;Reference number: A44017; MUID:93035397; PMID:1415269
A;Accession: A44017
A;Molecule type: DNA
A;Residues: 687-692, 'G', 694-718 <KAM1>
A;Cross-references: UNIPARC:UPI000011F7EB; GB:S45135; NID:g257377; PIDN:AAB23645.1; PID:
A;Experimental source: familial Alzheimer disease family SB
A;Note: sequence extracted from NCBI backbone (NCBIP:115374)
A;Accession: B44017
A;Molecule type: DNA
A;Residues: 687-718 <KAM2>
A;Cross-references: UNIPARC:UPI000016B394; GB:S45136; NID:g257379; PIDN:AAB23646.1; PID:
A;Experimental source: familial Alzheimer disease family Lit
A;Note: sequence extracted from NCBI backbone (NCBIP:115376)
A;Note: this sequence has a silent mutation
R;Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A;Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A;Reference number: A03134; MUID:87144572; PMID:2881207
A;Accession: A03134
A;Molecule type: mRNA
A;Residues: 1-288, 'V', 365-770 <KAN>
A;Cross-references: UNIPARC:UPI000002A2F2; GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:9
A;Note: alternative splice form APP(695)
R;Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A;Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular a
A;Reference number: A29030; MUID:87231971; PMID:3035574
A;Accession: A29030
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-770 <ROB>
A;Cross-references: UNIPARC:UPI000016A545; GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:
A;Note: the authors translated the codon GAG for residue 647 as Asp
R;Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffioti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A;Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A;Reference number: A47584; MUID:87120328; PMID:3810169
A;Accession: A47584
A;Molecule type: mRNA
A;Residues: 674-756, 'S', 758-770 <COL>
A;Cross-references: UNIPARC:UPI00001420B5; GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:
A;Experimental source: brain
R;Tanzi, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A;Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A;Reference number: A47585; MUID:87120329; PMID:2949367
A;Accession: A47585
A;Molecule type: mRNA
A;Residues: 674-703 <TANI>
A;Cross-references: UNIPARC:UPI000016A46F; GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:
R;Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A;Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pro
A;Reference number: S02638; MUID:88296437; PMID:2900137
A;Accession: S02638
A;Molecule type: mRNA
A;Residues: 672-678 <DYP>
A;Cross-references: UNIPARC:UPI0000035AB0
R;Tanzi, R.E.; McClatchey, A.I.; Lamperti, E.D.; Valla-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988
A;Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA associat

A;Reference number: S00707; MUID:88122640; PMID:2893290
A;Accession: S00707
A;Molecule type: mRNA
A;Residues: 286-344, 'I', 365-366 <TAN2>
A;Cross-references: UNIPARC:UPI00001421B0; EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:
A;Experimental source: promyelocytic leukemia cell line HL60
A;Note: alternative splice form APP(751)
R;Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.; Da
Nature 331, 525-527, 1988
A;Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibit
A;Reference number: S00925; MUID:88122639; PMID:2893289
A;Accession: S00925
A;Molecule type: mRNA
A;Residues: 1-344, 'I', 365-770 <PO2>
A;Cross-references: UNIPARC:UPI000002A2F6; GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA3
A;Note: alternative splice form APP(751)
R;Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A;Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibitor
A;Reference number: A38949; MUID:88122641; PMID:2893291
A;Accession: A38949
A;Molecule type: mRNA
A;Residues: 287-367 <KIT>
A;Cross-references: UNIPARC:UPI000014553B; GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:
A;Experimental source: glioblastoma cell line
A;Note: alternative splice form APP(770)
R;Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ashtoi
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A;Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of three I
A;Reference number: A30320
A;Accession: A30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 284-288, 'V', 365-770 <VIT1>
A;Cross-references: UNIPARC:UPI0000174094
A;Accession: B30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 122-288, 'V', 365-770 <VIT2>
A;Cross-references: UNIPARC:UPI0000174094
A;Accession: C30320
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 606-770 <VIT3>
A;Cross-references: UNIPARC:UPI0000174094
R;Zain, S.B.; Salim, M.; Chou, W.G.; Saidel-Sulkowska, E.M.; Majocha, R.E.; Marotta, C.
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A;Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease b
A;Reference number: A31087; MUID:88124954; PMID:2893379
A;Accession: A31087
A;Molecule type: mRNA

Query Match 93.1%; Score 27; DB 1; Length 770;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
DB 687 KLVFFA 692

RESULT 25
S30236
genome polyprotein - zucchini yellow mosaic virus (strain Singapore) (fragment)
N;Contains: coat protein; nuclear inclusion protein a; RNA-directed RNA polymerase (EC
C;Species: zucchini yellow mosaic virus, ZYMV
A;Variety: strain Singapore
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C;Accession: S30236
R;Wu, M.; Yeong, C.Y.; Lee, S.C.; Wong, S.M.
Nucleic Acids Res. 21, 1317, 1993
A;Title: Nucleotide sequence of the 3' half of zucchini yellow mosaic virus (Singapore
A;Reference number: S30236; MUID:93219099; PMID:8464715

A;Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37, 'X', 39-40, 'X', 42-44 <SCH>
A;Cross-references: UNIPARC:UPI00001777FD
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
PEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Cross-references: UNIPARC:UPI00001777FE
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status Predicted <TM>

Query Match 93.1%; Score 27; DB 2; Length 695;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 612 KLVFFA 617

RESULT 23
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
C;Accession: JH0773
R;Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A;Title: A xenopus homologue of the human beta-amyloid precursor protein: developmental
A;Reference number: JH0773; MUID:93129227; PMID:1282805
A;Accession: JH0773
A;Molecule type: mRNA
A;Residues: 1-747 <OKA>
A;Cross-references: UNIPARC:UPI00000FC880; GB:S52417; NID:G263150; PIDN:AAB24853.1; PID:
A;Experimental source: larva
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C;Keywords: alternative splicing; amyloid
F;287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>

Query Match 93.1%; Score 27; DB 2; Length 747;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|||||
Db 664 KLVFFA 669

RESULT 24
QRHUA4
Alzheimer's disease amyloid beta protein precursor [validated] - human
A;Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor X1a inhibitor
N;Contents: amyloid beta protein long, plaque form; amyloid beta protein short, vascular
protein precursor splice form APP(770)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000

C;Accession: S02260; S05194; A32277; A33260; A35486; I39452; I39451; I39453; I59562; A44
466; A28583; A29302; A60805; J00038; S06121; A60355; A59011; A38384; S29076; S38252; S3
R;Lemaire, H.G.; Salbaum, J.M.; Multhaup, G.; Kang, J.; Baynes, R.M.; Unterbeck, A.; Bey
Nucleic Acids Res. 17, 517-522, 1989
A;Title: The PreA4(695) precursor protein of Alzheimer's disease A4 amyloid is encoded b
A;Reference number: S02260; MUID:89128427; PMID:2783775
A;Accession: S02260
A;Molecule type: DNA
A;Residues: 1-288, 'V', 365-770 <LEM1>
A;Cross-references: UNIPARC:UPI000002A2F2; EMBL:X13466
A;Note: alternative splice form APP(695)
R;Lemaire, H.G.
submitted to the EMBL Data Library, November 1988
A;Reference number: S05194
A;Accession: S05194
A;Molecule type: DNA
A;Residues: 1-14, 'VM', 17-288, 'V', 365-770 <LEM2>
A;Cross-references: UNIPARC:UPI000016A57D; EMBL:X13466; PIDN:CAA31830.1; PID:
A;Note: alternative splice form APP(695)
R;La Pauci, G.; Lahiri, D.K.; Salton, S.R.J.; Robakis, N.K.
Biochem. Biophys. Res. Commun. 159, 297-304, 1989
A;Title: Characterization of the 5'-end region and the first two exons of the beta-prote
A;Reference number: A32277; MUID:89165870; PMID:2538123
A;Accession: A32277
A;Molecule type: DNA
A;Residues: 1-75 <LAP>
A;Cross-references: UNIPARC:UPI000016A57D; GB:M24546; GB:M24547; NID:G341202; PIDN:AAAC13
R;Johnstone, E.M.; Chaney, M.O.; Moore, R.E.; Ward, K.E.; Norris, F.H.; Little, S.P.
Biochem. Biophys. Res. Commun. 163, 1248-1255, 1989
A;Title: Alzheimer's disease amyloid peptide is encoded by two exons and shows similarit
A;Reference number: A33260; MUID:8932030; PMID:2675837
A;Accession: A33260
A;Molecule type: DNA
A;Residues: 656-737 <JOH>
A;Cross-references: UNIPARC:UPI000016A551; GB:M29270; NID:G178863; PIDN:AAAS1768.1; PID:
R;Prelti, F.; Levy, E.; van Duinen, S.G.; Bots, G.T.A.M.; Luyendijk, W.; Frangione, B.
Biochem. Biophys. Res. Commun. 170, 301-307, 1990
A;Title: Expression of a normal and variant Alzheimer's beta-protein gene in amyloid of
A;Reference number: A35486; MUID:90321244; PMID:2196878
A;Accession: A35486
A;Molecule type: DNA
A;Residues: 672-710 <PRE1>
A;Cross-references: UNIPARC:UPI0000148176
A;Note: 693-Gln was found in DNA isolated from HCHWA-D patients
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuha, H.; Sakaki, Y.
Gene 87, 257-263, 1990
A;Title: Genomic organization of the human amyloid beta-protein precursor gene.
A;Reference number: I39451; MUID:90236318; PMID:2110105
A;Accession: I39452
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-770 <YOS1>
A;Cross-references: UNIPARC:UPI000002DB1C; GB:M33112; NID:G178613; PIDN:AAB59502.1; PID:
A;Accession: I39451
A;Status: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL
A;Molecule type: DNA
A;Residues: 1-530, 'QWLMVPVPAFWKVR', <YOS2>
A;Cross-references: UNIPARC:UPI000016A54F; GB:M34875; NID:G178608; PIDN:AAB59501.1; PID:
R;Yoshikai, S.I.; Sasaki, H.; Doh-ura, K.; Furuha, H.; Sakaki, Y.
Gene 102, 291-292, 1991
A;Reference number: A59020; MUID:91340168; PMID:1908403
A;Contents: annotation; erratum
A;Note: revised physical map for reference I39451
R;Levy, E.; Carman, M.D.; Fernandez-Madrid, I.J.; Power, M.D.; Lieberburg, I.; van Duinen
Science 248, 1124-1126, 1990
A;Title: Mutation of the Alzheimer's disease amyloid gene in hereditary cerebral hemorrh
A;Reference number: I39453; MUID:90260663; PMID:2111584
A;Accession: I39453
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 656-737 <LEV>
A;Cross-references: UNIPARC:UPI000016A551; GB:M37896; NID:G178618; PIDN:AAAS1727.1; PID:
A;Note: a mutation with 693-Gln is presented

C;Accession: F70399
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70399
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-380 <AQF>
A;Cross-references: UNIPROT:O67225; UNIPARC:UPI0000056543; GB:AE000726; NID:g2983612; PID:
A;Experimental source: strain VF5
C;Genetics:
C;Superfamily: [Nife]-hydrogenase maturation factor, HypD type

Query Match 93.1%; Score 27; DB 2; Length 380;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 141 KIVFFA 146
|:|||||

RESULT 19
T48008
Hypothetical protein T17J13.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 31-Dec-2004
C;Accession: T48008
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Lemcke, K.; Mayer,
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24482
A;Accession: T48008
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-428 <RIE>
A;Cross-references: UNIPROT:Q9M108; UNIPARC:UPI00000488B7; EMBL:AL1138651
A;Experimental source: cultivar Columbia; BAC clone T17J13
C;Genetics:
A;Map position: 3
A;Introns: 137/3
A;Note: T17J13.120
C;Superfamily: N-hydroxycinnamoyl/benzoyl transferase

Query Match 93.1%; Score 27; DB 2; Length 428;
Best Local Similarity 83.3%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 271 KIVFFA 276
|:|||||

RESULT 20
A49795
Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A49795
R;Podlany, M.B.; Tolan, D.R.; Selkoe, D.J.
Am. J. Pathol. 138, 1423-1435, 1991
A;Title: Homology of the amyloid beta protein precursor in monkey and human supports a p
A;Reference number: A49795; MUID:91273117; PMID:1905108
A;Accession: A49795
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-695 <POD>
A;Cross-references: UNIPARC:UPI000002A2F2; GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
C;Keywords: alternative splicing

Query Match 93.1%; Score 27; DB 1; Length 695;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 612 KIVFFA 617
|:|||||

RESULT 21
A27485
Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
N;Alternate names: proteinase nexin II
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: A27485; S19727; I49485
R;Yanada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
Biochem. Biophys. Res. Commun. 149, 665-671, 1987
A;Title: Complementary DNA for the mouse homolog of the human amyloid beta protein precu
A;Reference number: A27485; MUID:88106489; PMID:3322280
A;Accession: A27485
A;Molecule type: mRNA
A;Residues: 1-695 <YAM>
A;Cross-references: UNIPROT:P12023; UNIPARC:UPI0000151C70; GB:M18373; NID:g191568; PIDN:
A;Experimental source: brain
R;de Strooper, B.; van Leuven, F.; van den Berghe, H.
Biochim. Biophys. Acta 1129, 141-143, 1991
A;Title: The amyloid beta protein precursor or proteinase nexin II from mouse is closer
A;Reference number: S19727; MUID:92096458; PMID:1756177
A;Accession: S19727
A;Molecule type: mRNA
A;Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
A;Cross-references: UNIPARC:UPI000002A2F9; EMBL:X59379
R;Izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
Gene 112, 189-195, 1992
A;Title: Positive and negative regulatory elements for the expression of the Alzheimer
A;Reference number: I49485; MUID:92209998; PMID:1555768
A;Accession: I49485
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
A;Cross-references: UNIPARC:UPI00000003B7; GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:
C;Genetics:
A;Map position: 16C3
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 93.1%; Score 27; DB 2; Length 695;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 612 KIVFFA 617
|:|||||

RESULT 22
S00550
Alzheimer's disease amyloid beta protein precursor - rat
N;Alternate names: beta-A4 amyloid protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: S00550; A41245; A39820; S46251
R;Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H.
EMBO J. 7, 1365-1370, 1988
A;Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat brai
A;Reference number: S00550; MUID:88312583; PMID:2900758
A;Accession: S00550
A;Molecule type: mRNA
A;Residues: 1-695 <SHI>
A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2EB; EMBL:X07648; NID:g55616; PID:
R;Schubert, D.; Schroeder, R.; Lacorbriere, M.; Saiton, T.; Cole, G.
Science 241, 223-226, 1988

Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
 C:Species: Ursus maritimus (polar bear)
 C>Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
 C:Accession: B60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079; PMID:1656157
 A:Accession: B60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: UNIPROT:Q29149; UNIPARC:UPI0000125049; EMBL:X56128; NID:G2165; PIDN:
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
 Best Local Similarity 83.3%; Pred. No. 13;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|:|
 Db 21 KLVFFA 26

RESULT 14
 PQ0438
 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 C:Accession: PQ0438; C60045
 R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992
 A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
 A:Reference number: PQ0438; MUID:93075180; PMID:1445331
 A:Accession: PQ0438
 A:Molecule type: DNA
 A:Residues: 1-82 <DAV>
 A:Cross-references: UNIPARC:UPI000016A551; GB:M83558; GB:M83657
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079; PMID:1656157
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 12-68 <JOH>
 A:Cross-references: UNIPARC:UPI0000125049; EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase i
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 93.1%; Score 27; DB 2; Length 82;
 Best Local Similarity 83.3%; Pred. No. 19;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|:|:|
 Db 32 KLVFFA 37

RESULT 15
 T06645
 hypothetical protein T20K18.220 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T06645
 R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Men
 submitted to the Protein Sequence Database, April 1999
 A:Reference number: Z15790
 A:Accession: T06645
 A:Molecule type: DNA
 A:Residues: 1-152 <BEV>
 A:Cross-references: UNIPROT:Q9ST29; UNIPARC:UPI00000A0722; EMBL:AL049640; GSPDB:GN000062;
 A:Experimental source: cultivar Columbia; BAC clone T20K18
 C:Genetics:

A:Gene: ATSP:T20K18.220

A:Map position: 4

A:Introns: 87/3; 109/3

C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match

Best Local Similarity 93.1%; Score 27; DB 2; Length 152;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

:|:|:|:|

Db 9 KLVFFA 14

RESULT 16

H85138

hypothetical protein AT4g12900 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C:Accession: H85138

R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring

A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A:Reference number: A85001; MUID:20083488; PMID:10617198

A:Accession: H85138

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-231 <STO>

A:Cross-references: UNIPROT:Q9SV79; UNIPARC:UPI00000A7E0E; GB:NC_001268; NID:G7267992; P

C:Genetics:

A:Gene: AT4g12900

A:Map position: 4

C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.100

Query Match

Best Local Similarity 93.1%; Score 27; DB 2; Length 231;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

:|:|:|:|

Db 12 KLVFFA 17

RESULT 17

T48903

wax synthase [imported] - Simmondsia chinensis

C:Species: Simmondsia chinensis

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C:Accession: T48903

R:Lardizabal, K.D.; Metz, J.G.; Sakamoto, T.; Hutton, W.C.; Pollard, M.R.; Lassner, M.W.

Plant Physiol. 122, 645-655, 2000

A:Title: Purification of a jojoba embryo wax synthase, cloning of its cDNA and productio

A:Reference number: Z25002

A:Accession: T48903

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-352 <LAR>

A:Cross-references: UNIPROT:Q9XGY6; UNIPARC:UPI00000A1C81; EMBL:AF149919; PIDN:AAD38041.

Query Match

Best Local Similarity 93.1%; Score 27; DB 2; Length 352;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

:|:|:|:|

Db 135 KLVFFA 140

RESULT 18

F70399

hydrogenase expression/formaton protein HypD - Aquifex aeolicus

C:Species: Aquifex aeolicus

C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

A;Residues: 1-42 <SHI>
A;Cross-references: UNIPROT:Q7M088; UNIPARC:UPI0000031588
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; amyloid

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 10;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 8
A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: A60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Molecule type: mRNA
A;Accession: A60045
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56125
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 9
F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C;Accession: F60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Molecule type: mRNA
A;Accession: F60045
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56127; NID:g1895; PIDN:CAA39592.1; PID:
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 10
D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: D60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.

Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: D60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56124
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 11
E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C;Species: Ovis sp. (sheep)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: E60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: E60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56130
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 12
G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C;Accession: G60045
R;Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A;Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A;Reference number: A60045; MUID:92017079; PMID:1656157
A;Accession: G60045
A;Molecule type: mRNA
A;Residues: 1-57 <JOH>
A;Cross-references: UNIPARC:UPI0000125049; EMBL:X56126
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C;Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 93.1%; Score 27; DB 2; Length 57;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 13
B60045

A;Cross-references: UNIPROT:Q9PHV5; UNIPARC:UPI00000C217E; GB:AL139075; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: CJ0560

Query Match 96.6%; Score 28; DB 2; Length 442;
Best Local Similarity 83.3%; Pred. No. 51;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 313 KLVFFA 318

RESULT 4
F71039
hypothetical protein PH1606 - *Pyrococcus horikoshii*
C;Species: *Pyrococcus horikoshii*
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004
C;Accession: F71039
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohkuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: F71039
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-447 <KAW>
A;Cross-references: UNIPROT:O59243; UNIPARC:UPI00000630DE; GB:AP000006; NID:G3236133; PI
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1606
C;Superfamily: *Pyrococcus horikoshii* hypothetical protein PH142

Query Match 96.6%; Score 28; DB 2; Length 447;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 207 KIIFFA 212

RESULT 5
A43271
nitric-oxide synthase (EC 1.14.13.39), calmodulin-independent - mouse
C;Species: *Mus musculus* (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: A43271; A42166; JN0458; A46186
R;Xie, Q.; Cho, H.J.; Calaycay, J.; Mumford, R.A.; Swiderek, K.M.; Lee, T.D.; Ding, A.;
Science 256, 225-228, 1992
A;Title: Cloning and characterization of inducible nitric oxide synthase from mouse macr
A;Reference number: A43271; MUID:92229444; PMID:1373522
A;Accession: A43271
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1144 <XIE>
A;Cross-references: UNIPROT:P29477; UNIPARC:UPI000000D36; GB:M87039; NID:G198406; PIDN:
R;Lyons, C.R.; Orloff, G.J.; Cunningham, J.M.
J. Biol. Chem. 267, 6370-6374, 1992
A;Title: Molecular cloning and functional expression of an inducible nitric oxide syntha
A;Reference number: A42166; MUID:92210618; PMID:1372907
A;Accession: A42166
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1144 <LYO>
A;Cross-references: UNIPARC:UPI000000D36; GB:M84373; NID:G200095; PIDN:AAA39834.1; PID:
R;Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.
Biochem. Biophys. Res. Commun. 191, 767-774, 1993
A;Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxid
A;Reference number: JN0457; MUID:93221515; PMID:7682072

A;Accession: JN0458
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-278, 'F', 280-682, 'H', 684-937, 939-1144 <WOO>
A;Cross-references: UNIPARC:UPI000017223A
A;Experimental source: liver
R;Lowenstein, C.J.; Glatt, C.S.; Bredt, D.S.; Snyder, S.H.
Proc. Natl. Acad. Sci. U.S.A. 89, 6711-6715, 1992
A;Title: Cloned and expressed macrophage nitric oxide synthase contrasts with the brain
A;Reference number: A46186; MUID:92357701; PMID:1379716
A;Accession: A46186
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-190, 'V', 192-765, 'P', 767-843, 'G', 845-1144 <LOW>
A;Cross-references: UNIPARC:UPI000017223B; GB:M92649; NID:G200109
A;Experimental source: BALB/c, RAW 264.7 cells, macrophage
A;Note: sequence extracted from NCBI backbone (NCBIP:113541)
C;Genetics:
A;Gene: NOS
C;Function:
A;Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
F;533-1121/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;535-671/Domain: flavodoxin homology <FLX>
F;194/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 96.6%; Score 28; DB 1; Length 1144;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 514 KLVFFA 519

RESULT 6
S23094
beta-amyloid protein precursor - rat
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-May-1996
C;Accession: S23094
R;Kojima, S.; Omori, M.
FEBS Lett. 304, 57-60, 1992
A;Title: Two-way cleavage of beta-amyloid protein precursor by multicatalytic proteinase
A;Reference number: S23094; MUID:92316198; PMID:1618299
A;Accession: S23094
A;Molecule type: protein
A;Residues: 1-33 <KOJ>
A;Cross-references: UNIPARC:UPI000001777FB
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase 1

Query Match 93.1%; Score 27; DB 2; Length 33;
Best Local Similarity 83.3%; Pred. No. 8.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 21 KLVFFA 26

RESULT 7
PN0512
beta-amyloid protein - guinea pig (fragment)
C;Species: *Cavia porcellus* (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fragmen
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein

103	25	86.2	606	2	S41830	NADH2 dehydrogenas	176	24	82.8	263	2	C97198	HAD superfamily hy
104	25	86.2	606	2	T45560	NADH2 dehydrogenas	177	24	82.8	268	2	D86736	conserved hypothet
105	25	86.2	606	2	T11373	NADH2 dehydrogenas	178	24	82.8	272	2	T24709	hypothetical prote
106	25	86.2	606	2	T10982	NADH2 dehydrogenas	179	24	82.8	274	2	T33371	hypothetical prote
107	25	86.2	606	2	T11060	NADH2 dehydrogenas	180	24	82.8	276	2	T32682	hypothetical prote
108	25	86.2	617	2	A72123	hypothetical prote	181	24	82.8	281	2	B54498	major merozoite su
109	25	86.2	655	2	T31691	hypothetical prote	182	24	82.8	286	2	C84857	hypothetical prote
110	25	86.2	726	2	T15810	hypothetical prote	183	24	82.8	286	2	AF2941	hypothetical prote
111	25	86.2	732	2	T32023	hypothetical prote	184	24	82.8	294	2	D98341	lactose transport
112	25	86.2	763	2	T21006	hypothetical prote	185	24	82.8	295	2	JC4744	NAD-dinitrogen-red
113	25	86.2	817	2	A82511	glycogen phosphory	186	24	82.8	295	2	I39751	NAD-dinitrogen-red
114	25	86.2	825	2	T46311	hypothetical prote	187	24	82.8	295	2	C70736	hypothetical prote
115	25	86.2	935	2	T40715	hypothetical prote	188	24	82.8	295	2	A36966	probable dTDP-rham
116	25	86.2	1121	2	T21303	hypothetical prote	189	24	82.8	296	2	D82515	ketoreductase XF27
117	25	86.2	1133	2	T30302	P-type ATPase - Te	190	24	82.8	302	2	A99074	hypothetical prote
118	25	86.2	1270	2	T21269	hypothetical prote	191	24	82.8	302	2	B35961	hypothetical 21K p
119	25	86.2	1291	2	T21267	hypothetical prote	192	24	82.8	304	2	C90565	hypothetical prote
120	25	86.2	1316	2	D87145	[beta], subunit of	193	24	82.8	311	2	S73625	methionyl-tRNA for
121	25	86.2	1316	2	S31146	DNA-directed RNA p	194	24	82.8	312	2	A46247	olfactory receptor
122	25	86.2	1316	2	G70535	probable rpoC prot	195	24	82.8	316	2	S61237	capsid protein - b
123	25	86.2	1318	2	T21266	hypothetical prote	196	24	82.8	316	2	F81712	ABC transporter, p
124	25	86.2	1327	2	T21268	hypothetical prote	197	24	82.8	318	2	A75275	methionyl-tRNA for
125	25	86.2	1462	2	T00345	hypothetical prote	198	24	82.8	318	2	H71561	probable integral
126	24	82.8	20	2	C60894	gamma crystallin I	199	24	82.8	322	2	F84948	NADH2 dehydrogenas
127	24	82.8	61	2	H71329	hypothetical prote	200	24	82.8	322	2	T24356	hypothetical prote
128	24	82.8	77	2	A01750	preprotein translo	201	24	82.8	328	2	T11938	NADH2 dehydrogenas
129	24	82.8	85	2	A33408	molybdopterin (mpt	202	24	82.8	330	2	H75505	tryptophanyl-tRNA
130	24	82.8	101	2	T26641	hypothetical prote	203	24	82.8	334	2	T20562	hypothetical prote
131	24	82.8	104	2	C75046	hypothetical prote	204	24	82.8	347	2	A81988	probable N-acetyl-
132	24	82.8	110	2	A10493	probable membrane	205	24	82.8	347	2	D81043	N-acetyl-gamma-glu
133	24	82.8	115	2	B25120	major merozoite su	206	24	82.8	347	2	S35229	hypD', protein - Br
134	24	82.8	132	2	G84717	actin depolymerizi	207	24	82.8	348	2	C64676	oligopeptide ABC t
135	24	82.8	136	2	T19479	hypothetical prote	208	24	82.8	348	2	C71841	probable peptide A
136	24	82.8	140	2	B95049	hypothetical prote	209	24	82.8	352	2	H97272	histidinol-phospha
137	24	82.8	140	2	H97919	(3R)-hydroxymyrist	210	24	82.8	356	2	T13430	hypothetical prote
138	24	82.8	144	2	A86722	hypothetical prote	211	24	82.8	356	2	D84280	hypothetical prote
139	24	82.8	146	2	E75134	hypothetical prote	212	24	82.8	356	2	T18590	hypothetical prote
140	24	82.8	148	2	T32362	hypothetical prote	213	24	82.8	357	2	T16596	hypothetical prote
141	24	82.8	149	2	JA0167	prolamin 17 precu	214	24	82.8	363	2	F70195	UDP-N-acetylglucos
142	24	82.8	153	2	A80099	probable membrane	215	24	82.8	364	2	H85856	probable transport
143	24	82.8	155	2	S59155	NADH2 dehydrogenas	216	24	82.8	364	2	A10784	probable binding-p
144	24	82.8	159	2	C71080	hypothetical prote	217	24	82.8	364	2	F91012	probable transport
145	24	82.8	162	2	T13659	NADH2 dehydrogenas	218	24	82.8	364	2	A64987	hypothetical ABC t
146	24	82.8	162	2	T13656	NADH2 dehydrogenas	219	24	82.8	365	2	T33499	hypothetical prote
147	24	82.8	162	2	T13563	NADH2 dehydrogenas	220	24	82.8	373	2	AE0847	hydrogenase isoenz
148	24	82.8	162	2	T13487	NADH2 dehydrogenas	221	24	82.8	373	2	A85922	pleiotrophic effec
149	24	82.8	164	2	T13562	NADH2 dehydrogenas	222	24	82.8	373	2	A91077	hydrogenase isoenz
150	24	82.8	168	2	A25522	major merozoite su	223	24	82.8	373	2	S15200	hydrogenase expres
151	24	82.8	187	2	A99124	hypothetical prote	224	24	82.8	379	2	I39743	hydrogenase homolo
152	24	82.8	188	2	G70475	conserved hypothet	225	24	82.8	381	2	A70454	conserved hypothet
153	24	82.8	188	2	T25683	hypothetical prote	226	24	82.8	384	2	H64161	hypothetical prote
154	24	82.8	200	2	A81632	hypothetical prote	227	24	82.8	385	2	S32877	hypD protein - Rhi
155	24	82.8	208	2	T05859	hypothetical prote	228	24	82.8	397	2	F95352	probable proline d
156	24	82.8	211	2	JC4540	transcription init	229	24	82.8	398	2	C81729	Mr/TnaB/TyO perm
157	24	82.8	211	2	S14920	hypothetical prote	230	24	82.8	399	2	G97727	proton/sodium-glut
158	24	82.8	212	2	B75109	hypothetical prote	231	24	82.8	399	2	D71728	proton/sodium-glut
159	24	82.8	214	2	T47892	hypothetical prote	232	24	82.8	399	2	A82842	conserved hypothet
160	24	82.8	220	2	A64141	probable glutamate	233	24	82.8	402	2	AE2804	MFS permease (impo
161	24	82.8	224	2	E95223	hypothetical prote	234	24	82.8	404	2	H96916	probable permease
162	24	82.8	224	2	H98087	probable haloacid	235	24	82.8	404	2	A97559	hypothetical prote
163	24	82.8	226	2	S62550	probable haloacid	236	24	82.8	404	2	AE2779	acyltransferase li
164	24	82.8	231	1	E84982	yonK protein - Esc	237	24	82.8	407	2	B81914	probable transmemb
165	24	82.8	231	2	B91008	probable seritonin	238	24	82.8	417	2	T18769	hypothetical prote
166	24	82.8	231	2	D85852	probable serotonin	239	24	82.8	420	2	B90553	hypothetical prote
167	24	82.8	231	2	C64703	hypothetical prote	240	24	82.8	421	2	H72492	probable proton/ao
168	24	82.8	232	2	A71495	probable polyaacch	241	24	82.8	422	2	E82904	hypothetical prote
169	24	82.8	233	2	A25814	Glycoprotein 185 -	242	24	82.8	423	2	JC7677	allatostatin recep
170	24	82.8	233	2	T32680	hypothetical prote	243	24	82.8	426	2	F81187	glucose/galactose
171	24	82.8	234	2	T23466	hypothetical prote	244	24	82.8	435	2	AD1340	maltodextrin ABC-t
172	24	82.8	238	2	F70107	hypothetical prote	245	24	82.8	435	2	H61711	maltodextrin ABC-t
173	24	82.8	255	2	C87434	2-deoxy-D-gluconat	246	24	82.8	437	2	H64251	replication initia
174	24	82.8	257	2	C83982	hypothetical prote	247	24	82.8	437	2	S50006	preprotein translo
175	24	82.8	261	2	D84166	hypothetical prote	248	24	82.8	437	2	JC5115	preprotein translo

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds
(without alignments)
44.518 Million cell updates/sec

Title: US-10-009-122-1
Perfect score: 29
Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : PIR 80:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	96.6	186	1 WMR219	19K globulin precu
2	28	96.6	186	2 JC4784	alpha-globulin pre
3	28	96.6	442	2 H81402	probable integral
4	28	96.6	447	2 F71039	hypothetical prote
5	28	96.6	1144	1 A43271	nitric-oxide synth
6	27	93.1	33	2 S23094	beta-amyloid prote
7	27	93.1	42	2 PN0512	beta-amyloid prote
8	27	93.1	57	2 A60045	Alzheimer's diseas
9	27	93.1	57	2 F60045	Alzheimer's diseas
10	27	93.1	57	2 D60045	Alzheimer's diseas
11	27	93.1	57	2 E60045	Alzheimer's diseas
12	27	93.1	57	2 G60045	Alzheimer's diseas
13	27	93.1	57	2 B60045	Alzheimer's diseas
14	27	93.1	82	2 PQ0438	Alzheimer's diseas
15	27	93.1	152	2 T06645	hypothetical prote
16	27	93.1	231	2 H85138	hypothetical prote
17	27	93.1	352	2 T48903	wax synthase [impo
18	27	93.1	380	2 F70399	hydrogenase expres
19	27	93.1	428	2 T48008	hypothetical prote
20	27	93.1	695	1 A49795	Alzheimer's diseas
21	27	93.1	695	2 A27485	Alzheimer's diseas
22	27	93.1	695	2 S00550	Alzheimer's diseas
23	27	93.1	747	2 JH0773	Alzheimer's diseas
24	27	93.1	770	1 QRHUA4	Alzheimer's diseas
25	27	93.1	1016	2 S30236	genome polypeptid
26	26	89.7	74	2 E64214	hypothetical prote
27	26	89.7	109	2 B72213	conserved hypotet
28	26	89.7	156	2 H95252	PTS system, IIB co
29	26	89.7	156	2 F98117	hypothetical prote

probable permease	190	2	A95895
uncharacterized co	194	2	B97211
hypothetical prote	247	2	T32514
transcription regu	253	2	D82405
hypothetical prote	277	2	T31855
hypothetical prote	300	2	T26245
hypothetical prote	321	2	H71729
hypothetical prote	349	2	T26247
sorbitol dehydroge	352	2	AH2097
hypothetical prote	382	2	G83808
probable LPS biosy	402	2	E86038
lipid A-core surfa	402	2	D91191
tyrosine-tRNA liga	405	2	A70146
ABC transporter, A	620	2	H93382
protein Tif9.8 [im	1119	2	A86340
hypothetical prote	20	2	JU0330
hypothetical prote	20	2	A99091
hypothetical prote	62	2	E84530
hypothetical prote	81	2	F90736
molybdopterin bios	81	2	A82251
molybdenum cofacto	81	2	G85586
molybdopterin bios	81	2	H64814
molybdopterin conv	81	2	A80598
hypothetical prote	83	2	AC0598
gliding motility p	108	2	C84516
cofilin - yeast (S	141	1	B70457
hypothetical prote	143	1	A44397
phosphoribosyl-AMP	193	2	B90157
hypothetical prote	207	2	B81256
HDEL receptor ERD2	219	1	A35617
hypothetical prote	219	2	A75004
glutaredoxin-relat	221	2	G72322
hypothetical prote	222	2	T47768
conserved hypotet	225	2	A90260
amino acid ABC tra	248	2	F71849
glutamine transpor	248	2	C64666
hypothetical prote	254	2	T28170
conserved hypotet	256	2	AC1561
conserved hypotet	256	2	AE1203
conserved hypotet	262	2	A81056
conserved hypotet	262	2	A81820
NAD ADP-ribosyltra	269	2	S05343
carboxyphosphoen	276	2	AI2038
hypothetical prote	287	2	D63355
glycerol kinase [g	293	2	H90318
methionyl-tRNA for	311	2	D64240
NADH2 dehydrogenas	330	2	B82822
hypothetical prote	337	2	AG0963
UDP-N-acetylglucos	339	2	B72402
cell fusion protei	340	1	MM3E5
methionyl-tRNA for	342	2	AE2238
probable LPS biosy	363	2	S56273
probable LPS biosy	380	2	F86038
hydrogenase expres	380	2	E91191
hypothetical prote	383	2	AF1893
hypothetical prote	385	2	T31493
membrane glycoprot	400	2	H69009
hypothetical prote	409	2	S29124
hypothetical prote	455	2	T34366
LPS glycosyltransf	466	2	A95179
hypothetical prote	466	2	B97030
hypothetical prote	466	2	H98045
potassium channel	477	2	B28988
hypothetical prote	490	2	A35312
hypothetical prote	509	2	S51348
hypothetical prote	520	2	A81548
hypothetical prote	594	2	F86499
conserved hypotet	603	2	T11490
NADH2 dehydrogenas	603	2	F72237
NADH2 dehydrogenas	604	2	T11867
NADH2 dehydrogenas	606	1	QXBQ5M
NADH2 dehydrogenas	606	2	T11150
NADH2 dehydrogenas	606	2	C58851

THIS PAGE BLANK (USP 10)

CC of the invention are useful in the manufacture of a medicament for
 CC inhibiting or treating amyloidosis or amyloid deposits e.g. Type I and
 CC Type II diabetes and/or for cytoprotection. They are also useful for
 CC treating secondary amyloidosis associated with chronic infection e.g.
 CC tuberculosis and chronic inflammation e.g. rheumatoid arthritis, and
 CC familial inflammation, fever, neurodegenerative diseases e.g. scrapie,
 CC bovine spongy form encephalitis, Creutzfeldt-Jacob disease, Alzheimer's
 CC disease, cerebral amyloid angiopathy
 XX
 SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
 |:||||
 Db 1 KLVFFA 6

RESULT 74

AAU11658
 ID AAU11658 standard; peptide; 6 AA.

XX AAU11658;

XX
 DT 09-APR-2002 (first entry)

XX Peptide #11, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.

XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.

XX Key Location/Qualifiers
 FH Modified-site 6
 FT /note= "C-terminal amide"

XX WO200185093-A2.

XX 15-NOV-2001.

XX 22-DEC-2000; 2000WO-IB002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.

XX Green AM, Gervais F;

XX WPI; 2002-075222/10.

XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.

XX Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
 |:||||
 Db 1 KLVFFA 6

RESULT 75

AAU11650
 ID AAU11650 standard; peptide; 6 AA.

XX AAU11650;

XX 09-APR-2002 (first entry)

XX Peptide #3, used as a carrier for amyloid-beta40 (Abeta40) inhibitor.

XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
 KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
 KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

XX Synthetic.

XX WO200185093-A2.

XX 15-NOV-2001.

XX 22-DEC-2000; 2000WO-IB002078.

XX 23-DEC-1999; 99US-0171877P.

XX (NEUR-) NEUROCHEM INC.

XX Green AM, Gervais F;

XX WPI; 2002-075222/10.

XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.

XX Disclosure; Page 10; 68pp; English.

XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
 |:||||
 Db 1 KLVFFA 6

Search completed: December 29, 2005, 17:33:38
 Job time : 82.7742 secs

CC not only reduces the formation of neurotoxic aggregates but also have the
 CC ability to reduce the neurotoxicity of performed A-beta fibrils. The
 CC present sequence represents a beta-AP peptide, which is used in the
 CC exemplification of the present invention

XX Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
 | : | | |
 Db 1 KLVFFA 6

RESULT 72
 AAU96820
 ID AAU96820 standard; peptide; 6 AA.

XX AAU96820;

30-JUL-2002 (first entry)

DE Amyloid targeting peptide #10.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1. .6

FT /note= "Preferably D-form residue"

FT Modified-site 6

FT /note= "Ala is amidated"

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 XX plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
 XX agent is of general formula A_t-t-(A₁)_n-k-z-A₁-a_b (I) where z = 0 - 1;
 XX A_t = an amyloid targeting moiety; A₁-n-k = a linker moiety; and A₁-a_b
 XX = a labelling moiety. Also included are imaging amyloid deposition or
 XX diagnosing an amyloid-related condition in a patient involving
 XX administering (I) to the patient, and ultrasound imaging (I) in the
 XX patient to determine the presence of amyloid or amyloid-related condition
 XX ; and a kit for preparing a radiopharmaceutical preparation comprising
 XX (I), a reducing agent, a buffering agent, a transchelating agent, and

CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 5; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
 | : | | |
 Db 1 KLVFFA 6

RESULT 73

ABB83305

ID ABB83305 standard; peptide; 6 AA.

XX ABB83305;

29-AUG-2002 (first entry)

DE Amyloid-beta (Abeta) peptide fragment.

XX Human; islet amyloid polypeptide; IAPP; antidiabetic; amylin;
 KW fibrillar accumulation; amyloidosis; diabetes; cytoprotection; neurotropic;
 KW chronic infection; tuberculosis; inflammation; rheumatoid arthritis;
 KW fever; neurodegenerative disease; scrapie; neuroprotective; antipruritic;
 KW bovine spongiform encephalitis; Creutzfeldt-Jacob disease; amyloid-beta;
 KW Alzheimer's disease; cerebral amyloid angiopathy; anti-diabetic;
 KW tuberculostatic; antiarthritic; antirheumatic; cerebroprotective.

XX Unidentified.

XX WO200224727-A2.

XX 28-MAR-2002.

XX 19-SEP-2001; 2001WO-CA001333.

XX 19-SEP-2000; 2000US-0233482P.

XX (UTOR) UNIV TORONTO.

XX Fraser P;

XX WPI; 2002-519078/55.

XX New antidiabetic peptide useful for inhibiting amyloidosis and/or
 XX for cytoprotection in the treatment of amyloidosis disorders e.g. type I
 XX or type II.

XX Disclosure; Page 5; 77pp; English.

XX The present invention relates to antidiabetic agents (ABB83281-
 XX ABB83298), derived from human islet amyloid polypeptide (IAPP, ABB83307).
 XX The present sequence is a peptide fragment of the amyloid-beta (Abeta)
 XX peptide. Aggregation of IAPP, also known as amylin, or Abeta results in
 XX fibrillar accumulations, leading to amyloidosis. The antidiabetic
 XX peptides prevent fibril formation and amyloidosis and hence control
 XX folding or deposition of amyloid proteins. The antidiabetic peptides

DB 1 KLVFFA 6
|:|||||

RESULT 70
ABG71009
ID ABG71009 standard; peptide; 6 AA.
XX AC ABG71009;
XX DB 05-DEC-2002 (first entry)
XX DE Long form beta-amyloid protein fragment #6.
XX KW Beta-amyloid; amyloid modulator; amyloidogenic protein; amyloidosis;
XX KW familial amyloid polyneuropathy; familial amyloid cardiomyopathy;
XX KW isolated cardiac amyloid; systemic senile amyloidosis; scrapie; myeloma;
XX KW bovine spongiform encephalopathy; BSE; Creutzfeldt-Jakob disease;
XX KW adult onset diabetes; Gerstmann-Strausler-Scheinker syndrome;
XX KW insulinoma; atrial amyloidosis; idiopathic amyloidosis; haemodialysis;
XX KW macroglobulinaemia-associated amyloidosis; reactive amyloidosis;
XX KW primary localised cutaneous nodular amyloidosis; Sjogren's syndrome;
XX KW hereditary cerebral haemorrhage with amyloidosis; Nuckle-Wells syndrome;
XX KW hereditary non-neuropathic systemic amyloidosis;
XX KW familial Mediterranean Fever.
XX OS Homo sapiens.
XX XX US2002098173-A1.
XX PN 25-JUL-2002.
XX PD 04-OCT-2001; 2001US-00972475.
XX PF 14-MAR-1995; 95US-00404831.
XX PR 07-JUN-1995; 95US-00475579.
XX PR 27-OCT-1995; 95US-00548998.
XX PR 14-MAR-1996; 96US-00617267.
XX XX (PRAE-) PRAECIS PHARM INC.
XX PA Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
XX PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX XX WPI; 2002-697709/75.
XX PT Amyloid modulator useful for treating a disorder associated with
XX PT amyloidosis, comprises an amyloidogenic protein and/or a peptide fragment
XX PT coupled to a modifying group.
XX PS Example 12; Page 35; 41pp; English.
XX XX The invention describes an amyloid modulator comprising an amyloidogenic
XX CC protein and/or peptide fragment coupled to a modifying group so that the
XX CC compound modulates the aggregation of natural amyloid proteins or
XX CC peptides. The modulator is used for treating a disorder associated with
XX CC amyloidosis e.g. familial amyloid polyneuropathy (Portuguese, Japanese
XX CC and Swedish types), familial amyloid cardiomyopathy (Danish type),
XX CC spongiform encephalopathy, Creutzfeldt-Jakob disease, adult onset
XX CC diabetes, Gerstmann-Strausler-Scheinker syndrome, insulinoma, isolated
XX CC atrial amyloidosis, idiopathic (primary) amyloidosis, myeloma or
XX CC macroglobulinaemia-associated amyloidosis, primary localised cutaneous
XX CC nodular amyloidosis associated with Sjogren's syndrome, reactive
XX CC (secondary) amyloidosis, familial Mediterranean Fever and familial
XX CC amyloid nephropathy with urticaria and deafness (Muckle-Wells syndrome),
XX CC hereditary cerebral haemorrhage with amyloidosis of Icelandic type,
XX CC amyloidosis associated with long term haemodialysis, hereditary non-
XX CC neuropathic systemic amyloidosis (familial amyloid polyneuropathy III),
XX CC familial amyloidosis of Finnish type, amyloidosis associated with
XX CC renal carcinoma of the thyroid, fibrinogen-associated hereditary
XX CC amyloidosis and lysozyme-associated hereditary systemic
XX CC amyloidosis. The compound is capable of altering and inhibiting beta-

CC amyloid protein (beta-AP) aggregation of natural amyloidogenic proteins
CC or peptides when contacted with a molar excess amount of natural beta-APs
CC relative to the modulator. This sequence represents a fragment of the
CC long form of beta-amyloid used in the creation of an amyloid modulator
XX XX Sequence 6 AA;
XX Query Match 93.1%; Score 27; DB 5; Length 6;
XX Best Local Similarity 83.3%; Pred. NO. 2e+06;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
DB 1 KLVFFA 6
|:|||||

RESULT 71
ABG05157
ID ABG05157 standard; peptide; 6 AA.
XX AC ABG05157;
XX XX 02-APR-2002 (first entry)
XX DE Beta amyloid peptide (16-21) SEQ ID NO:9.
XX KW Beta amyloid peptide; beta-AP; beta amyloid precursor protein; A-beta;
XX KW APP-770; amyloid aggregation; amyloidogenic; Alzheimer's disease;
XX KW neurotic; neuroprotective; immunosuppressive; antimicrobial; auditory;
XX KW antidiabetic; antipyretic; dermatological; cardiovascular; nephrotropic;
XX KW amyloid aggregation inhibitor; neurotoxicity inhibitor; Down's syndrome;
XX KW amyloidogenic disease; beta amyloid deposition; amyloidosis;
XX KW hereditary cerebral haemorrhage; familial amyloid polyneuropathy.
XX OS Homo sapiens.
XX OS Synthetic.
XX XX US6319498-B1.
XX PN 20-NOV-2001.
XX PD 14-MAR-1996; 96US-00617267.
XX PF 14-MAR-1995; 95US-00404831.
XX PR 07-JUN-1995; 95US-00475579.
XX PR 27-OCT-1995; 95US-00548998.
XX XX (PRAE-) PRAECIS PHARM INC.
XX PA Findeis MA, Benjamin H, Garnick MB, Geffer ML, Hundal A;
XX PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ;
XX XX WPI; 2002-146668/19.
XX DR Amyloid modulator compound useful for treatment of an amyloidogenic
XX PT disease such as Alzheimer's disease comprises an aggregation core domain
XX PT and a modifying group attached to it.
XX XX Disclosure; Col 18; 54pp; English.
XX PS The present invention describes an amyloid modulator compound (I)
XX CC comprising an aggregation core domain and a modifying group attached to
XX CC it. (I) has neurotropic, neuroprotective, immunosuppressive, antimicrobial,
XX CC antidiabetic, antipyretic, dermatological, cardiovascular, nephrotropic
XX CC and auditory activities, and can be used as a natural amyloid aggregation
XX CC inhibitor and a neurotoxicity inhibitor of natural beta amyloid peptide
XX CC (beta-AP). (I) are used in the manufacture of a medicament for the
XX CC diagnosis or treatment of an amyloidogenic disease e.g. Alzheimer's
XX CC disease and other clinical occurrences of beta amyloid deposition such as
XX CC Down's syndrome individuals and in patients with hereditary cerebral
XX CC haemorrhage with amyloidosis, and for treating a disorder associated with
XX CC amyloidosis such as familial amyloid polyneuropathy. (I) reduces the
XX CC toxicity of natural beta-AP aggregates to cultured neuronal cells. (I)

```

CC protein
XX Sequence 6 AA;
SQ

Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVPFA 6
DB 1 KLVVFA 6

RESULT 68
AAB48476
ID AAB48476 standard; peptide; 6 AA.
XX AC AAB48476;
XX DT 02-MAR-2001 (first entry)
XX DE Antifibrillogenic peptide #3.
XX KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
XX KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
XX KW Alzheimer's disease.
XX OS Homo sapiens.
XX PN WO200068263-A2.
XX PD 16-NOV-2000.
XX PF 04-MAY-2000; 2000WO-CA000515.
XX PR 05-MAY-1999; 99US-0132592P.
XX PA (NEUR-) NEUROCHEM INC.
XX PI Chalifour R, Gervais F, Gupta A;
XX WPI; 2001-031852/04.
XX DR
XX PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
XX PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
XX PT its isomer or peptidomimetic.
XX PS Claim 7; Page 25; 46pp; English.
XX SQ
XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
XX for inhibiting amyloidosis and/or for cytoprotection. The peptides of
XX AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
XX useful for treating amyloidosis disorders such as Alzheimer's disease.
XX Peptides AAB48474-B48496 were identified from the glycoaminoglycan
XX binding region and the prot-prot interaction region of the human amyloid
XX protein
XX Sequence 6 AA;
XX Query Match          93.1%; Score 27; DB 4; Length 6;
XX Best Local Similarity 83.3%; Pred. No. 2e+06;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVPFA 6
DB 1 KLVVFA 6

RESULT 69
AAB82632
ID AAB82632 standard; peptide; 6 AA.
XX AC AAB82632;

```

```

XX 02-OCT-2001 (first entry)
XX All-D peptide used in Alzheimer's disease vaccine.
XX DE
XX KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
XX KW therapy; antigen.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 1..6
XX FT Modified-site 6 /note= "all D-form residues"
XX FT /note= "C-terminal amide"
XX PN WO200139796-A2.
XX PD 07-JUN-2001.
XX PF 29-NOV-2000; 2000WO-CA001413.
XX PR 29-NOV-1999; 99US-0168594P.
XX PR 28-NOV-2000; 2000US-00724842.
XX PA (NEUR-) NEUROCHEM INC.
XX PI Chalifour R, Hebert L, Kong X, Gervais F;
XX WPI; 2001-441458/47.
XX DR
XX PT Preventing/treating amyloid-related disease, especially Alzheimer's
XX PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
XX PT which elicits production of antibodies to prevent fibrillogenesis and
XX PT associated cellular toxicity.
XX PS Disclosure; Page 11; 31pp; English.
XX SQ
XX The present sequence is that of an all-D peptide suitable for use for
XX preparing vaccines for preventing or treating Alzheimer's disease and
XX other amyloid related disorders in humans. It is based on a portion of
XX amyloid-beta peptide (see AAB82622), and may be modified by removing or
XX inserting 1 or more amino acid residues, or by substituting 1 or more
XX amino acid residues with other amino acid residues or non-amino acid
XX fragments. Vaccines of the invention are produced using 'non-self'
XX peptides synthesised from the unnatural D-configuration amino acids to
XX avoid the drawbacks of 'self' proteins. The all-D peptides need not be
XX aggregated to be operative or immunogenic. They preferably interact with
XX at least 1 region of an amyloid protein, e.g. the beta-sheet region or
XX GAG-binding site region, the amyloid-beta peptide, or their immunogenic
XX fragments, protein conjugates, immunogenic derivative peptides and
XX immunogenic peptidomimetics. Examples include all-D peptides
XX corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
XX 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
XX in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
XX preventing fibrillogenesis and associated cellular toxicity. The amyloid
XX related diseases may be localised amyloidosis, e.g. diabetes type II,
XX neurodegenerative diseases, e.g. bovine spongiform encephalitis,
XX Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
XX prion protein related disorders, or systemic amyloidosis associated with
XX chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
XX rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
XX amyloidosis found in long-term haemodialysis patients. The present all-D
XX peptide was demonstrated to elicit antibody production in rabbits, and
XX provided greater anti-fibrillogenic activity than its all-L equivalent
XX Sequence 6 AA;
XX Query Match          93.1%; Score 27; DB 4; Length 6;
XX Best Local Similarity 83.3%; Pred. No. 2e+06;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVPFA 6

```

XX AAW02310-W02332 represent the peptide portions of the beta-amyloid
CC modulator compounds of the invention. Beta-amyloid peptide is a 4
CC kilodalton peptide that is the major protein component of amyloid
CC plaques. Amyloid plaques are present both in the brain lesions, and in
CC the walls of cerebral blood vessels in Alzheimer's disease patients. The
CC amyloid modulators of the invention comprise an amyloidogenic protein or
CC peptide (such as this sequence) coupled directly or indirectly to at
CC least one modifying group. The modifying group is preferably a cyclic,
CC heterocyclic, or polycyclic group, such as deca-, a cholanyl group, a
CC biotin containing group, or a fluorescein containing group. These
CC compounds then modulate the aggregation of these sequences to natural
CC amyloid proteins or peptides when contacted with the natural
CC amyloidogenic proteins or peptides. The modulator compounds can be used
CC in the treatment of disorders associated with amyloidosis, such as
CC familial amyloid polynuropathy, familial amyloid cardiomyopathy,
CC isolated cardiac amyloidosis, systemic senile amyloidosis, scrapie,
CC bovine spongiform encephalopathy, Creutzfeldt-Jakob disease, adult-onset
CC diabetes, insulinoma, familial Mediterranean fever, familial amyloid
CC nephropathy with urticaria and deafness, hereditary cerebral haemorrhage
CC and other types of amyloidosis. The modulators are also useful for the
CC treatment of disorders associated with beta-amyloidosis, especially
CC Alzheimer's disease
XX
SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6
|:||||
|:||||

RESULT 66
AAW89378
ID AAW89378 standard; peptide; 6 AA.
XX
AC AAW89378;
XX
DT 02-MAR-1999 (first entry)
XX
DE Beta-amyloid peptide derivative A-beta-16-21.
XX
KW Human; beta-amyloid peptide; Alzheimer's disease; amyloidogenic protein;
KW aggregation; neurotoxicity; amyloidosis; Down's syndrome; cardiomyopathy;
KW familial amyloid polynuropathy; bovine spongiform encephalopathy;
KW Creutzfeldt-Jakob disease; bAP.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US5854204-A.
XX
PD 29-DEC-1998.
XX
PF 14-MAR-1996; 96US-00612785.
XX
XX 14-MAR-1995; 95US-00404831.
PR 07-JUN-1995; 95US-00475579.
PR 27-OCT-1995; 95US-00548998.
XX
XX (PRAE-) PRAECIS PHARM INC.
XX
XX Hundal A, Geffer ML, Kasman L, Musso G, Molineaux S, Benjamin H;
PI Findeis MA, Chin J, Lee J, Kelley M, Reed M, Wakefield J;
PI Garnick MB, Kubasek W, Signer ER;
XX
XX WPI; 1999-094964/08.
DR
XX New peptide(s) derived from beta-amyloid peptide that inhibit amyloid
PT aggregation - and neurotoxicity, specifically for treatment and

PT prevention of Alzheimer's disease.
XX
XX Example 12; Col 64; 52pp; English.
XX
CC The present invention describes beta-amyloid peptide (bAP) derivatives.
CC The bAP derivatives inhibit aggregation of amyloidogenic proteins and
CC peptides, specifically bAP, and their neurotoxicity, so are useful for
CC treating and preventing any disease involving amyloidosis, specifically
CC Alzheimer's disease but also Down's syndrome, familial amyloid
CC polynuropathy or cardiomyopathy, bovine spongiform encephalopathy and
CC Creutzfeldt-Jakob disease. The bAP derivatives are also used to diagnose
CC these diseases, in vitro or in vivo, by detecting binding of bAP to
CC labelled bAP derivatives. Some bAP derivatives inhibit bAP aggregation
CC even when bAP is present in molar excess. The present sequence represents
CC a bAP derivative
XX
SQ Sequence 6 AA;

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6
|:||||
|:||||

RESULT 67
AAB48484
ID AAB48484 standard; peptide; 6 AA.
XX
AC AAB48484;
XX
DT 02-MAR-2001 (first entry)
XX
DE Antifibrillogenic peptide #11.
XX
KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KW Alzheimer's disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /notes "C-terminal amide"
FT
XX
PN W0200068263-A2.
XX
PD 16-NOV-2000.
XX
PF 04-MAY-2000; 2000WO-CA0000515.
XX
PR 05-MAY-1999; 99US-0132592P.
XX
XX (NEUR-) NEUROCHEM INC.
XX
PI Chalfour R, Gervais F, Gupta A;
XX
XX WPI; 2001-031852/04.
DR
XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
PT its isomer or peptidomimetic.
XX
XX Claim 7; Page 25; 46pp; English.
XX
XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC useful for treating amyloidosis disorders such as Alzheimer's disease.
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
CC binding region and the prot-prot interaction region of the human amyloid

DR WPI; 2005-394926/40.
 DR N-PSDB; AEA03074.
 XX
 PT New composition for treating a tumor or neoplastic disease in a subject
 PT comprises conjugates comprising superantigen polypeptides or nucleic
 PT acids with other molecules that produce a tumoricidal response.
 XX
 XX Example 3; SEQ ID NO 101; 125pp; English.
 PS
 CC The invention relates to a composition for treating a tumor or neoplastic
 CC disease in a subject. Also described: (1) a mammalian cell comprising an
 CC exogenous nucleic acid encoding a superantigen expressed in the cell,
 CC which cell also produces or expresses all alpha-anomers of
 CC monoglycosylceramide or diglycosylceramide, where expression of the
 CC superantigen and the mono- or diglycosylceramide is capable of eliciting
 CC an antitumor immune response in a mammal into which the cell is
 CC introduced; (2) treating a tumor or neoplastic disease in a subject; (3)
 CC preparing a population of immunotherapeutic T or natural killer T (NKT)
 CC cells useful to treat a tumor or neoplastic disease in a subject; (4) an
 CC apoptotic cell preparation or lysate useful for treating a tumor or
 CC neoplastic disease in a subject, comprising a cell population that has
 CC been transfected with naked DNA encoding a superantigen, and treated to
 CC undergo apoptosis or lysis; and (5) a cell that has ingested or been
 CC transfected with the above apoptotic preparation or lysate, thus,
 CC rendering the cell effective in presenting material expressed from
 CC transfecting nucleic acid or material ingested to the immune system of a
 CC mammal to elicit an anti-tumor immune response. The composition and
 CC methods are useful for treating tumors or neoplastic diseases. The
 CC present sequence represents a VEGF protein sequence, which is used in an
 CC example from the present invention. Note - The sequence data for this
 CC patent is not represented in the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site.
 XX
 XX Sequence 1144 AA;
 SQ

Query Match 96.6%; Score 28; DB 9; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|||||
 Db 514 KWVFFA 519

RESULT 64
 ABB68472
 ID ABB68472 standard; protein; 1443 AA.
 AC ABB68472;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster polypeptide SEQ ID NO 32208.
 DE
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US009231.
 PP
 XX 23-MAR-2000; 2000US-0191637P.
 PR
 XX 11-JUL-2000; 2000US-00614150.
 PR
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI; 2001-656860/75.
 DR

DR N-PSDB; ABL12575.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 XX Disclosure; SEQ ID NO 32208; 21pp + Sequence Listing; English.
 PS
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL130511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 1443 AA;
 SQ

Query Match 96.6%; Score 28; DB 4; Length 1443;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|||||
 Db 1204 KIIFFA 1209

RESULT 65
 AAW02314
 ID AAW02314 standard; peptide; 6 AA.
 AC AAW02314;
 XX
 XX 02-MAY-1997 (first entry)
 DT
 XX Beta-amyloid modulator peptide #5.
 DE
 XX Beta-amyloid; modulator; amyloid plaque; brain lesion; amyloidosis;
 KW cerebral blood vessel; Alzheimer's disease; amyloidogenic protein;
 KW familial amyloid polynuropathy; familial amyloid cardiomyopathy;
 KW isolated cardiac amyloidosis; systemic senile amyloidosis; insulinoma;
 KW bovine spongiform encephalopathy; Creutzfeldt-Jakob disease; urticaria;
 KW adult-onset diabetes; familial Mediterranean fever; therapy; deafness;
 KW scrapie; familial amyloid nephropathy; hereditary cerebral haemorrhage.
 KW
 XX Synthetic.
 OS
 XX WO9628471-A1.
 PN
 XX 19-SEP-1996.
 PD
 XX 14-MAR-1996; 96WO-US003492.
 PP
 XX 14-MAR-1995; 95US-00404831.
 PR
 XX 07-JUN-1995; 95US-00475579.
 PR
 XX 27-OCT-1995; 95US-00548998.
 PR
 XX (PHAR-) PHARM PEPTIDES INC.
 PA
 XX Findeis MA, Benjamin H, Garnick MB, Gefter ML, Hundal A;
 PI Kasman L, Musso G, Signer ER, Wakefield J, Reed MJ, Molineaux S;
 PI Kubasek W, Chin J, Lee J, Kelley M;
 XX
 XX WPI; 1996-433762/43.
 DR
 XX Modulators of amyloid aggregation - comprising, e.g. amyloidogenic
 PT protein coupled (in)directly to at least 1 modifying gp., useful in
 PT treatment of Alzheimer's disease.
 XX
 XX Claim 16; Page 91; 106pp; English.
 PS

or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (I) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polynucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for bronchial asthma or a chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (I) has respiratory and antiasthmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.

XX Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 8; Length 1144;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
|:|||||
DB 514 KVVFFFA 519

RESULT 62

ADJ76136
ID ADJ76136 standard; protein; 1144 AA.

AC ADJ76136;

XX 20-MAY-2004 (first entry)

DE Marker gene related amino acid sequence SEQ ID NO:1388.

XX bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker.

XX Mus musculus.

XX EP1394274-A2.

XX 03-MAR-2004.

XX 04-AUG-2003; 2003EP-00254857.

XX 06-AUG-2002; 2002JP-00229312.

XX 20-MAR-2003; 2003JP-00077212.

XX (GENO-) GENOX RES INC.

XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;

XX WPI; 2004-193155/19.

XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample

PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.

XX Claim 16; SEQ ID NO 1388; 241pp; English.

XX The present invention describes a method of testing for bronchial asthma
CC or chronic obstructive pulmonary disease. The method comprises
CC determining the expression level of a marker gene in a biological sample
CC from a subject, comparing the expression level determined with the
CC expression level of the marker gene in a biological sample from a healthy
CC subject, and judging whether the subject has bronchial asthma or chronic
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC genes (S1) whose expression levels increase when respiratory epithelial
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC testing for bronchial asthma or chronic obstructive pulmonary disease;
CC (2) a kit for screening for a candidate compound for a therapeutic agent;
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC an animal model for bronchial asthma or chronic obstructive pulmonary
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC method for producing an animal model for bronchial asthma or chronic
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC asthma or chronic obstructive pulmonary disease, comprising the compound,
CC a marker gene or an antisense nucleic acid corresponding to a portion of
CC the marker gene, a ribozyme, a polynucleotide that suppresses the
CC expression of the gene through an RNAi effect or an antibody recognising
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC probe has been immobilised to assay a marker gene. (I) has respiratory
CC and antiasthmatic activities, and can be used in gene therapy. The method
CC is useful for testing for or screening for a therapeutic agent for
CC bronchial asthma or chronic obstructive pulmonary disease. The present
CC sequence is used in the exemplification of the present invention.

XX Sequence 1144 AA;

Query Match 96.6%; Score 28; DB 8; Length 1144;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
|:|||||
DB 514 KVVFFFA 519

RESULT 63

AEA03075
ID AEA03075 standard; protein; 1144 AA.

XX AEA03075;

XX 28-JUL-2005 (first entry)

XX VEGF amino acid sequence SEQ ID NO:101.

XX tumor; neoplasm; gene therapy; immunotherapy; cytostatic;
KW vascular endothelial cell growth factor.

XX Unidentified.

XX US2005112141-A1.

XX 26-MAY-2005.

XX 08-SEP-2004; 2004US-00937758.

XX 30-AUG-2000; 2000US-00650884.

XX (TERM/) TERMAN D S.

XX Terman DS;

expression of inducible nitric oxide synthase. The antisense compounds have immunomodulator, antidiabetic, cardiovascular, cardiant, neuroprotective, disorder and vasotropic activity. The antisense oligonucleotides are useful for inhibiting the expression of inducible nitric oxide synthase in cells or tissues. In particular, the antisense oligonucleotides are useful for treating diseases or disorders associated with inducible nitric oxide synthase, e.g. diabetes, immunological disorder, cardiovascular disorder, neurological disorder or ischaemia/reperfusion injury. The antisense oligonucleotides are also useful for research and diagnostics. The present sequence is that of mouse inducible nitric oxide synthase

Sequence 1144 AA;
 Query Match 96.6%; Score 28; DB 4; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|||||
 Db 514 KVVFFA 519

RESULT 58
 ABU79138
 ID ABU79138 standard; protein; 1144 AA.
 AC ABU79138;
 XX
 DT 18-JUN-2003 (first entry)
 DE Inducible nitric oxide synthase protein.
 XX
 KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW gene therapy; mammalian cell receptor; cytostatic;
 KW tumour associated lipid; anergy; T cell; antigen presenting cell; APC;
 KW tumouricidal immunocyte; antitumour.
 XX
 OS Unidentified.
 XX
 FN US2002177551-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 30-MAY-2001; 2001US-00870759.
 XX
 PR 31-MAY-2000; 2000US-0208128P.
 XX
 PA (TERM/) Terman D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 2003-361759/34.
 XX
 DR N-PSDB; ACA64740.
 XX
 PT A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces anergy or apoptosis
 PT in T cells and antigen presenting cells.
 XX
 PS Example 2; Page; 167pp; English.
 XX
 CC The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a

superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidal APC to the host), producing (M3) a tumouricidal APC activated immunocytes to the host), producing (M4) a tumour associated lipid to population ex vivo in a mammal (by allowing a tumour associated lipid to contact APCs, in which receptors for the tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population, and administering APCs to the host), producing a tumouricidal T cell population ex vivo in a mammal (by allowing a tumour associated lipid to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumour associated antigens, are deleted or functionally deactivated to produce a tumouricidal population of T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host), treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo), producing (M6) a tumouricidal T cell population in vivo in a mammal (by allowing a tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumour associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence represents an anti-tumour protein which is co-administered with or incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patent office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"

Sequence 1144 AA;
 Query Match 96.6%; Score 28; DB 6; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |:|||||
 Db 514 KVVFFA 519

RESULT 59
 ADF43404
 ID ADF43404 standard; protein; 1144 AA.
 XX
 AC ADF43404;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE iNOS polypeptide seqid 124.
 XX
 KW receptor; lipid-based tumour associated antigen; cytostatic;
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
 KW infectious disease; iNOS.
 XX
 OS Unidentified.
 XX
 XX US2003157113-A1.
 XX
 PD 21-AUG-2003.
 XX
 PF 28-DEC-2000; 2000US-00751708.
 XX
 PR 28-DEC-1999; 99US-0173371P.
 XX

DE Inducible nitrogen monoxide synthase.
 XX nitrogen monoxide synthase; inducible; treatment; prevention;
 KW vascular disease; restenosis.
 XX
 OS Mus musculus.
 XX
 PN DE4411402-A1.
 XX
 PD 05-OCT-1995.
 XX
 XX 31-MAR-1994; 94DE-04411402.
 XX
 XX 31-MAR-1994; 94DE-04411402.
 XX
 PA (SCHR/) SCHRADER J.
 XX
 XX Schrader J, Goedecke A;
 XX
 DR WPI; 1995-345550/45.
 DR N-PSDB; AAQ94252.
 XX
 XX Eukaryotic expression vector for nitrogen-monoxide synthase gene -
 PT useful in the treatment and prevention of diseases of blood vessels by
 PT gene therapy.
 XX
 XX Claim 5; Fig 1; 28pp; German.
 PS
 XX Inducible nitrogen monoxide synthase (iNOS) was isolated from mice, and
 CC is encoded by AAQ94252. iNOS is homodimer with a mol. wt. of 130 kDa per
 CC subunit. The activity of iNOS is independent of calmodulin and cellular
 CC calcium levels. Vectors contg. the DNA are used in the treatment or
 CC prevention of vascular diseases, high blood pressure, arteriosclerosis,
 CC stenosis or restenosis of blood vessels, esp. coronary vessels after
 CC percutane transluminal coronary angioplasty. See AAR77363 and AAR77362
 CC for endothelial and brain-derived NOS
 XX
 XX Sequence 1144 AA;
 SQ

Query Match 96.6%; Score 28; DB 2; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIVFFA 6
 Db 514 KVVFFA 519
 |:|||||
 RESULT 57
 AAAG64500
 ID AAAG64500 standard; protein; 1144 AA.
 XX
 AC AAG64500;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE Mouse inducible nitric oxide synthase 2.
 XX
 KW Antisense oligonucleotide; inducible nitric oxide synthase;
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
 KW cardiant; neuroprotective; vasotrophic; ischaemia; reperfusion injury;
 KW 2'-O-methoxyethyl; phosphorothioate; mouse.
 XX
 OS Mus sp.
 XX
 PN WO200152902-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 15-JAN-2001; 2001WO-US001381.
 XX
 XX 24-JAN-2000; 2000US-00490208.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CF, Dean NM, Cowsert LM;
 PI
 XX WPI; 2001-465340/50.
 DR
 DR N-PSDB; AAH47974.
 XX
 XX New antisense oligonucleotides for modulating the expression of inducible
 PT nitric oxide synthase in cells or tissues, particularly useful for
 PT treating e.g. immunological, cardiovascular or neurological disorders, or
 PT ischemia.
 XX
 XX Example 17; Page 110-114; 144pp; English.
 PS
 XX The invention relates to antisense compounds, especially
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
 CC nitric oxide synthase and which specifically hybridise to and modulate

XX Mumford RA, Calaycay JR, Xie Q, Nathan CF;
 PI
 XX WPI; 1998-361696/31.
 DR
 DR N-PSDB; AAV07247.
 XX
 XX DNA encoding inducible nitric oxide synthase proteins - useful for
 PT producing recombinant proteins.
 XX
 XX Claim 1; Col 25-32; 39pp; English.
 PS
 XX The invention relates to two DNA molecules encoding inducible nitric
 CC oxide synthase (iNOS) proteins, where the DNA molecules comprise defined
 CC sequences of 4041 and 4165 base pairs given in the specification and the
 CC proteins have 1144 amino acids. Also claimed are expression vectors
 CC containing the DNA molecules, and recombinant host cells containing the
 CC vectors. The DNA molecules are useful for producing the recombinant
 CC proteins. The present sequence represents inducible nitric oxide, long
 CC isoform. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 1144 AA;
 SQ

Query Match 96.6%; Score 28; DB 2; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KIVFFA 6
 Db 514 KVVFFA 519
 |:|||||
 RESULT 57
 AAAG64500
 ID AAAG64500 standard; protein; 1144 AA.
 XX
 AC AAG64500;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE Mouse inducible nitric oxide synthase 2.
 XX
 KW Antisense oligonucleotide; inducible nitric oxide synthase;
 KW modulate expression; immunomodulator; antidiabetic; cardiovascular;
 KW cardiant; neuroprotective; vasotrophic; ischaemia; reperfusion injury;
 KW 2'-O-methoxyethyl; phosphorothioate; mouse.
 XX
 OS Mus sp.
 XX
 PN WO200152902-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 15-JAN-2001; 2001WO-US001381.
 XX
 XX 24-JAN-2000; 2000US-00490208.
 PR
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Bennett CF, Dean NM, Cowsert LM;
 PI
 XX WPI; 2001-465340/50.
 DR
 DR N-PSDB; AAH47974.
 XX
 XX New antisense oligonucleotides for modulating the expression of inducible
 PT nitric oxide synthase in cells or tissues, particularly useful for
 PT treating e.g. immunological, cardiovascular or neurological disorders, or
 PT ischemia.
 XX
 XX Example 17; Page 110-114; 144pp; English.
 PS
 XX The invention relates to antisense compounds, especially
 CC oligonucleotides, which are targeted to a nucleic acid encoding inducible
 CC nitric oxide synthase and which specifically hybridise to and modulate

CC a small inhibitory dsRNA, or a ribozyme. As such, the compositions and
 CC methods are useful for diagnosing and treating diseases or conditions
 CC associated with abnormal apoptosis in mammalian tissues, such as cancer,
 CC inflammation, autoimmune or neurodegenerative disorders. Accordingly,
 CC they exhibit cytostatic, antiinflammatory, immunosuppressive and
 CC neuroprotective activities. These may also be used for drug screening
 CC purposes and in gene therapy. This polypeptide sequence is a human target
 CC protein, an enzyme associated with the regulation of apoptosis whose
 CC expression is modulated by novel agents of the invention.

XX Sequence 925 AA;

SQ Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|
 DB 292 KVVFFA 297

RESULT 53

ADY17516
 ID ADY17516 standard; protein; 925 AA.

XX AC
 ADY17516;

XX DT 05-MAY-2005 (first entry)

XX DE PRO polypeptide SEQ ID NO 3322.

XX KW Antinflammatory; Immune disorder; Dermatological; Immunosuppressive;
 KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
 KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
 KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
 KW Antiallergic; diagnosis.

XX OS Homo sapiens.

XX PN WO2005016962-A2.

XX PD 24-FEB-2005.

XX PF 11-AUG-2004; 2004WO-US026249.

XX PR 11-AUG-2003; 2003US-0493546P.

XX PA (GETH) GENENTECH INC.

XX PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;

XX WPI; 2005-182330/19.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.

PS Claim 8, SEQ ID NO 3322; 158pp; English.

XX The invention relates to an isolated nucleic acid encoding a PRO
 CC polypeptide. The polypeptide, agonist or an antagonist, antibody,
 CC composition, and method are useful for diagnosing and treating an immune
 CC related disorder, e.g. systemic lupus erythematosus, rheumatoid
 CC arthritis. The present sequence represents a PRO polypeptide.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 9; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|

DB 292 KVVFFA 297

RESULT 54

AEA23525
 ID AEA23525 standard; protein; 925 AA.

XX AC AEA23525;

XX DT 11-AUG-2005 (first entry)

XX DE Human PRO polypeptide SEQ ID NO 67.

XX KW immune disorder; PRO; Antiinflammatory; Dermatological;
 KW Immunosuppressive; Antirheumatic; Antiarthritic; Osteopathic;
 KW Muscular-Gen.; Vasotropic; Antianemic; Antipsoriatic; Immunostimulant.

XX OS Homo sapiens.

XX PN WO2005051988-A2.

XX PD 09-JUN-2005.

XX PF 02-MAR-2004; 2004WO-US006460.

XX PR 03-MAR-2003; 2003US-0451884P.

XX PA (GETH) GENENTECH INC.

XX PI Abbas A, Bodary S, Clark H, Schoenfeld J, Williams PM, Wood WI,
 PI Wu TD;

XX WPI; 2005-417958/42.

XX DR N-PSDB; AEA23524.

XX New nucleic acid encoding PRO polypeptide, useful for diagnosing and
 PT treating an immune related disorder, e.g. systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, autoimmune hemolytic anemia, or
 PT psoriasis.

XX Disclosure; SEQ ID NO 67; 966pp; English.

XX The invention relates to an isolated nucleic acid. The polypeptide,
 CC compound or composition, and methods are useful for diagnosing and
 CC treating an immune related disorder, e.g. systemic lupus erythematosus,
 CC rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis,
 CC spondyloarthropathies, systemic sclerosis, idiopathic inflammatory
 CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
 CC autoimmune hemolytic anemia, autoimmune or immune-mediated skin diseases
 CC including bullous skin diseases, erythema multiforme and contact
 CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The
 CC present sequence represents the amino acid sequence of a human PRO
 CC polypeptide.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 9; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |:|

DB 292 KVVFFA 297

RESULT 55

AAR77360
 ID AAR77360 standard; protein; 1144 AA.

XX AC AAR77360;

XX DT 10-MAY-1996 (first entry)

XX

CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 292 KVVFFA 297
 |:|:|:|

RESULT 51
 ADP25011
 ID ADP25011 standard; protein; 925 AA.

AC ADP25011;

DT 18-NOV-2004 (first entry)

DE PRO polypeptide SEQ ID NO:2189.

XX PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.

XX Unidentified.

XX WO2004041170-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WL;
 PI Wu TD;

DR WPI; 2004-419628/39.

DR N-PSDB; ADP25010.

XX New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.

XX Claim 7; SEQ ID NO 2189; 2940pp; English.

XX The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as
 CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal

CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 Db 292 KVVFFA 297
 |:|:|:|

RESULT 52

ADR97294

ID ADR97294 standard; protein; 925 AA.

AC ADR97294;

XX 02-DEC-2004 (first entry)

DE Human RIG-I-DEAD/H box protein, an apoptosis related target Seq 2.

XX human; enzyme; apoptosis; cancer; inflammation; autoimmune;
 KW neurodegenerative disorder; cytostatic; antiinflammatory;
 KW immunosuppressive; neuroprotective; gene therapy; RIG-I-DEAD/H box.

XX Homo sapiens.

XX WO2004078783-A2.

XX 16-SEP-2004.

XX 05-MAR-2004; 2004WO-GB000957.

XX 07-MAR-2003; 2003GB-00005267.

XX (BIRX-) BIRX THERAPEUTICS LTD.

XX Murphy FJ, Sheehan DE, Keating KE, Hayes I, Seera L;

DR WPI; 2004-662402/64.

DR N-PSDB; ADR97293.

XX Identifying an agent that modulates the function of an apoptosis-
 PT associated polypeptide, useful for diagnosing or treating e.g. cancer,
 PT comprises comparing the binding of the polypeptide to the candidate agent
 PT and to a control agent.

XX Claim 1; SEQ ID NO 2; 304pp; English.

XX This invention relates to novel agents that modulates the function of
 CC human apoptosis-associated proteins specified within the specification.
 CC Specifically, it refers to a method for the identification of target
 CC genes whose expression is correlated with an early stage in the
 CC regulation of apoptosis. The present invention describes a method of
 CC contacting either candidate agents or control agents to the target genes
 CC and assessing the difference of binding and inhibitory activity, where
 CC the candidate agent is selected from a low molecular weight organic
 CC molecule, an antibody or fragment thereof, an antisense oligonucleotide,

CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (I) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |.:|||
 Db 292 KVVFFA 297

RESULT 49
 ADN04860
 ID ADN04860 standard; protein; 925 AA.

XX AC ADN04860;

XX DT 01-JUL-2004 (first entry)

XX DE Antipsoriatic protein sequence #610.

XX KW antipsoriatic; gene therapy; psoriasis; diagnosis.

XX OS Homo sapiens.

XX PN WO2004028479-A2.

XX PD 08-APR-2004.

XX PF 25-SEP-2003; 2003WO-US030907.

XX PR 25-SEP-2002; 2002US-0414006P.

XX PA (GETH) GENENTECH INC.

XX PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;
 XX WU TD;

DR WPI: 2004-305105/28.

DR N-PSDB; ADN04859.

XX New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.

PS Claim 9; SEQ ID NO 1254; 3069pp; English.

XX The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.

XX SQ Sequence 925 AA;

Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |.:|||

Db 292 KVVFFA 297

RESULT 50

ADN14233

ID ADN14233 standard; protein; 925 AA.

XX AC ADN14233;

XX DT 21-OCT-2004 (first entry)

XX DE Human NF-kappaB pathway-associated protein SeqID234.

XX KW NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;
 KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
 KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
 KW immunosuppressive; vulnery; gene therapy; immune disorder;
 KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
 KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
 KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;
 KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
 KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;
 KW viral replication; host cell survival; evasion of immune response;
 KW rheumatoid arthritis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW atherosclerosis; hyper immune activity;
 KW autoimmune disorder; hyper immune activity;
 KW aberrant acute phase response; hypercongenital condition; birth defect;
 KW necrotic lesion; wound; organ transplant rejection;
 KW aberrant signal transduction; proliferating disorder; cancer;
 KW HIV propagation; human.

XX OS Homo sapiens.

XX PN WO2004065577-A2.

XX PD 05-AUG-2004.

XX PF 13-JAN-2004; 2004WO-US000798.

XX PR 14-JAN-2003; 2003US-0440068P.

XX PR 12-MAY-2003; 2003US-0469757P.

XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.

XX PI Nadler SG, Neubauer MG, Feder JN, Carman J;

DR WPI: 2004-562168/54.

DR N-PSDB; ADN14232.

XX New isolated polynucleotides and polypeptides associated with NF-kappaB
 PT pathway, useful for diagnosing, treating, or preventing disorders or
 PT diseases associated with NF-kappaB pathway.

PS Claim 6; SEQ ID NO 234; 237pp; English.

XX This invention relates to the novel association of protein sequences (and
 CC the genes which encode them) to the NF-kappaB pathway. The invention may
 CC be useful for the production of compounds with an antiinflammatory,
 CC cytostatic, hepatotropic, virucide, antirheumatic, antirheumatic,
 CC gastrointestinal-Gen, antiasthmatic, antirheumatic, antirheumatic,
 CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or
 CC vulnery activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper

SQ Sequence 925 AA;
 Query Match 96.6%; Score 28; DB 7; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 |:|||||
 Db 292 KVVFFA 297
 RESULT 47
 ADJ75428
 ID ADJ75428 standard; protein; 925 AA.
 XX
 AC ADJ75428;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Marker gene related amino acid sequence SEQ ID NO:680.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 OS Homo sapiens.
 XX
 PN EP1394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 PF 04-AUG-2003; 2003EP-00254857.
 XX
 PR 06-AUG-2002; 2002JP-00229312.
 PR 20-MAR-2003; 2003JP-00077212.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 XX
 DR WPI; 2004-193155/19.
 XX
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 PS Example 11; SEQ ID NO 680; 241pp; English.
 XX
 CC The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a

CC probe has been immobilised to assay a marker gene. (I) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 925 AA;
 Query Match 96.6%; Score 28; DB 8; Length 925;
 Best Local Similarity 83.3%; Pred. No. 7.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 |:|||||
 Db 292 KVVFFA 297
 RESULT 48
 ADJ75495
 ID ADJ75495 standard; protein; 925 AA.
 XX
 AC ADJ75495;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Marker gene related amino acid sequence SEQ ID NO:747.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 OS Homo sapiens.
 XX
 PN EP1394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 PF 04-AUG-2003; 2003EP-00254857.
 XX
 PR 06-AUG-2002; 2002JP-00229312.
 PR 20-MAR-2003; 2003JP-00077212.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 XX
 DR WPI; 2004-193155/19.
 XX
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 PS Example 11; SEQ ID NO 747; 241pp; English.
 XX
 CC The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial


```
SQ Sequence 922 AA;
Query Match          96.6%; Score 28; DB 8; Length 922;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 291 KIVFFA 296

RESULT 45
ADF76335
ID ADF76335 standard; protein; 925 AA.
XX
AC ADF76335;
XX
DT 26-FEB-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein SegID 8.
XX
KW human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neuroepitide; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
PN WO2003072035-A2.
XX
PD 04-SEP-2003.
XX
PF 21-FEB-2003; 2003WO-US005241.
XX
PR 22-FEB-2002; 2002US-0359461P.
XX
PA (GETH ) GENENTECH INC.
XX
PI Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;
XX
DR WPI; 2003-721702/68.
DR N-PSDB; ADF76334.
XX
XX New PRO polypeptides, useful for diagnosing and treating an immune
PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
PT diabetes mellitus.
XX
PS Claim 10; SEQ ID NO 8; 918pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neuropeptides and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is the amino acid sequence of a human PRO protein of the
CC invention.
```

```
XX
SQ Sequence 925 AA;
Query Match          96.6%; Score 28; DB 7; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 292 KIVFFA 297

RESULT 46
ADJ70225
ID ADJ70225 standard; protein; 925 AA.
XX
AC ADJ70225;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SegID2031.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy tagged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 2031; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC tagged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
```


XX PS Disclosure; SEQ ID NO 12723; 21pp + Sequence Listing; English.

XX CC The invention relates to an isolated nucleic acid detection reagent

XX CC capable of detecting 1000 or more genes from *Drosophila*. The invention is

XX CC useful in developmental biology and in elucidating cell signalling and

XX CC cell-cell interactions in higher eukaryotes for the development of

XX CC insecticides, therapeutics and pharmaceutical drugs. The invention

XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-

XX CC ABB72072). The sequence data for this patent did not form part of the

XX CC printed specification, but was obtained in electronic format directly

XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 564 AA;

Query Match 96.6%; Score 28; DB 4; Length 564;

Best Local Similarity 83.3%; Pred. No. 4.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

DB 53 KIIFFA 58

RESULT 43

ADQ66704

ID ADQ66704 standard; protein; 854 AA.

XX AC ADQ66704;

XX DT 07-OCT-2004 (first entry)

XX DE Novel human protein sequence #1677.

XX KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;

XX KW gene therapy; diagnostic marker; morbid state; osteoporosis;

XX KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

XX KW cancer.

XX OS Homo sapiens.

XX FN EPI1440981-A2.

XX PD 28-JUL-2004.

XX PF 21-JAN-2004; 2004EP-00001196.

XX PR 21-JAN-2003; 2003JP-00102206.

XX PR 09-MAY-2003; 2003JP-00131392.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Iisogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

XX PI Yamamoto J, Isono Y, Nagai K, Irie R;

XX DR WPI; 2004-535376/52.

XX DR N-PSDB; ADQ64516.

XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,

XX PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.

XX FS Claim 1; SEQ ID NO 3865; 2449pp; English.

XX CC The invention relates to 2495 novel polynucleotides (I) and their encoded

XX CC polypeptides, sequences hybridizing to these nucleotides, sequences

XX CC encoding partial polypeptides and sequences having 70% or 90% identity to

XX CC the nucleotide and protein sequences. The nucleotides and polypeptides

XX CC are useful as diagnostic markers or therapeutic target for the diseases

XX CC or morbid states. They are also useful for treating osteoporosis,

XX CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,

XX CC dementia and various cancers. This sequence corresponds to a protein

XX CC sequence of the invention.

XX SQ Sequence 854 AA;

Query Match 96.6%; Score 28; DB 8; Length 854;

Best Local Similarity 83.3%; Pred. No. 7.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

DB 221 KVVFFA 226

RESULT 44

ABM83252

ID ABM83252 standard; protein; 922 AA.

XX AC ABM83252;

XX DT 18-NOV-2004 (first entry)

XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:3501.

XX KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX KW Homo sapiens.

XX FN WO2004023973-A2.

XX PD 25-MAR-2004.

XX PF 12-SEP-2003; 2003WO-US028227.

XX PR 12-SEP-2002; 2002US-0410259P.

XX PR 12-SEP-2002; 2002US-0410260P.

XX PA (INCY-) INCYTE CORP.

XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;

XX PI Harthehorne TA, Suchorolski MT, Altus CM, Pitts SU, Elder LV;

XX PI Mooney EM, Delegeane AM, Panesar IS, Barville SC, Reddy TP;

XX PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;

XX PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;

XX PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;

XX PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;

XX PI Patury S, Shi X, Suarez CJ;

XX DR WPI; 2004-329368/30.

XX DR N-PSDB; ACN41904.

XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful

XX PT in diagnosing a condition, disease or disorder associated with human

XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or

XX PT in gene mapping.

XX PS Claim 27; Page; 190pp; English.

XX CC The invention relates to novel diagnostic and therapeutic polynucleotides

XX CC selected from one of the 2722 sequences defined in the specification. A

XX CC polynucleotide of the invention may have a use in gene therapy. The human

XX CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be

XX CC used to diagnose a particular condition, disease or disorder associated

XX CC with human molecules, e.g. cell proliferative disorders,

XX CC autoimmune/inflammatory disorder, developmental disorder, endocrine

XX CC disorder, neurological disorders, gastrointestinal disorders, or

XX CC infections caused by virus, bacteria, fungi or parasite. The dithp

XX CC molecules may also be used in genetic mapping, in identifying individuals

XX CC from minute biological samples, in detecting single nucleotide

XX CC polymorphisms, as molecular weight markers, and for somatic or germline

XX CC gene therapy. The present sequence represents a dithp protein of the

XX CC invention. Note: The sequence data for this patent is not represented in

XX CC the printed specification, but was obtained in electronic format directly

XX CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

```
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239933P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0244647P.
PR 08-NOV-2000; 2000US-0244647P.
PR 08-NOV-2000; 2000US-0244676P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
(HUMA-) HUMAN GENOME SCI INC.
XX
XX

PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
DR N-PSDB; AAK56573.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Claim 11; SEQ ID NO 11385; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX SQ Sequence 190 AA;
Query Match 96.6%; Score 28; DB 4; Length 190;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
DB 14 KVVFFA 19
|:||||
RESULT 42
ABB61977
ID ABB61977 standard; protein; 564 AA.
XX
AC ABB61977;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 12723.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR N-PSDB; ABL06080.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
```

KW plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
 KW carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
 KW tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
 KW wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
 KW gene; ds; plant.
 XX Oryza sativa.
 XX OS
 XX WO2003000905-A2.
 XX PD
 XX 03-JAN-2003.
 XX PF
 XX 21-JUN-2002; 2002WO-IB002450.
 XX PR
 XX 22-JUN-2001; 2001US-0300112P.
 XX PR
 XX 26-SEP-2001; 2001US-0325277P.
 XX PR
 XX 20-DEC-2001; 2001US-0342327P.
 XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX PI Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
 FI Glazebrook J, Katagiri F, Kreps J, Provart N, Rickie D;
 XX DR WPI; 2003-229341/22.
 XX DR N-PSDB; ABC07947.
 XX CC
 XX PT New plant genes encoding polypeptides having an activity involved in or
 PT associated with the synthesis, metabolism or degradation of carbohydrates
 PT in the plant grain useful in generating plants having improved
 PT nutritional properties.
 XX CC
 XX PS Claim 15; SEQ ID NO 214; 130pp; English.
 XX CC
 XX CC This invention, in the area of plant biotechnology, relates to novel
 CC polynucleotides comprising a nucleotide sequence encoding a protein which
 CC is involved in or associated with the synthesis, metabolism or
 CC degradation of carbohydrates in the plant grain and the expression of
 CC which is up-regulated during grain filling. The plant is selected from
 CC corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
 CC sugarbeet, wheat, and rice. The invention may be useful for the
 CC improvement of protein, oil, starch, fibre and moisture content of the
 CC cereal grains. In addition, carbohydrate levels may be modified to a more
 CC desirable level using the present invention. The present sequence is the
 CC amino acid sequence of a rice protein of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/publishedpct_sequences.
 XX CC
 XX SQ Sequence 186 AA;
 XX
 XX Query Match 96.6%; Score 28; DB 7; Length 186;
 XX Best Local Similarity 83.3%; Pred. No. 1.6e+02;
 XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db |::|||
 4 KIVFFA 9
 RESULT 41
 AAM83792
 ID AAM83792 standard; protein; 190 AA.
 XX AC AAM83792;
 XX XX
 XX 07-NOV-2001 (first entry)
 XX DE Human immune/haematopoietic antigen SEQ ID NO:11385.
 XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
 KW cytostatic; gene therapy; vaccine; metastasis.
 XX KW
 XX OS Homo sapiens.

XX WO200157182-A2.
 PN
 XX 09-AUG-2001.
 XX
 XX 17-JAN-2001; 2001WO-US001354.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.
 PR 24-FEB-2000; 2000US-0184664P.
 PR 02-MAR-2000; 2000US-0186350P.
 PR 16-MAR-2000; 2000US-0189874P.
 PR 17-MAR-2000; 2000US-0190076P.
 PR 18-APR-2000; 2000US-0198123P.
 PR 19-MAY-2000; 2000US-0205515P.
 PR 07-JUN-2000; 2000US-0209467P.
 PR 28-JUN-2000; 2000US-0214886P.
 PR 30-JUN-2000; 2000US-0215135P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 11-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 14-JUL-2000; 2000US-0217496P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226682P.
 PR 23-AUG-2000; 2000US-0227182P.
 PR 30-AUG-2000; 2000US-0227009P.
 PR 01-SEP-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 12-SEP-2000; 2000US-0232081P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234224P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.

```

Db          38 KVVFFA 43
|:||||
|:||||
|:||||
|:||||

RESULT 38
AAOI1219
ID  AAOI1219 standard; protein; 175 AA.
XX
XX
AC  AAOI1219;
XX
XX
DT  06-NOV-2001 (first entry)
XX
XX
DE  Human polypeptide SEQ ID NO 25111.
XX
XX
KW  Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW  vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW  tissue growth factor; immunomodulatory; cancer; leukaemia;
KW  nervous system disorders; arthritis; inflammation.
XX
XX
OS  Homo sapiens.
XX
XX
FN  WO200164835-A2.
XX
XX
PD  07-SEP-2001.
XX
XX
PF  26-FEB-2001; 2001WO-US004927.
XX
XX
PR  28-FEB-2000; 2000US-00515126.
XX
XX
PR  18-MAY-2000; 2000US-00577409.
XX
XX
PA  (HYSE-) HYSEQ INC.
XX
XX
PI  Tang YT, Liu C, Drmanac RT;
XX
XX
WPI; 2001-514838/56.
XX
XX
N-PSDB; AAI91150.
XX
XX
Isolated nucleic acids and polypeptides, useful for preventing diagnosing
and treating e.g. leukemia, inflammation and immune disorders.
XX
XX
Claim 20; SEQ ID NO 25111; 1399pp + Sequence Listing; English.
XX
XX
The invention relates to human polynucleotides (AAI79941-AAI93841) and
the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
cytokine, cell proliferation or cell differentiation or which may induce
production of other cytokines in other cell populations. The
polynucleotides and polypeptides are useful in gene therapy, vaccines or
peptide therapy. The polypeptides have various cytokine-like activities,
e.g. stem cell growth factor activity, haematopoiesis regulating
activity, tissue growth factor activity, immunomodulatory activity and
activin/inhibin activity and may be useful in the diagnosis and/or
treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX
SQ  Sequence 175 AA;

Query Match          96.6%; Score 28; DB 4; Length 175;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KIVFFA 6
|:||||
|:||||
|:||||
|:||||
Db          128 KVVFFA 133

RESULT 39
ADC07962
ID  ADC07962 standard; protein; 186 AA.
XX
XX
AC  ADC07962;
XX
XX
DT  18-DEC-2003 (first entry)
XX
XX
DE  Rice protein sequence Seq ID214 related to grain filling.
XX
XX
18-DEC-2003 (first entry)
Rice protein sequence Seq ID228 related to grain filling.
plant biotechnology; carbohydrate synthesis; carbohydrate metabolism;
carbohydrate degradation; carbohydrate; plant grain; grain filling; corn;
tomato; banana; canola; cotton; peanut; sorghum; tobacco; sugarbeet;
wheat; rice; protein; oil; starch; fibre; moisture content; cereal grain;
gene; ds; plant.
Oryza sativa.
WO2003000905-A2.
03-JAN-2003.
21-JUN-2002; 2002WO-IB002450.
22-JUN-2001; 2001US-0300112P.
26-SEP-2001; 2001US-0325277P.
20-DEC-2001; 2001US-0342327P.
(SYGN ) SYNGENTA PARTICIPATIONS AG.
Zhu T, Cheng W, Briggs S, Cooper B, Goff SA, Moughamer T;
Glazebrook J, Katagiri F, Kreps J, Provart N, Rickes D;
WPI; 2003-229341/22.
N-PSDB; ADC07961.
New plant genes encoding polypeptides having an activity involved in or
associated with the synthesis, metabolism or degradation of carbohydrates
in the plant grain useful in generating plants having improved
nutritional properties.
Claim 15; SEQ ID NO 228; 130pp; English.
This invention, in the area of plant biotechnology, relates to novel
polynucleotides comprising a nucleotide sequence encoding a protein which
is involved in or associated with the synthesis, metabolism or
degradation of carbohydrates in the plant grain and the expression of
which is up-regulated during grain filling. The plant is selected from
corn, tomato, banana, canola, cotton, peanut, sorghum, tobacco,
sugarbeet, wheat, and rice. The invention may be useful for the
improvement of protein, oil, starch, fibre and moisture content of the
cereal grains. In addition, carbohydrate levels may be modified to a more
desirable level using the present invention. The present sequence is the
amino acid sequence of a rice protein of the invention. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
Sequence 186 AA;

Query Match          96.6%; Score 28; DB 7; Length 186;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1 KIVFFA 6
|:||||
|:||||
|:||||
|:||||
Db          4 KVVFFA 9

RESULT 40
ADC07948
ID  ADC07948 standard; protein; 186 AA.
XX
XX
AC  ADC07948;
XX
XX
DT  18-DEC-2003 (first entry)
XX
XX
DE  Rice protein sequence Seq ID214 related to grain filling.
XX
XX

```

The present sequence represents the calmodulin-binding site of mouse iNOS amino acid sequence. The present invention describes endothelial nitric oxide synthase (eNOS) mutants having one or more mutations in an amino acid sequence corresponding to a functional domain of a mammalian eNOS. At least one of the mutations is at a position corresponding to an amino acid residue in a calmodulin-binding domain that is phosphorylated in mammalian cells, and not an amino acid substitution to Ala or Asp. Also described: (1) an isolated eNOS polypeptide mutant that is substantially homologous, or has a 95-99% sequence identity to the amino acid sequence of the novel eNOS polypeptide mutant; (2) an isolated polynucleotide encoding the polypeptide mutant; (3) a recombinant vector comprising the polynucleotide operably linked to at least one regulatory sequence; (4) a pharmaceutical composition comprising the polypeptide mutant or the polynucleotide; (5) a binding partner of the polypeptide mutant; (6) modulating eNOS activity in a cell by administering to the cell the polypeptide mutant; (7) modulating eNOS activity in a cell by administering the polypeptide mutant or the polynucleotide to the cell, such that the polypeptide mutant is expressed in the cell; (8) diagnosing a condition associated with aberrant eNOS activity by contacting a cell of a patient with the polynucleotide, and detecting a level of eNOS activity indicative of the medical condition; and (9) prophylactic and therapeutic methods of treating a condition associated with aberrant eNOS activity by administering the polypeptide mutant or polynucleotide to the patient. The eNOS mutant has vasotropic, antiarteriosclerotic, hypotensive, antidiabetic, vulnerary, antilipemic and anorectic activities, and has reduced calcium dependence and increased activity.

CC encoding allergen specific T-cell epitope peptide, inserting a DNA into
 CC the variable region of storage protein of the plant and expressing the
 CC peptide in the transgenic plant. The invention describes the accumulation
 CC of human T cell epitope in rice albumen, a method of accumulating T cell
 CC epitope-attached peptide (7crp) in seeds, a method of inserting the 7crp
 CC into the variable region of glutelin (the major storage protein of rice),
 CC and expressing and accumulating 7crp as part of the glutelin. The rice
 CC capable of producing the 7crp is useful as an edible vaccine against
 CC Japanese (Cryptomeria japonica) cedar pollen antigen. The pollen allergen
 CC is Cryj1 or Cryj2. The T-cell epitope is integrated on an edible region
 CC such as the seed of a plant. The method of the invention is useful for
 CC producing a plant accumulated with allergen specific T-cell epitope, and
 CC manufacturing a transgenic plant, preferably rice, integrated with T-cell
 CC epitope. The method is useful for preventing or treating allergic disease
 CC such as hay fever. The method enables the production of allergen specific
 CC T-cell epitope at a low cost and also reduces the amount for
 CC administration. The allergen specific T-cell epitope accumulated in a
 CC seed is stable for storage. This sequence represents rice 26 kDa peptide.
 XX
 SQ Sequence 23 AA;

Query Match 96.6%; Score 28; DB 8; Length 23;
 Best Local Similarity 83.3%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
 |:||||
 Db 4 KVVFFFA 9

RESULT 34

AAB05910
 ID AAB05910 standard; peptide; 37 AA.

XX
 AC AAB05910;

XX
 DT 16-OCT-2000 (first entry)

XX Mouse inducible nitric oxide synthase calmodulin-binding region.

XX Mouse; inducible nitric oxide synthase; iNOS;

XX endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;

KW AMP-activated protein kinase; AMPK; calmodulin; CaM;

KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;

KW obstructive airways disease.

XX
 OS Mus sp.

XX WO200028076-A1.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-AU000968.

XX 06-NOV-1998; 98AU-00006976.

XX (SVIN-) ST VINCENTS INST MEDICAL RES.

XX Stapleton DI, Chen Z, Michell BJ, Kemp BE, Mitchellhill KI;

XX WPI; 2000-376583/32.

XX Identifying modulators of AMP-activated protein kinase-mediated

PT activation of a nitric oxide synthase (NOS), for use in ischemic heart

PT disease, comprises testing for the increase or decrease in

PT phosphorylation of NOS.

XX Example 4; Fig 5; 41pp; English.

XX The present sequence is the calmodulin (CaM)-binding region of mouse
 CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of
 CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-
 CC arginine. The sequence is provided for comparison with endothelial nitric

CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is
 CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of
 CC Ca²⁺-CaM. Phosphorylation results in inhibition of eNOS. In the presence
 CC of Ca²⁺-CaM, phosphorylation by AMPK occurs predominantly at Ser-1177 and
 CC eNOS is activated. Modulators which activate AMPK may be used in the
 CC treatment of ischaemic heart disease by promoting glucose and fatty acid
 CC metabolism, and improving nutrient and oxygen supply to the myocytes.
 CC They may also be used for the treatment of pulmonary hypertension and
 CC obstructive airways disease

XX Sequence 37 AA;

Query Match 96.6%; Score 28; DB 3; Length 37;

Best Local Similarity 83.3%; Pred. No. 32;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFFA 6
 |:||||
 Db 18 KVVFFFA 23

RESULT 35

ADK34080

ID ADK34080 standard; peptide; 37 AA.

XX
 AC ADK34080;

XX 20-MAY-2004 (first entry)

XX Human nNOS calmodulin binding domain peptide seqid 7.

XX vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;

KW eNOS; endothelial nitric oxide synthase; angiogenesis;

KW microvascular dysfunction; human; calmodulin binding domain;

KW neuronal nitric oxide; nNOS.

XX Homo sapiens.

XX WO2004016761-A2.

XX 26-FEB-2004.

XX 15-AUG-2003; 2003WO-US025626.

XX 16-AUG-2002; 2002US-0403637P.

XX (SCHD) SCHERING AG.

XX Dole WP, Kauser K, Qian HS, Rubanyi G;

XX WPI; 2004-203789/19.

XX Treating critical limb ischemia (CLI), or angiogenesis comprises

PT administering to a patient a polynucleotide encoding a mammalian

PT endothelial nitric oxide synthase (eNOS) polypeptide.

XX Example 1; SEQ ID NO 7; 82pp; English.

XX The invention describes a method of creating critical limb ischaemia
 CC (CLI) comprising administering to a patient a polynucleotide encoding a
 CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also
 CC described are: a method for treating angiogenesis by administering to a
 CC patient a polynucleotide encoding eNOS; and ameliorating microvascular
 CC dysfunction by administering to the patient the polynucleotide encoding
 CC the eNOS polypeptide. The method is useful for treating critical limb
 CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.
 CC This is the amino acid sequence of a human neuronal nitric synthase
 CC (nNOS) calmodulin binding domain peptide.

XX Sequence 37 AA;

Query Match 96.6%; Score 28; DB 8; Length 37;

Best Local Similarity 83.3%; Pred. No. 32;

Query Match 96.6%; Score 28; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|||||
Db 1 KVVFFA 6

RESULT 32
ADQ09761
ID ADQ09761 standard; peptide; 22 AA.
XX
AC ADQ09761;
XX
DT 23-SEP-2004 (first entry)
XX
DE Rice 26kDa globulin signal sequence SEQ ID NO:117.
XX
KW prolamine; rice; plant; seed; transgenic plant; signal.
XX
OS Oryza sativa.
XX
PN WO2004056993-A1.
XX
PD 08-JUL-2004.
XX
PF 09-DEC-2003; 2003WO-JP015753.
XX
PR 20-DEC-2002; 2002JP-00369700.
XX
PA (NAA-1) NAT AGRIC & BIO-ORIENTED RES ORG.
XX
PI Kuroda M;
XX
DR WPI; 2004-525439/50.
DR N-PSDB; ADQ09760.
XX
PT Novel nucleic acid molecule antisense to nucleic acid sequence encoding
prolamine, useful for reducing expression dose of protein in seed, and
for producing transgenic plant, preferably rice plant having reduced
storage protein.
XX
PS Example 13; SEQ ID NO 117; 272pp; Japanese.
XX
CC The present invention describes a nucleic acid molecule (I) comprising a
consecutive nucleic acid sequence (SI) of at least 15 bp in length and
complementary with a nucleic acid sequence encoding a prolamine
polypeptide or a nucleic acid sequence having a homology of at least
about 70% to (SI). Also described: (1) a nucleic acid molecule (NI)
comprising a nucleic acid sequence (A) having about 70% homology to a
nucleic acid sequence encoding a prolamine polypeptide and a nucleic acid
sequence (B) having about 70% homology to the complement of the nucleic
acid sequence encoding a prolamine polypeptide; (2) a factor (II) capable
of causing RNA interference of the gene sequence encoding a prolamine
polypeptide; (3) a nucleic acid cassette (III) containing (1); (4)
producing (III); (5) a vector (IV) comprising (1); (6) a plant cell (V)
comprising (1); (7) a plant tissue (VI) comprising (V); (8) a plant (VII)
containing (1) or (V); (9) a seed (VIII) produced by (VII); (10) starch
preparation produced from (VII) or (VIII); and (11) a composition
containing gene product of foreign gene produced from (VII) or (VIII).
(1) is useful for decreasing the expression level of a protein in the
seed of a plant, for expressing a foreign gene in the seed of a plant and
for decreasing the expression of a natural protein in the seed of a
plant. The method of decreasing the amount of expression level of a
protein in the seed of a plant involves providing (I), introducing (I)
into the cell of the plant, redifferentiating the cell, producing a
transgenic plant, and obtaining the seed from the transgenic plant. The
method after the step of introduction, further involves selecting the
cell introduced with (I), by determining resistance with respect to
antibiotics. The method of expressing a foreign gene in the seed of a
plant, involves providing (I) and the nucleic acid molecule encoding a

CC foreign gene product, introducing (I) and the nucleic acid molecule
CC encoding a foreign gene product into cell of the plant, re-
CC differentiating the cell, producing a transgenic plant, and obtaining the
CC seed from the transgenic plant. The method further involves isolating the
CC gene product of the foreign gene from the seed. (I) is useful for
CC producing transgenic plants having reduced expression of storage proteins
CC and for reducing the expression dose of a protein in a seed of a plant.
CC The present sequence represents a rice 26kDa globulin signal sequence,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 22 AA;
Query Match 96.6%; Score 28; DB 8; Length 22;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|||||
Db 4 KVVFFA 9

RESULT 33
ADT93984
ID ADT93984 standard; peptide; 23 AA.
XX
AC ADT93984;
XX
DT 27-JAN-2005 (first entry)
XX
DE Rice 26 kDa peptide.
XX
KW Storage protein; allergen specific T cell epitope;
KW vesicle anchoring signal; transgenic plant; rice albumen;
KW T cell epitope-attached peptide; 7crp; seed; glutelin; edible vaccine;
KW Japanese cedar pollen antigen; Cryj1; Cryj2; allergic disease; hay fever;
KW antiallergic; plant; 26 kDa.
XX
OS Oryza sativa.
XX
PN WO2004094637-A1.
XX
PD 04-NOV-2004.
XX
PF 23-APR-2004; 2004WO-JP005938.
XX
PR 24-APR-2003; 2003JP-00120639.
XX (NORQ) NAT INST AGROBIOLOGICAL SCI.
XX Takaiwa F, Takagi H;
PI WPI; 2004-784905/77.
DR
PT Novel DNA having sequence encoding allergen specific T-cell epitope
peptide, useful for accumulating T-cell epitope peptide in plants and for
treating allergic diseases such as pollinosis.
XX
PS Disclosure; SEQ ID NO 5; 79pp; Japanese.
XX
CC This invention relates to a DNA (I) having a sequence under the control
of a storage protein promoter, chosen from a sequence encoding storage
protein signal sequence at the 5' end of a sequence encoding allergen
specific T cell epitope peptide and/or a sequence encoding vesicle
anchoring signal sequence at the 3' end, and a DNA sequence encoding a
polypeptide having allergen specific T-cell epitope peptide inserted in
the variable region of a storage protein. Also disclosed is a vector (II)
for T-cell epitope accumulated plant preparation, and a method of
accumulating allergen specific T-cell epitope in a plant. The method
involves introducing (I) or (II) to a plant, obtaining DNA encoding
allergen specific T-cell epitope peptide, adding a DNA encoding a storage
protein signal sequence to the 5' end and/or a vesicle anchoring signal
sequence to the 3' end of the obtained DNA, and expressing the DNA in a
plant under the control of a storage protein promoter, or obtaining DNA

QY 1 KIVEFA 6
|:||||
Db 1 KIVEFA 6

RESULT 30
ADY37928
ID ADY37928 standard; peptide; 6 AA.
XX
AC ADY37928;
XX
DT 19-MAY-2005 (first entry)
XX
DE Amyloid-targeting peptide, SEQ ID NO:8, for use in imaging agent.
XX
KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimers disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.
XX
OS Synthetic.
XX
PN US2005048000-A1.
XX
PD 03-MAR-2005.
XX
PF 03-DEC-2003; 2003US-00728028.
XX
PR 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
PR 29-JAN-2003; 2003US-0443291P.
XX
PA (NEUR-) NEUROCHEM INT LTD.
XX
PI Gervais F, Kong X, Chalifour R, Migneault D;
DR WPI; 2005-212201/22.
XX
PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 8; 34pp; English.
XX
CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.
XX
SQ Sequence 6 AA;
Query Match 96.8%; Score 28; DB 9; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVEFA 6
|:||||
Db 1 KIVEFA 6

RESULT 31
ADY37936
ID ADY37936 standard; peptide; 6 AA.
XX
AC ADY37936;
XX
DT 19-MAY-2005 (first entry)
XX
DE Amyloid-targeting peptide, SEQ ID NO:16, for use in imaging agent.
XX
KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimers disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "C-terminal amide"
XX
XX US2005048000-A1.
XX
PD 03-MAR-2005.
XX
PF 03-DEC-2003; 2003US-00728028.
XX
PR 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
PR 29-JAN-2003; 2003US-0443291P.
XX
PA (NEUR-) NEUROCHEM INT LTD.
XX
PI Gervais F, Kong X, Chalifour R, Migneault D;
DR WPI; 2005-212201/22.
XX
PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 16; 34pp; English.
XX
CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.
XX
SQ Sequence 6 AA;

agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; having amyloid-beta deposits. The present sequence represents a peptide that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.

Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVFVFA 6

RESULT 29

ADQ37329
ID ADQ37329 standard; peptide; 6 AA.

XX AC ADQ37329;

DT 07-OCT-2004 (first entry)

DE Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;
KW amyloid-beta fibril formation; immune response; nootropic;
KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW anticonvulsant; anti-HIV; cardiovascular; tranquilliser; uteropathic;
KW cardiant; antidepressant; endocrine; hypnotic;
KW amyloid-beta fibril formation modulator; immune system modulator;
KW Alzheimer's disease; mild cognitive impairment;
KW mild-to-moderate cognitive impairment; vascular dementia;
KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW senile dementia; Down's syndrome; inclusion body myositis;
KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW behavioural dysfunction; neurological condition; psychological condition;

vacine antigen.
XX Synthetic.
OS Key Location/Qualifiers
FH Modified-site 6
FT /note="amidated"
XX WO2004058239-A1.
PN 15-JUL-2004.
XX 24-DEC-2003; 2003WO-CA002021.
PD 24-DEC-2002; 2002US-0436379P.
PF 23-JUN-2003; 2003US-0482214P.
XX (NEUR-) NEUROCHEM INT LTD.
XX Gervais F, Bellini F;
XX WPI; 2004-543342/52.
DR Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.

Disclosure; Page 70; 143pp; English.

The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have nootropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; having amyloid-beta deposits. The present sequence represents a peptide that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.

Sequence 6 AA;

Query Match 96.6%; Score 28; DB 8; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1..6 /note= "D-form residues"
 FT Modified-site 6 /note= "amidated"
 FT
 XX WO2004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 XX
 XX 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 67; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX Sequence 6 AA;
 SQ

Query Match 96.6%; Score 28; DB 8; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 Db 1 KIVFFPA 6

RESULT 28

ADQ37321

ID ADQ37321 standard; peptide; 6 AA.

XX AC ADQ37321;

XX DT 07-OCT-2004 (first entry)

XX DE Antifibrillogenic amyloidosis inhibiting peptide.

XX KW amyloid-beta; amyloid-beta related disease;

XX KW amyloid-beta fibril formation; immune response; neurotropic;

XX KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;

XX KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;

XX KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;

XX KW cardiant; antidepressant; endocrine; hypnotic;

XX KW amyloid-beta fibril formation modulator; immune system modulator;

XX KW Alzheimer's disease; mild cognitive impairment;

XX KW mild-to-moderate cognitive impairment; vascular dementia;

XX KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

XX KW senile dementia; Down's syndrome; inclusion body myositis;

XX KW age-related macular degeneration; hypothyroidism;

XX KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;

XX KW behavioural dysfunction; neurological condition; psychological condition;

XX KW vaccine antigen.
 XX Synthetic.
 XX OS
 XX WO2004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 XX
 XX 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 67; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,

XX The present invention describes compositions (C) comprising: (a) a first

RESULT 25
AAU11656
ID AAU11656 standard; peptide; 6 AA.
AC AAU11656;
XX
XX
DT 09-APR-2002 (first entry)
XX
DE Peptide #9, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX
OS Synthetic.
XX
FN WO200185093-A2.
XX
XX
PD 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Green AM, Gervais F;
XX
XX WPI; 2002-075222/10.
XX
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
FT disease comprises contacting blood vessel wall cell with amyloid-beta 40
FT inhibitor.
XX
XX Disclosure; Page 10; 68pp; English.
XX
XX The present invention relates to a new method of inhibiting cerebral
CC amyloid angiopathy. The new method of the invention involves contacting a
CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
CC can be used for treating disease states characterised by cerebral amyloid
CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
CC The present sequence represents one of a group of peptides (AAU11648-
CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
CC was used in the invention to treat a disease state characterised by
CC cerebral amyloid angiopathy (CAA)
XX
XX Sequence 6 AA;
Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KVVFFA 6
|:|||||
|:|||||
RESULT 26
AAE35452
ID AAE35452 standard; peptide; 6 AA.
AC AAE35452;
XX
XX 17-JUN-2003 (first entry)
XX
XX Abeta peptide #23.
DE
XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
KW

psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotic;
KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH Misc-difference 1.6
FT /note= "D-form residues"
FT Modified-site 6
FT /note= "C-terminal amide"
XX
XX WO200296937-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-CA000763.
XX
XX 29-MAY-2001; 2001US-00867847.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Hebert L, Chalifour RJ, Kong X;
XX
XX WPI; 2003-201269/19.
XX
XX Prevention and/or treatment of an amyloid-related disease e.g.
FT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
XX
XX Claim 1; Page 59; 44pp; English.
XX
XX The invention relates to a method for prevention and/or treatment of an
CC amyloid-related disease which comprises administration of an all-D -
CC amyloid-beta peptide. The method is used for preventing and/or treating
CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
CC the mammal; and reducing or inhibiting the formation of plaques. It is
CC also used for treating AA (reactive) amyloid diseases including
CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
CC disease. AA deposits are also produced as a result of chronic microbial
CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
CC present sequence is an Abeta peptide used to illustrate the method of the
CC invention
XX
XX Sequence 6 AA;
Query Match 96.6%; Score 28; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KVVFFA 6
|:|||||
|:|||||
RESULT 27
ADQ37277
ID ADQ37277 standard; peptide; 6 AA.
XX
XX ADQ37277;
AC
XX
XX 07-OCT-2004 (first entry)
XX
XX Vaccine antigen amyloid-beta related amino acid sequence.
DE

```

CC
SQ      Sequence 6 AA;
      Query Match      96.6%; Score 28; DB 5; Length 6;
      Best Local Similarity 83.3%; Pred. NO. 2e+06;
      Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFFA 6
      |:|:|:|
DB      1 KVVFFFA 6

RESULT 24
AAU11664
ID      AAU11664 standard; peptide; 6 AA.
XX
AC      AAU11664;
XX
DT      09-APR-2002 (first entry)
XX
DE      Peptide #17, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
KW      Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
KW      CAA; nontropic; neuroprotective; cerebroprotective; Alzheimer's disease;
KW      cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      Modified-site 6
FT      /note= "C-terminal amide"
XX
PN      WO200185093-A2.
XX
PD      15-NOV-2001.
XX
PF      22-DEC-2000; 2000WO-IB002078.
XX
PR      23-DEC-1999; 99US-0171877P.
XX
PA      (NEUR-) NEUROCHEM INC.
XX
PI      Green AM, Gervais F;
XX
WPI; 2002-075222/10.
XX
DR      Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX      disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX      inhibitor.
XX
PS      Disclosure; Page 10; 68pp; English.
XX
CC      The present invention relates to a new method of inhibiting cerebral
CC      amyloid angiopathy. The new method of the invention involves contacting a
CC      blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
CC      can be used for treating disease states characterised by cerebral amyloid
CC      angiopathy, particularly Alzheimer's disease, hereditary cerebral
CC      haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
CC      The present sequence represents one of a group of peptides (AAU11648-
CC      AAU11669, AAU11910 & AAU11911) that were used in the invention as a
CC      carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
CC      was used in the invention to treat a disease state characterised by
CC      cerebral amyloid angiopathy (CAA)
XX
SQ      Sequence 6 AA;
      Query Match      96.6%; Score 28; DB 5; Length 6;
      Best Local Similarity 83.3%; Pred. NO. 2e+06;
      Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFFA 6
      |:|:|:|
DB      1 KVVFFFA 6

AAU96826
ID      AAU96826 standard; peptide; 6 AA.
XX
AC      AAU96826;
XX
DT      30-JUL-2002 (first entry)
XX
DE      Amyloid targeting peptide #16.
XX
KW      Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
KW      transmissible cerebral amyloidosis; transmissible virus dementia;
KW      scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
KW      bovine spongiform encephalopathy; inflammation associated amyloid;
KW      primary amyloidosis; feline spongiform encephalopathy;
KW      Alzheimer's disease; prion-mediated disease; blood-brain barrier;
KW      dialysis-related amyloidosis; light chain-related amyloidosis;
KW      cerebral amyloid angiopathy.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      Misc-difference 1..6
FT      /note= "Preferably D-form residue"
FT      Modified-site 6
FT      /note= "Ala is amidated"
XX
PN      WO200207781-A2.
XX
PD      31-JAN-2002.
XX
PF      25-JUL-2001; 2001WO-CA001071.
XX
PR      25-JUL-2000; 2000US-0220808P.
XX
PR      24-JUL-2001; 2001US-00915092.
XX
PA      (NEUR-) NEUROCHEM INC.
XX
PI      Gervais F, Kong X, Chalifour R, Migneault D;
XX
WPI; 2002-371447/40.
XX
DR      New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX      plaques and/or for the treatment of amyloidosis disorders.
XX
PS      Claim 49; Page 21; 57pp; English.
XX
CC      The invention relates to an amyloid-targeting imaging agent comprising an
CC      amyloid targeting moiety, a linker moiety and a labelling moiety. The
CC      agent is of general formula A_t-(A_1)_n_k z-(A_1)_a_b (I) where z = 0 - 1;
CC      A_t = an amyloid targeting moiety; A_1)_n_k = a linker moiety; and A_1)_a_b
CC      = a labelling moiety. Also included are imaging amyloid deposition or
CC      diagnosing an amyloid-related condition in a patient involving
CC      administering (I) to the patient, and ultrasound imaging (I) in the
CC      patient to determine the presence of amyloid or amyloid-related condition
CC      ; and a kit for preparing a radiopharmaceutical preparation comprising
CC      (I), a reducing agent, a buffering agent, a transchelating agent, and
CC      instructions for the preparation and use of the radiopharmaceutical in
CC      the imaging of amyloid or an amyloid-related condition. The agents are
CC      used for imaging amyloid deposition and for diagnosing an amyloid related
CC      condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
CC      cerebral amyloidosis (transmissible virus dementias), familial CJD,
CC      scrapie, transmissible mink encephalopathy, bovine spongiform
CC      encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
CC      primary amyloidosis, feline spongiform encephalopathy, non-transmissible
CC      cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
CC      dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
CC      amyloid angiopathy. The agents are capable of crossing the blood-brain
CC      barrier and are capable of binding specifically to amyloid plaques. The
CC      present sequence is a peptide forming the amyloid targeting moiety of the
CC      agent of the invention

```

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1..6

FT Modified-site 6

FT /note= "all D-form residues"

FT /note= "C-terminal amide"

XX WO200139796-A2.

XX 07-JUN-2001.

XX 29-NOV-2000; 2000WO-CA001413.

XX 29-NOV-1999; 99US-0168594P.

XX 28-NOV-2000; 2000US-00724842.

XX (NEUR-) NEUROCHEM INC.

XX Chalifour R, Hebert L, Kong X, Gervais F;

XX WPI; 2001-441458/47.

XX Preventing/treating amyloid-related disease, especially Alzheimer's disease, comprises administering antigenic all-D peptide, eg. as vaccine, which elicits production of antibodies to prevent fibrillogenesis and associated cellular toxicity.

XX Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in preparing vaccines for preventing or treating Alzheimer's disease and other amyloid related disorders in humans. It is based on a portion of amyloid-beta peptide (see AAB2622), and may be modified by removing or inserting 1 or more amino acid residues, or by substituting 1 or more amino acid residues with other amino acid residues or non-amino acid fragments. Vaccines of the invention are produced using 'non-self' peptides synthesised from the unnatural D-configuration amino acids to avoid the drawbacks of 'self' proteins. The all-D peptides need not be aggregated to be operative or immunogenic. They preferably interact with at least 1 region of an amyloid protein, e.g. the beta-sheet region or GAG-binding site region, the amyloid-beta peptide, or their immunogenic fragments, protein conjugates, immunogenic derivative peptides and immunogenic peptidomimetics. Examples include all-D peptides corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and 36-42 of the amyloid-beta peptide and the all-D derivative peptides given in AAB2623-64. The vaccine elicits a preferential TH-2 or TH-1 response, preventing fibrillogenesis and associated cellular toxicity. The amyloid related diseases may be localised amyloidosis, e.g. diabetes type II, neurodegenerative diseases, e.g. bovine spongiform encephalitis, and Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and prion protein related disorders, or systemic amyloidosis associated with chronic infection (e.g. tuberculosis) or chronic inflammation (e.g. rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

XX Query Match 96.6%; Score 28; DB 4; Length 6;

XX Best Local Similarity 83.3%; Pred. No. 2e+06;

XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

Db 1 KVVFFA 6

RESULT 22

ID AAU96818 standard; peptide; 6 AA.

XX AAU96818;

XX

30-JUL-2002 (first entry)

XX Amyloid targeting peptide #8.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD; transmissible cerebral amyloidosis; transmissible virus dementia; scrapie; transmissible mink encephalopathy; BSE; type II diabetes; bovine spongiform encephalopathy; inflammation associated amyloid; primary amyloidosis; feline spongiform encephalopathy; Alzheimer's disease; prion-mediated disease; blood-brain barrier; dialysis-related amyloidosis; light chain-related amyloidosis; cerebral amyloid angiopathy.

OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1..6

FT /note= "Preferably D-form residue"

FT WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

XX 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an amyloid targeting moiety, a linker moiety and a labelling moiety. The agent is of general formula A t-(A l n k) z-A l a b (I) where z = 0 - 1; A t = an amyloid targeting moiety; A l n k = a linker moiety; and A l a b = a labelling moiety. Also included are imaging amyloid deposition or diagnosing an amyloid-related condition in a patient involving administering (I) to the patient, and ultrasound imaging (I) in the patient to determine the presence of amyloid or amyloid-related condition; and a kit for preparing a radiopharmaceutical preparation comprising (I), a reducing agent, a buffering agent, a transchelating agent, and instructions for the preparation and use of the radiopharmaceutical in the imaging of amyloid or an amyloid-related condition. The agents are used for imaging amyloid deposition and for diagnosing an amyloid related condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible cerebral amyloidosis (transmissible virus dementia), familial CJD, scrapie, transmissible mink encephalopathy, bovine spongiform encephalopathy (BSE), inflammation-associated amyloid, type II diabetes, primary amyloidosis, feline spongiform encephalopathy, non-transmissible cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy. The agents are capable of crossing the blood-brain barrier and are capable of binding specifically to amyloid plaques. The present sequence is a peptide forming the amyloid targeting moiety of the agent of the invention

XX Sequence 6 AA;

XX Query Match 96.6%; Score 28; DB 5; Length 6;

XX Best Local Similarity 83.3%; Pred. No. 2e+06;

XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

Db 1 KVVFFA 6

AC AAB48490;
 XX
 XX 02-MAR-2001 (first entry)
 XX
 XX Antifibrillogenic peptide #17.
 DE
 XX Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
 KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
 KW Alzheimer's disease.
 XX
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 6
 FT /note= "C-terminal amide"
 FT
 XX WO200068263-A2.
 PN
 XX 16-NOV-2000.
 PD
 XX 04-MAY-2000; 2000WO-CA000515.
 XX
 XX 05-MAY-1999; 99US-0132592P.
 XX
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Chalifour R, Gervais F, Gupta A;
 XX
 XX WPI; 2001-031852/04.
 DR
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 PT
 XX Claim 7; Page 25; 46pp; English.
 PS
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 DB |:|:|:|
 1 KVVFFFA 6
 RESULT 20
 AAB82630
 ID AAB82630 standard; peptide; 6 AA.
 XX
 XX AAB82630;
 AC
 XX 02-OCT-2001 (first entry)
 XX
 XX All-D peptide used in Alzheimer's disease vaccine.
 DE
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 1. .6
 FT /note= "all D-form residues"
 FT

XX WO200139796-A2.
 FN
 XX 07-JUN-2001.
 PD
 XX 29-NOV-2000; 2000WO-CA001413.
 PF
 XX 29-NOV-1999; 99US-0168594P.
 XX
 XX 28-NOV-2000; 2000US-00724842.
 PR
 XX (NEUR-) NEUROCHEM INC.
 XX
 XX Chalifour R, Hebert L, Kong X, Gervais F;
 PI
 XX WPI; 2001-441458/47.
 DR
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX
 XX Disclosure; Page 11; 31pp; English.
 PS
 XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self',
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC prion protein related disorders, scrapie, cerebral amyloid angiopathy, and
 CC Creutzfeldt-Jakob disease, scrapie, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFFA 6
 DB |:|:|:|
 1 KVVFFFA 6
 RESULT 21
 AAB82638
 ID AAB82638 standard; peptide; 6 AA.
 XX
 XX AAB82638;
 AC
 XX 02-OCT-2001 (first entry)
 XX
 XX All-D peptide used in Alzheimer's disease vaccine.
 DE
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 KW
 XX

CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |||||
 Db 1 KIVFFA 6

RESULT 17
 ABG26598
 ID ABG26598 standard; protein; 99 AA.

XX

AC ABG26598;

XX

DT 18-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #26589.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

XX

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

XX

DR N-PSDB; AAS90785.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

XX

PT diagnostics, forensics, gene mapping, identification of mutations

XX

PT responsible for genetic disorders or other traits and to assess

XX

PT biodiversity.

XX

PS Claim 20; SEQ ID NO 56957; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)

XX

CC sequences. (I) is useful as hybridisation probes, polymerase chain

XX

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

XX

CC and in recombinant production of (II). The polynucleotides are also used

XX

CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 99 AA;

Query Match 100.0%; Score 29; DB 4; Length 99;
 Best Local Similarity 100.0%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |||||
 Db 63 KIVFFA 68

RESULT 18
 AAB48482

ID AAB48482 standard; peptide; 6 AA.

XX

AC AAB48482;

XX

DT 02-MAR-2001 (first entry)

XX

DE Antifibrillogenic peptide #9.

XX

KW Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;

XX

KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;

XX

KW Alzheimer's disease.

XX

OS Homo sapiens.

XX

PN WO200068263-A2.

XX

PD 16-NOV-2000.

XX

PF 04-MAY-2000; 2000WO-CA000515.

XX

PR 05-MAY-1999; 99US-0132592P.

XX

PA (NEUR-) NEUROCHEM INC.

XX

PI Chalifour R, Gervais F, Gupta A;

XX

DR WPI; 2001-031852/04.

XX

PT Antifibrillogenic agent useful for inhibiting amyloidosis and/or for

XX

PT cytoprotection for treating amyloidosis disorders, comprises a peptide,

XX

PT its isomer or peptidomimetic.

XX

PS Claim 7; Page 25; 46pp; English.

XX

CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used

XX

CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of

XX

CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore

XX

CC useful for treating amyloidosis disorders such as Alzheimer's disease.

XX

CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan

XX

CC binding region and the prot-prot interaction region of the human amyloid

XX

SQ Sequence 6 AA;

Query Match 96.6%; Score 28; DB 4; Length 6;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
 |||||
 Db 1 KIVFFA 6

RESULT 19
 AAB48490

ID AAB48490 standard; peptide; 6 AA.

XX

CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in


```

XX SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |||||
Db 1 KIVFFA 6

RESULT 15
ADV37921
ID ADV37921 standard; peptide; 6 AA.
XX
AC ADV37921;
XX
DT 19-MAY-2005 (first entry)
XX
DE Amyloid-targeting peptide, SEQ ID NO:1, for use in imaging agent.
XX
KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimer's disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.
XX
OS Synthetic.
XX
FN US2005048000-A1.
XX
PD 03-MAR-2005.
XX
PF 03-DEC-2003; 2003US-00728028.
XX
PR 25-JUL-2000; 2000US-0220808P.
PR 24-JUN-2001; 2001US-00915092.
PR 29-JAN-2003; 2003US-0443291P.
XX
PA (NEUR-) NEUROCHEM INT LTD.
XX
PI Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.
XX
PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 1; 34pp; English.
XX
CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementia), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADV37921-ADV37947 and ADV37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.

```

```

XX SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |||||
Db 1 KIVFFA 6

RESULT 16
ADV37929
ID ADV37929 standard; peptide; 6 AA.
XX
AC ADV37929;
XX
DT 19-MAY-2005 (first entry)
XX
DE Amyloid-targeting peptide, SEQ ID NO:9, for use in imaging agent.
XX
KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimer's disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.
XX
OS Synthetic.
XX
FN US2005048000-A1.
XX
PD 03-MAR-2005.
XX
PF 03-DEC-2003; 2003US-00728028.
XX
PR 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
PR 29-JAN-2003; 2003US-0443291P.
XX
PA (NEUR-) NEUROCHEM INT LTD.
XX
PI Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2005-212201/22.
XX
PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX
PS Disclosure; SEQ ID NO 9; 34pp; English.
XX
CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidosis (also known as transmissible virus
CC dementia), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease, prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-10

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New:*

1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB.pep:*

4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB.pep:*

5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB.pep:*

6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB.pep:*

7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB.pep:*

8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	93.1	19	6	US-10-923-605-5
2	27	93.1	19	6	US-10-934-818-5
3	27	93.1	40	7	US-11-016-706-36
4	27	93.1	40	7	US-11-098-674-12
5	27	93.1	42	6	US-10-923-605-1
6	27	93.1	42	6	US-10-934-818-1
7	27	93.1	42	6	US-11-016-706-37
8	27	93.1	43	6	US-10-934-818-6
9	27	93.1	43	6	US-10-250-581-1
10	27	93.1	43	6	US-10-581-1
11	27	93.1	770	6	US-10-982-545-15
12	27	93.1	269	6	US-10-789-273-38
13	25	86.2	269	6	US-10-467-657-330
14	25	86.2	400	6	US-10-793-626-1056
15	24	82.8	50	6	US-10-467-657-7892
16	24	82.8	347	6	US-10-467-657-2014
17	24	82.8	402	6	US-10-467-657-9070
18	24	82.8	426	6	US-10-467-657-2120
19	24	82.8	524	6	US-10-689-742-13
20	24	82.8	660	7	US-11-186-284-125
21	24	82.8	677	6	US-10-131-826A-230
22	24	82.8	708	6	US-10-821-234-917
23	23	79.3	5	7	US-11-098-674-1
24	23	79.3	229	6	US-10-131-826A-410
25	23	79.3	311	6	US-10-793-626-2450

26	23	79.3	481	6	US-10-995-561-959	Sequence 959, App
27	23	79.3	522	7	US-11-080-991-104	Sequence 104, App
28	23	79.3	528	6	US-10-793-626-1930	Sequence 1930, App
29	23	79.3	533	6	US-10-467-657-2868	Sequence 2868, App
30	23	79.3	3623	6	US-10-995-561-593	Sequence 593, App
31	22	75.9	47	6	US-10-467-657-5436	Sequence 5436, App
32	22	75.9	98	6	US-10-467-657-4746	Sequence 4746, App
33	22	75.9	167	7	US-11-210-316-18	Sequence 18, Appl
34	22	75.9	211	6	US-10-467-657-6932	Sequence 6932, App
35	22	75.9	215	6	US-10-131-826A-4	Sequence 4, Appl
36	22	75.9	228	6	US-10-467-657-568	Sequence 568, App
37	22	75.9	228	6	US-10-467-657-4838	Sequence 4838, App
38	22	75.9	233	6	US-10-821-234-1322	Sequence 1322, App
39	22	75.9	239	6	US-10-467-657-432	Sequence 432, App
40	22	75.9	265	6	US-10-793-626-2500	Sequence 2500, App
41	22	75.9	330	6	US-10-793-626-2476	Sequence 2476, App
42	22	75.9	330	6	US-10-793-626-2734	Sequence 2734, App
43	22	75.9	338	6	US-10-878-556A-19	Sequence 19, Appl
44	22	75.9	344	6	US-10-131-826A-376	Sequence 376, App
45	22	75.9	358	7	US-11-055-822-572	Sequence 572, App
46	22	75.9	358	7	US-11-055-822-836	Sequence 836, App
47	22	75.9	432	7	US-11-194-246-308	Sequence 308, App
48	22	75.9	449	6	US-10-467-657-678	Sequence 678, App
49	22	75.9	453	7	US-11-082-389-198	Sequence 198, App
50	22	75.9	510	7	US-11-210-316-22	Sequence 22, Appl
51	22	75.9	539	7	US-11-210-316-25	Sequence 26, Appl
52	22	75.9	601	6	US-10-467-657-7120	Sequence 7120, App
53	22	75.9	635	6	US-10-821-234-1673	Sequence 1673, App
54	22	75.9	858	6	US-10-613-744-6	Sequence 6, Appl
55	22	75.9	2233	6	US-10-873-528-2	Sequence 2, Appl
56	21	72.4	43	6	US-10-467-657-7886	Sequence 7886, App
57	21	72.4	52	6	US-10-467-657-2216	Sequence 2216, App
58	21	72.4	76	6	US-10-467-657-5690	Sequence 5690, App
59	21	72.4	91	6	US-10-821-234-1703	Sequence 1703, App
60	21	72.4	123	6	US-10-793-626-430	Sequence 430, App
61	21	72.4	134	6	US-10-467-657-5166	Sequence 5166, App
62	21	72.4	134	6	US-10-793-626-2374	Sequence 2374, App
63	21	72.4	155	6	US-10-467-657-2420	Sequence 2420, App
64	21	72.4	175	6	US-10-965-694-23	Sequence 23, Appl
65	21	72.4	182	6	US-10-793-626-2836	Sequence 2836, App
66	21	72.4	182	6	US-10-467-657-3510	Sequence 3510, App
67	21	72.4	190	6	US-10-467-657-3436	Sequence 3436, App
68	21	72.4	211	6	US-10-821-234-1372	Sequence 1372, App
69	21	72.4	216	6	US-10-467-657-8102	Sequence 8102, App
70	21	72.4	221	6	US-10-467-657-2390	Sequence 2390, App
71	21	72.4	221	6	US-10-467-657-5750	Sequence 5750, App
72	21	72.4	254	6	US-10-467-657-6144	Sequence 6144, App
73	21	72.4	272	7	US-11-073-150-46	Sequence 46, Appl
74	21	72.4	272	7	US-11-073-457-46	Sequence 46, Appl
75	21	72.4	272	7	US-11-073-460-46	Sequence 45, Appl
76	21	72.4	278	6	US-10-957-569-45	Sequence 45, Appl
77	21	72.4	370	6	US-10-821-234-1105	Sequence 1105, App
78	21	72.4	440	7	US-11-082-389-106	Sequence 106, App
79	21	72.4	463	6	US-10-467-657-6352	Sequence 6352, App
80	21	72.4	463	6	US-10-467-657-7604	Sequence 7604, App
81	21	72.4	482	6	US-10-793-626-24	Sequence 24, Appl
82	21	72.4	496	7	US-11-067-121-12	Sequence 12, Appl
83	21	72.4	525	6	US-10-995-561-1030	Sequence 1030, App
84	21	72.4	525	7	US-11-082-389-350	Sequence 350, App
85	21	72.4	569	7	US-11-082-389-104	Sequence 104, App
86	21	72.4	582	7	US-11-090-439-58	Sequence 58, Appl
87	21	72.4	592	6	US-10-467-657-4888	Sequence 4888, App
88	21	72.4	615	6	US-10-995-561-940	Sequence 940, App
89	21	72.4	662	6	US-10-995-561-943	Sequence 943, App
90	21	72.4	702	7	US-10-995-561-942	Sequence 942, App
91	21	72.4	738	7	US-11-147-047-48	Sequence 48, Appl
92	21	72.4	747	7	US-11-018-018-1	Sequence 1, Appl
93	21	72.4	747	7	US-11-047-757-1	Sequence 1, Appl
94	21	72.4	754	6	US-10-995-561-941	Sequence 941, App
95	21	72.4	1061	7	US-11-000-463-347	Sequence 347, App
96	21	72.4	1070	7	US-11-147-047-49	Sequence 49, Appl
97	21	72.4	1091	7	US-11-000-463-348	Sequence 348, App
98	21	72.4	3507	7	US-11-075-185-7	Sequence 7, Appl

99	20	69.0	19	6	US-10-467-657-8712	Sequence 8712, Ap	172	20	69.0	325	6	US-10-454-437-142	Sequence 142, App
100	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	173	20	69.0	329	6	US-10-793-626-1942	Sequence 1942, Ap
101	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	174	20	69.0	335	6	US-10-467-657-3818	Sequence 3818, Ap
102	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	175	20	69.0	337	6	US-10-485-517-234	Sequence 234, App
103	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	176	20	69.0	342	7	US-11-082-389-214	Sequence 214, App
104	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	177	20	69.0	343	6	US-10-467-657-4824	Sequence 4824, Ap
105	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	178	20	69.0	343	6	US-10-467-657-7256	Sequence 7256, Ap
106	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	179	20	69.0	343	6	US-10-467-657-4840	Sequence 4840, Ap
107	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	180	20	69.0	355	6	US-10-467-657-7996	Sequence 7996, Ap
108	20	69.0	42	6	US-10-467-657-8811	Sequence 8811, Ap	181	20	69.0	355	6	US-10-995-561-636	Sequence 636, App
109	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	182	20	69.0	355	6	US-10-454-437-102	Sequence 102, App
110	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	183	20	69.0	357	6	US-10-467-657-2500	Sequence 2500, Ap
111	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	184	20	69.0	357	6	US-10-467-657-6648	Sequence 6648, Ap
112	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	185	20	69.0	362	6	US-10-995-561-637	Sequence 637, App
113	20	69.0	54	6	US-10-467-657-4978	Sequence 4978, Ap	186	20	69.0	389	7	US-11-018-018-2	Sequence 2, Appli
114	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	187	20	69.0	389	7	US-11-047-757-2	Sequence 2, Appli
115	20	69.0	83	6	US-10-510-386-114	Sequence 114, App	188	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
116	20	69.0	95	6	US-10-467-657-3518	Sequence 2518, Ap	189	20	69.0	396	6	US-10-386-238	Sequence 238, App
117	20	69.0	102	6	US-10-793-626-2592	Sequence 2592, Ap	190	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appl
118	20	69.0	105	6	US-10-467-657-9209	Sequence 9209, Ap	191	20	69.0	399	7	US-11-018-018-3	Sequence 3, Appli
119	20	69.0	108	6	US-10-467-657-4266	Sequence 4266, Ap	192	20	69.0	399	7	US-11-047-757-3	Sequence 3, Appli
120	20	69.0	114	6	US-10-821-234-1140	Sequence 1140, Ap	193	20	69.0	406	6	US-10-467-657-7420	Sequence 7420, Ap
121	20	69.0	114	6	US-10-467-657-124	Sequence 124, App	194	20	69.0	409	6	US-10-821-234-1425	Sequence 1425, Ap
122	20	69.0	114	6	US-10-467-657-4414	Sequence 1414, Ap	195	20	69.0	413	6	US-10-467-657-1858	Sequence 1858, Ap
123	20	69.0	114	6	US-10-467-657-3162	Sequence 3162, Ap	196	20	69.0	414	6	US-10-878-556A-1	Sequence 1, Appli
124	20	69.0	114	6	US-10-467-657-3754	Sequence 3754, Ap	197	20	69.0	418	6	US-10-467-657-5788	Sequence 5788, Ap
125	20	69.0	114	6	US-10-467-657-8674	Sequence 8674, Ap	198	20	69.0	432	7	US-11-113-424-186	Sequence 186, App
126	20	69.0	115	6	US-10-793-626-1554	Sequence 1554, Ap	199	20	69.0	436	7	US-10-467-657-7694	Sequence 7694, App
127	20	69.0	116	6	US-10-467-657-5514	Sequence 5514, Ap	200	20	69.0	436	7	US-11-082-389-256	Sequence 256, App
128	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	201	20	69.0	443	6	US-10-467-657-362	Sequence 362, App
129	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appl	202	20	69.0	444	6	US-10-793-626-1860	Sequence 1860, Ap
130	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appli	203	20	69.0	448	6	US-10-873-528-30	Sequence 30, Appl
131	20	69.0	131	6	US-10-467-657-5308	Sequence 5308, Ap	204	20	69.0	448	6	US-10-763-112A-112	Sequence 112, App
132	20	69.0	137	6	US-10-821-234-1701	Sequence 1701, Ap	205	20	69.0	448	6	US-10-763-112A-69	Sequence 1075, Ap
133	20	69.0	140	6	US-10-467-657-2486	Sequence 2486, Ap	206	20	69.0	449	6	US-10-467-657-7095	Sequence 7094, Ap
134	20	69.0	144	6	US-10-793-626-1640	Sequence 1640, Ap	207	20	69.0	450	6	US-11-186-284-123	Sequence 123, App
135	20	69.0	144	6	US-10-793-626-2856	Sequence 2856, Ap	208	20	69.0	450	6	US-10-995-561-901	Sequence 901, App
136	20	69.0	156	6	US-10-467-657-1958	Sequence 1958, Ap	209	20	69.0	450	6	US-10-467-657-8028	Sequence 8028, Ap
137	20	69.0	156	6	US-10-467-657-1280	Sequence 1280, Ap	210	20	69.0	451	6	US-10-763-112A-76	Sequence 76, Appl
138	20	69.0	179	6	US-10-467-657-2232	Sequence 2232, Ap	211	20	69.0	451	6	US-10-467-657-7104	Sequence 7104, Ap
139	20	69.0	182	6	US-10-980-388-89	Sequence 89, Appl	212	20	69.0	456	7	US-10-467-657-4150	Sequence 4150, Ap
140	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	213	20	69.0	466	7	US-11-102-240-104	Sequence 104, App
141	20	69.0	186	6	US-10-467-657-3918	Sequence 3918, Ap	214	20	69.0	470	7	US-11-186-284-123	Sequence 123, App
142	20	69.0	195	7	US-11-019-955-24	Sequence 24, Appl	215	20	69.0	471	6	US-10-995-561-901	Sequence 901, App
143	20	69.0	197	6	US-10-793-626-2856	Sequence 2856, Ap	216	20	69.0	477	6	US-10-131-826A-452	Sequence 452, App
144	20	69.0	200	6	US-10-793-626-394	Sequence 394, App	217	20	69.0	481	6	US-10-467-657-3124	Sequence 3124, Ap
145	20	69.0	200	6	US-10-793-626-1242	Sequence 1242, Ap	218	20	69.0	481	6	US-11-090-439-16	Sequence 16, Appl
146	20	69.0	204	6	US-10-980-388-102	Sequence 102, App	219	20	69.0	485	6	US-10-204-029-7	Sequence 7, Appli
147	20	69.0	210	6	US-10-467-657-6318	Sequence 6318, Ap	220	20	69.0	488	6	US-10-821-234-1654	Sequence 1654, Ap
148	20	69.0	214	6	US-10-508-283-108	Sequence 108, App	221	20	69.0	488	6	US-11-186-284-121	Sequence 121, App
149	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	222	20	69.0	489	6	US-10-467-657-7846	Sequence 7846, Ap
150	20	69.0	239	6	US-10-467-657-8743	Sequence 8743, Ap	223	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
151	20	69.0	241	7	US-11-019-955-27	Sequence 27, Appl	224	20	69.0	495	7	US-11-082-389-178	Sequence 178, App
152	20	69.0	250	7	US-11-082-389-216	Sequence 216, App	225	20	69.0	508	7	US-11-082-389-1067	Sequence 1067, Ap
153	20	69.0	257	7	US-11-102-240-94	Sequence 94, Appl	226	20	69.0	514	6	US-10-793-626-12	Sequence 12, Appl
154	20	69.0	266	6	US-10-995-561-544	Sequence 544, App	227	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
155	20	69.0	267	6	US-10-995-561-543	Sequence 543, App	228	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
156	20	69.0	268	7	US-11-019-955-28	Sequence 28, Appl	229	20	69.0	558	6	US-11-078-189-19	Sequence 19, Appl
157	20	69.0	271	6	US-10-793-626-1156	Sequence 1156, Ap	230	20	69.0	560	6	US-10-623-155-225	Sequence 225, App
158	20	69.0	272	6	US-10-467-657-5520	Sequence 2520, Ap	231	20	69.0	563	6	US-10-821-234-1067	Sequence 1067, Ap
159	20	69.0	276	6	US-10-873-528-134	Sequence 134, App	232	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
160	20	69.0	280	6	US-10-858-730-200	Sequence 200, App	233	20	69.0	585	6	US-10-967-457-18	Sequence 18, Appl
161	20	69.0	280	6	US-10-467-657-2130	Sequence 2130, Ap	234	20	69.0	585	6	US-10-939-890-500	Sequence 500, App
162	20	69.0	285	7	US-11-082-389-324	Sequence 324, App	235	20	69.0	585	7	US-11-078-663-18	Sequence 18, Appl
163	20	69.0	288	6	US-10-467-657-1272	Sequence 1272, Ap	236	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
164	20	69.0	291	7	US-11-102-883-22	Sequence 22, Appl	237	20	69.0	626	6	US-10-467-657-6426	Sequence 6426, Ap
165	20	69.0	292	7	US-11-102-883-24	Sequence 24, Appl	238	20	69.0	637	6	US-10-467-657-7618	Sequence 7618, Ap
166	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	239	20	69.0	647	7	US-10-873-528-53	Sequence 53, Appl
167	20	69.0	299	6	US-10-467-657-2190	Sequence 2190, Ap	240	20	69.0	657	7	US-11-080-991-32	Sequence 32, Appl
168	20	69.0	312	7	US-11-055-822-16	Sequence 16, Appl	241	20	69.0	657	7	US-11-080-991-48	Sequence 48, Appl
169	20	69.0	316	7	US-11-082-389-62	Sequence 62, Appl	242	20	69.0	669	7	US-11-119-683-2	Sequence 2, Appli
170	20	69.0	321	6	US-10-467-657-2504	Sequence 2504, Ap	243	20	69.0	675	6	US-10-467-657-4004	Sequence 4004, Ap
171	20	69.0	324	6	US-10-467-657-7692	Sequence 7692, Ap	244	20	69.0	690	6	US-10-939-890-501	Sequence 501, App
			324	6	US-10-467-657-8440	Sequence 8440, Ap							

```
245 20 69.0 692 7 US-11-103-957-29
246 20 69.0 708 7 US-11-174-150-25
247 20 69.0 710 7 US-11-078-189-18
248 20 69.0 721 6 US-10-467-962B-49
249 20 69.0 736 7 US-11-174-150-26
250 20 69.0 736 7 US-11-078-189-9
251 20 69.0 739 7 US-11-082-389-94
252 20 69.0 739 7 US-11-078-189-12
253 20 69.0 739 7 US-11-107-048-6
254 20 69.0 741 6 US-10-467-657-6266
255 20 69.0 745 7 US-11-147-109-2
256 20 69.0 748 6 US-10-821-234-1479
257 20 69.0 817 6 US-10-793-626-2948
258 20 69.0 852 6 US-10-467-657-5004
259 20 69.0 856 6 US-10-467-657-8534
260 20 69.0 874 6 US-10-510-386-28
261 20 69.0 896 7 US-11-192-219-3
262 20 69.0 898 7 US-11-166-730-3
263 20 69.0 902 7 US-11-057-058-64
264 20 69.0 916 6 US-10-467-657-4242
265 20 69.0 923 7 US-11-192-219-4
266 20 69.0 989 7 US-10-821-234-975
267 20 69.0 1013 7 US-11-103-957-9
268 20 69.0 1047 6 US-10-510-386-200
269 20 69.0 1165 7 US-11-192-219-2
270 20 69.0 1167 6 US-10-601-368-18
271 20 69.0 1217 7 US-11-074-176-252
272 20 69.0 1730 7 US-11-192-967-4
273 20 69.0 1730 7 US-11-193-715-4
274 20 69.0 2644 6 US-10-770-726-45
275 20 69.0 7968 7 US-11-186-731-5
276 19 65.5 13 7 US-11-016-706-29
277 19 65.5 27 7 US-11-157-930-14
278 19 65.5 35 6 US-10-821-234-1704
279 19 65.5 43 7 US-11-075-400-28
280 19 65.5 44 7 US-11-000-463-372
281 19 65.5 46 6 US-10-467-657-9119
282 19 65.5 47 6 US-10-467-657-9186
283 19 65.5 57 6 US-10-467-657-5448
284 19 65.5 71 7 US-11-000-463-772
285 19 65.5 80 6 US-10-986-501-200
286 19 65.5 83 6 US-10-467-657-5366
287 19 65.5 86 6 US-10-467-657-3962
288 19 65.5 98 6 US-10-467-657-3376
289 19 65.5 100 7 US-11-123-896-137
290 19 65.5 103 6 US-10-793-626-1708
291 19 65.5 103 6 US-10-793-626-2074
292 19 65.5 104 6 US-10-793-626-2512
293 19 65.5 106 7 US-11-064-174-50
294 19 65.5 107 6 US-10-793-626-1586
295 19 65.5 107 6 US-10-467-657-1018
296 19 65.5 107 6 US-10-467-657-2102
297 19 65.5 107 7 US-11-000-463-300
298 19 65.5 115 6 US-10-432-483-10
299 19 65.5 117 6 US-10-467-657-2282
300 19 65.5 122 6 US-10-467-657-606

SEQUENCE 29, Appl
SEQUENCE 25, Appl
SEQUENCE 18, Appl
SEQUENCE 49, Appl
SEQUENCE 26, Appl
SEQUENCE 9, Appl
SEQUENCE 94, Appl
SEQUENCE 12, Appl
SEQUENCE 6, Appl
SEQUENCE 6266, Ap
SEQUENCE 2, Appl
SEQUENCE 1479, Ap
SEQUENCE 2948, Ap
SEQUENCE 5004, Ap
SEQUENCE 8534, Ap
SEQUENCE 28, Appl
SEQUENCE 3, Appl
SEQUENCE 3, Appl
SEQUENCE 64, Appl
SEQUENCE 4242, Ap
SEQUENCE 4, Appl
SEQUENCE 975, App
SEQUENCE 9, Appl
SEQUENCE 200, App
SEQUENCE 2, Appl
SEQUENCE 18, Appl
SEQUENCE 252, App
SEQUENCE 4, Appl
SEQUENCE 4, Appl
SEQUENCE 45, Appl
SEQUENCE 5, Appl
SEQUENCE 29, Appl
SEQUENCE 14, Appl
SEQUENCE 1704, Ap
SEQUENCE 28, Appl
SEQUENCE 372, App
SEQUENCE 9119, Ap
SEQUENCE 9186, Ap
SEQUENCE 5448, Ap
SEQUENCE 772, App
SEQUENCE 200, App
SEQUENCE 5366, Ap
SEQUENCE 3962, Ap
SEQUENCE 3376, Ap
SEQUENCE 137, App
SEQUENCE 1708, Ap
SEQUENCE 2074, Ap
SEQUENCE 2512, Ap
SEQUENCE 50, Appl
SEQUENCE 1586, Ap
SEQUENCE 1018, Ap
SEQUENCE 2102, Ap
SEQUENCE 300, App
SEQUENCE 10, Appl
SEQUENCE 10, Appl
SEQUENCE 2282, Ap
SEQUENCE 606, App

; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match 93.1%; Score 27; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 4 KLVFFA 9

RESULT 2
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abetal3-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; NAME/KEY: MOD_RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match 93.1%; Score 27; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 1.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 4 KLVFFA 9

RESULT 3
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
```

ALIGNMENTS

```
RESULT 1
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: US/09/322,289
```

; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; PRIOR FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 4
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTO-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 3.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 5
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605

; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match 93.1%; Score 27; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 6
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match 93.1%; Score 27; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 7
US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24

; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match 93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 3.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 8

US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:

; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 9

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 10

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:

; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 3.7;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 11

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US2005024890A1
; GENERAL INFORMATION:

; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (INAC-Ni), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; OTHER INFORMATION: C31
US-10-982-545-15

Query Match 93.1%; Score 27; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|
Db 687 KLVFFA 692

RESULT 12

US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Guriq
; APPLICANT: Saidanna, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; TITLE OF INVENTION: BETA-AMYLOID PEPTIDE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-789-273-38

Query Match 93.1%; Score 27; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 56;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:|
Db 687 KLVFFA 692

RESULT 13

US-10-467-657-330
; Sequence 330, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 330
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-330

Query Match 86.2%; Score 25; DB 6; Length 269;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
|:|
Db 11 KIVFF 15

RESULT 14

US-10-793-626-1056
; Sequence 1056, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:

; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P034800US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1056
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1056

Query Match 86.2%; Score 25; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
DB 7 KIVFF 11

RESULT 15
US-10-467-657-7892
; Sequence 7892, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7892
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7892

Query Match 82.8%; Score 24; DB 6; Length 50;
Best Local Similarity 80.0%; Pred. No. 19;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
DB 33 KIIFP 37

RESULT 16
US-10-467-657-2014
; Sequence 2014, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657

; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2014
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2014

Query Match 82.8%; Score 24; DB 6; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
DB 73 IVFFA 77

RESULT 17
US-10-467-657-9070
; Sequence 9070, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9070
; LENGTH: 402
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9070

Query Match 82.8%; Score 24; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
DB 264 IVFFA 268

RESULT 18
US-10-467-657-2120
; Sequence 2120, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2120
; LENGTH: 426

```
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2120

Query Match      82.8%; Score 24; DB 6; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFA 6
      |||||
Db      414 IVFFA 418

RESULT 19
US-10-689-742-13
; Sequence 13, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M
; APPLICANT: LaValle, Edward R
; APPLICANT: Racie, Lisa A
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: 00766.000091.10
; CURRENT APPLICATION NUMBER: US/10/689,742
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: 09/746,783
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-689-742-13

Query Match      82.8%; Score 24; DB 6; Length 524;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFA 6
      |||||
Db      404 IVFFA 408

RESULT 20
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978

; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-284-125

Query Match      82.8%; Score 24; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |||||
Db      531 KAVFFA 536

RESULT 21
US-10-131-826A-230
; Sequence 230, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 230
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo Sapien
```


US-10-131-826A-230

Query Match 82.8%; Score 24; DB 6; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
DB 557 IVFFA 561

RESULT 22

US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917

Query Match 82.8%; Score 24; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|:|
DB 579 KAVFFA 584

RESULT 23

US-11-098-674-1
; Sequence 1, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-11-098-674-1

Query Match 79.3%; Score 23; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.3e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5

DB |:|:|

1 KLVFF 5

RESULT 24

US-10-131-826A-410
; Sequence 410, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 410
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-410

Query Match 79.3%; Score 23; DB 6; Length 229;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
DB 118 KIVFF 122

RESULT 25

US-10-793-626-2450
; Sequence 2450, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:

```
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2450
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2450

Query Match      79.3%; Score 23; DB 6; Length 311;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
      |:|:|
Db      296 VVFFA 300

RESULT 26
US-10-995-561-959
; Sequence 959, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 959
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-959

Query Match      79.3%; Score 23; DB 6; Length 481;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |:|:|
Db      275 KVVFFA 280

RESULT 27
US-11-080-991-104
; Sequence 104, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petteer Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104
```

```
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-104

Query Match      79.3%; Score 23; DB 7; Length 522;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
      |:|:|
Db      260 IIVFA 264

RESULT 28
US-10-793-626-1930
; Sequence 1930, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1930
; LENGTH: 528
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1930

Query Match      79.3%; Score 23; DB 6; Length 528;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFF 5
      |:|:|
Db      477 KLVFF 481

RESULT 29
US-10-467-657-2868
; Sequence 2868, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2868
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2868

Query Match      79.3%; Score 23; DB 6; Length 533;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 2 IVFFA 6
|:|
Db 371 IIVFA 375

RESULT 30
US-10-995-561-593
; Sequence 593, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 593
; LENGTH: 3623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-593

Query Match 79.3%; Score 23; DB 6; Length 3623;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|
Db 2544 KIVFF 2548

RESULT 31
US-10-467-657-5436
; Sequence 5436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5436
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5436

Query Match 75.9%; Score 22; DB 6; Length 47;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|
Db 36 KIVFF 40

RESULT 32
US-10-467-657-4746
; Sequence 4746, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4746
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4746

Query Match 75.9%; Score 22; DB 6; Length 98;
Best Local Similarity 80.0%; Pred. No. 98;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|
Db 62 KIVFF 66

RESULT 33
US-11-210-316-18
; Sequence 18, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (34)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (85)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (98)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (112)
; OTHER INFORMATION: Xaa = any amino acid
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (151)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-18

Query Match

75.9%; Score 22; DB 7; Length 167;

Best Local Similarity 60.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 3; Conservative 2;

Qy 2 IVFFA 6
Db 105 VIFFA 109

RESULT 34

US-10-467-657-6932
; Sequence 6932, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6932
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6932

Query Match 75.9%; Score 22; DB 6; Length 211;
Best Local Similarity 80.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1;

Qy 2 IVFFA 6
Db 19 LVFFA 23

RESULT 35

US-10-131-826A-4
; Sequence 4, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 4
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-4

Query Match 75.9%; Score 22; DB 6; Length 215;
Best Local Similarity 80.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1;

Qy 2 IVFFA 6
Db 166 LVFFA 170

RESULT 36

US-10-467-657-568
; Sequence 568, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 568
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-568

Query Match 75.9%; Score 22; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 2.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1;

Qy 2 IVFFA 6
Db 156 LVFFA 160

RESULT 37

US-10-467-657-4838
; Sequence 4838, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia

; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4838
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4838

Query Match 75.9%; Score 22; DB 6; Length 228;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 156 LVFFA 160

RESULT 38

US-10-821-234-1322
; Sequence 1322, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt. Seq. genes Version 1.0
; SEQ ID NO 1322
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1322

Query Match 75.9%; Score 22; DB 6; Length 233;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 166 LVFFA 170

RESULT 39

US-10-467-657-432
; Sequence 432, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12

; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 432
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-432

Query Match 75.9%; Score 22; DB 6; Length 239;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 128 KVVFFA 133

RESULT 40

US-10-793-626-2500
; Sequence 2500, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2500
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2500

Query Match 75.9%; Score 22; DB 6; Length 265;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 230 KVVFFA 235

RESULT 41

US-10-793-626-2476
; Sequence 2476, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2476
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2476

Query Match 75.9%; Score 22; DB 6; Length 330;

Best Local Similarity 80.0%; Pred. No. 3.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1;

Qy 1 KIVFF 5
||:|
Db 3 KIMFF 7

RESULT 42

US-10-793-626-2734
; Sequence 2734, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2734
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2734

Query Match 75.9%; Score 22; DB 6; Length 330;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
||:|
Db 3 KIMFF 7

RESULT 43

US-10-878-556A-19
; Sequence 19, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLIC INFORMATION:
; DATABASE ACCESSION NUMBER: sw_hum/cn03_human
; DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-19

Query Match 75.9%; Score 22; DB 6; Length 338;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
||:|
Db 76 KLIFP 80

RESULT 44

US-10-131-826A-376
; Sequence 376, Application US/10131826A

; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 376
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-376

Query Match 75.9%; Score 22; DB 6; Length 344;
Best Local Similarity 60.0%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
||:|
Db 279 KLIFP 283

RESULT 45

US-11-055-822-572
; Sequence 572, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS

; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 572
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-572

Query Match 75.9%; Score 22; DB 7; Length 358;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
||| ||
Db 61 KIVWFA 66

RESULT 46
US-11-055-822-836
; Sequence 836, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121CPCN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 836
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-836

Query Match 75.9%; Score 22; DB 7; Length 358;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
||| ||
Db 61 KIVWFA 66

RESULT 47
US-11-194-246-308
; Sequence 308, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MEI
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 308
; LENGTH: 432
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-308

Query Match 75.9%; Score 22; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
||| ||
Db 4 KILFF 8

RESULT 48
US-10-467-657-678
; Sequence 678, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 678
; LENGTH: 449

```
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-678

Query Match          75.9%; Score 22; DB 6; Length 449;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 428 KIMFF 432

RESULT 49
US-11-082-389-198
; Sequence 198, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 198
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-198

Query Match          75.9%; Score 22; DB 7; Length 453;
Best Local Similarity 80.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 401 LVFFA 405

RESULT 50
US-11-210-316-22
; Sequence 22, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
```

```
; APPLICANT: Kinney, Anthony J.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 22
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (102)
; OTHER INFORMATION: Xaa = any amino acid
US-11-210-316-22

Query Match          75.9%; Score 22; DB 7; Length 510;
Best Local Similarity 60.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 96 VIFFA 100

RESULT 51
US-11-210-316-26
; Sequence 26, Application US/11210316
; Publication No. US20050282278A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Hitz, William D.
; TITLE OF INVENTION: Plant Sugar Transport Proteins
; FILE REFERENCE: BB1163USDIV
; CURRENT APPLICATION NUMBER: US/11/210,316
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/10/051,902
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/083,044
; PRIOR FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 26
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-11-210-316-26

Query Match          75.9%; Score 22; DB 7; Length 539;
Best Local Similarity 60.0%; Pred. No. 4.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 121 VIFFA 125

RESULT 52
US-10-467-657-7120
; Sequence 7120, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
```


; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7120
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7120

Query Match 75.9%; Score 22; DB 6; Length 601;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
:|||||
Db 251 RIVFF 255

RESULT 53
US-10-821-234-1673
; Sequence 1673, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1673
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1673

Query Match 75.9%; Score 22; DB 6; Length 635;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
:|||||
Db 259 KIVFF 263

RESULT 54
US-10-613-744-6
; Sequence 6, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347

; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-6

Query Match 75.9%; Score 22; DB 6; Length 858;
Best Local Similarity 80.0%; Pred. No. 7.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
:|||||
Db 348 LVFFA 352

RESULT 55
US-10-873-528-2
; Sequence 2, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe PG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21129WO
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2233
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-2

Query Match 75.9%; Score 22; DB 6; Length 2233;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
:|||||
Db 1895 KVQFFA 1900

RESULT 56
US-10-467-657-7886
; Sequence 7886, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 7886
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7886

Query Match 72.4%; Score 21; DB 6; Length 43;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 14 KVRFFA 19

RESULT 57

US-10-467-657-2216
; Sequence 2216, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2216
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2216

Query Match 72.4%; Score 21; DB 6; Length 52;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 42 RIVWFA 47

RESULT 58

US-10-467-657-5690
; Sequence 5690, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5690
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5690

Query Match 72.4%; Score 21; DB 6; Length 76;

Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 23 QIVFF 27

RESULT 59

US-10-821-234-1703
; Sequence 1703, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: PCT SEQ_genes Version 1.0
; SEQ ID NO 1703
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1703

Query Match 72.4%; Score 21; DB 6; Length 91;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 22 EIVFF 26

RESULT 60

US-10-793-626-430
; Sequence 430, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P0348005
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 430
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-430

Query Match 72.4%; Score 21; DB 6; Length 123;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
Db 78 IVFFS 82

RESULT 61

US-10-467-657-5166
; Sequence 5166, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5166
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5166

Query Match 72.4%; Score 21; DB 6; Length 123;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
Db 29 ILFFA 33

RESULT 62
US-10-793-626-2374
; Sequence 2374, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2374
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2374

Query Match 72.4%; Score 21; DB 6; Length 134;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
|:|:|
Db 7 KIYF 11

RESULT 63
US-10-467-657-2420
; Sequence 2420, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2420
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2420

Query Match 72.4%; Score 21; DB 6; Length 155;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
Db 18 MVFFA 22

RESULT 64
US-10-965-694-23
; Sequence 23, Application US/10965694
; Publication No. US20050271644A1
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Johannes
; APPLICANT: Muller-Reible, Clemens
; APPLICANT: Fregin, Andreas
; APPLICANT: Rost, Simone
; APPLICANT: Strom, Tim
; TITLE OF INVENTION: VITAMIN K EPOXID RECYCLING POLYPEPTIDE VKORC1, A THERAPEUTIC TARGET
; TITLE OF INVENTION: OF COUMARIN AND THEIR DERIVATIVES
; FILE REFERENCE: MBP-025XX
; CURRENT APPLICATION NUMBER: US/10/965,694
; CURRENT FILING DATE: 2004-10-14
; PRIOR APPLICATION NUMBER: US 60/511,041
; PRIOR FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Fugu rubripes
US-10-965-694-23

Query Match 72.4%; Score 21; DB 6; Length 175;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
|:|:|
Db 91 IVFYA 95

RESULT 65
US-10-793-626-2836
; Sequence 2836, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2836

```
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2836
```

```
Query Match          72.4%; Score 21; DB 6; Length 182;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
       |:|:|
Db      14 KVTFFS 19
```

```
RESULT 66
US-10-467-657-3510
; Sequence 3510, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3510
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3510
```

```
Query Match          72.4%; Score 21; DB 6; Length 182;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 IVFFA 6
       |:|:|
Db      17 ILFFA 21
```

```
RESULT 67
US-10-467-657-3436
; Sequence 3436, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3436
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3436
```

```
Query Match          72.4%; Score 21; DB 6; Length 190;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
       |:|:|
Db      46 KTVFFA 51
```

```
RESULT 68
US-10-821-234-1372
; Sequence 1372, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: Pt Seq_genes Version 1.0
; SEQ ID NO 1372
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1372
```

```
Query Match          72.4%; Score 21; DB 6; Length 211;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
       |:|:|
Db      33 KTVFFA 38
```

```
RESULT 69
US-10-467-657-8102
; Sequence 8102, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASNIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8102
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8102
```

```
Query Match          72.4%; Score 21; DB 6; Length 216;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 IVFFA 6
       |:|:|
Db      18 LIFFA 22
```

```
RESULT 70
US-10-467-657-290
; Sequence 290, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 290
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-290

Query Match      72.4%; Score 21; DB 6; Length 221;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFA 6
DB      41 LIFFA 45

RESULT 71
US-10-467-657-5750
; Sequence 5750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5750
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5750

Query Match      72.4%; Score 21; DB 6; Length 221;
Best Local Similarity 60.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFA 6
DB      41 LIFFA 45

RESULT 72
US-10-467-657-6144
; Sequence 6144, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6144
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6144

Query Match      72.4%; Score 21; DB 6; Length 254;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 IVFFA 6
DB      159 LIFFA 163

RESULT 73
US-10-632-150-46
; Sequence 46, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-46

Query Match      72.4%; Score 21; DB 6; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
DB      211 KLIFFA 216

RESULT 74
US-11-073-457-46
; Sequence 46, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
```

```
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6144
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6144
```

```
Query Match      72.4%; Score 21; DB 6; Length 254;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 IVFFA 6
DB      159 LIFFA 163
```

```
RESULT 73
US-10-632-150-46
; Sequence 46, Application US/10632150
; Publication No. US20050251871A1
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/10/632,150
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US/09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-632-150-46
```

```
Query Match      72.4%; Score 21; DB 6; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KIVFFA 6
DB      211 KLIFFA 216
```

```
RESULT 74
US-11-073-457-46
; Sequence 46, Application US/11073457
; Publication No. US20050260556A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
```

```
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-46

Query Match      72.4%; Score 21; DB 7; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFEA 6
      |::||
Db      211 KLMYFA 216

RESULT 75
US-11-073-460-46
; Sequence 46, Application US/11073460
; Publication No. US20050272066A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFERATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-46

Query Match      72.4%; Score 21; DB 7; Length 272;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFEA 6
      |::||
Db      211 KLMYFA 216

Search completed: December 29, 2005, 18:50:19
Job time : 4.29032 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-10
Perfect score: 29
Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : Published Applications AA Main:
1: /cgn2_6/prodata1/pubpaa/US07_PUBCOMB.pep:
2: /cgn2_6/prodata1/pubpaa/US08_PUBCOMB.pep:
3: /cgn2_6/prodata1/pubpaa/US09_PUBCOMB.pep:
4: /cgn2_6/prodata1/pubpaa/US10A_PUBCOMB.pep:
5: /cgn2_6/prodata1/pubpaa/US10B_PUBCOMB.pep:
6: /cgn2_6/prodata1/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	3	US-09-867-847-11
2	29	100.0	6	3	US-09-867-847-19
3	29	100.0	6	3	US-09-915-092-1
4	29	100.0	6	3	US-09-915-092-9
5	29	100.0	6	3	US-09-747-408-1
6	29	100.0	6	3	US-09-747-408-10
7	29	100.0	6	5	US-10-728-028-1
8	29	100.0	6	5	US-10-728-028-9
9	29	100.0	6	5	US-10-825-958-9
10	29	100.0	6	5	US-10-825-958-17
11	29	100.0	58	4	US-10-425-115-280164
12	29	100.0	90	4	US-10-424-599-165325
13	29	100.0	93	4	US-10-424-599-240310
14	29	100.0	99	5	US-10-450-763-56957
15	28	96.6	6	3	US-09-867-847-18
16	28	96.6	6	3	US-09-867-847-26
17	28	96.6	6	3	US-09-915-092-8
18	28	96.6	6	3	US-09-915-092-16
19	28	96.6	6	3	US-09-747-408-9
20	28	96.6	6	3	US-09-747-408-17
21	28	96.6	6	5	US-10-728-028-8
22	28	96.6	6	5	US-10-728-028-16
23	28	96.6	6	5	US-10-825-958-16
24	28	96.6	6	5	US-10-825-958-24
25	28	96.6	37	4	US-10-641-924-7
26	28	96.6	37	4	US-10-642-255-7
27	28	96.6	60	4	US-10-437-963-173619

28	28	96.6	87	4	US-10-437-963-133986
28	28	96.6	109	4	US-10-437-963-105773
29	30	96.6	135	4	US-10-437-963-141578
30	30	96.6	175	4	US-10-437-963-122124
31	28	96.6	186	5	US-10-481-032A-214
32	28	96.6	186	5	US-10-481-032A-228
33	28	96.6	188	4	US-10-437-963-172476
34	35	96.6	188	4	US-10-437-963-172452
35	36	96.6	416	4	US-10-055-475-14
36	37	96.6	416	6	US-11-042-922-14
37	28	96.6	514	4	US-10-055-475-13
38	28	96.6	514	6	US-11-042-922-13
39	28	96.6	564	6	US-11-097-143-12723
40	28	96.6	925	4	US-10-408-765A-2031
41	42	96.6	925	4	US-10-755-889-234
42	28	96.6	925	5	US-10-370-715B-8
43	43	96.6	925	5	US-10-631-467-680
44	44	96.6	925	5	US-10-631-467-747
45	28	96.6	1144	3	US-09-870-759-124
46	28	96.6	1144	3	US-09-751-708A-124
47	28	96.6	1144	4	US-10-428-817A-120
48	49	96.6	1144	5	US-10-937-758A-101
49	28	96.6	1144	5	US-10-631-467-1388
50	50	96.6	1144	5	US-10-631-467-1464
51	51	96.6	1443	6	US-11-097-143-32208
52	52	96.6	1443	6	US-10-437-963-109646
53	53	96.6	1640	4	US-09-867-847-7
54	27	93.1	6	3	US-09-867-847-20
55	55	27	93.1	6	US-09-972-475-9
56	27	93.1	6	3	US-09-915-092-10
57	27	93.1	6	3	US-09-915-092-28
58	58	27	93.1	6	US-09-956-625-25
59	27	93.1	6	3	US-09-747-408-3
60	60	27	93.1	6	US-09-747-408-11
61	27	93.1	6	3	US-10-463-729-9
62	62	27	93.1	6	US-10-728-028-10
63	63	27	93.1	6	US-10-728-028-27
64	64	27	93.1	6	US-10-728-028-28
65	65	27	93.1	6	US-10-825-958-7
66	27	93.1	6	5	US-10-825-958-18
67	67	27	93.1	6	US-10-666-095-3
68	27	93.1	7	3	US-09-867-847-12
69	27	93.1	7	3	US-09-867-847-27
70	70	27	93.1	7	US-09-867-847-28
71	27	93.1	7	3	US-09-972-475-7
72	72	27	93.1	7	US-09-915-092-2
73	73	27	93.1	7	US-09-915-092-17
74	27	93.1	7	3	US-09-915-092-18
75	27	93.1	7	3	US-09-747-408-2
76	76	27	93.1	7	US-09-747-408-18
77	27	93.1	7	3	US-09-747-408-19
78	78	27	93.1	7	US-10-463-729-7
79	27	93.1	7	4	US-10-463-729-9
80	27	93.1	7	5	US-10-728-028-2
81	81	27	93.1	7	US-10-728-028-17
82	27	93.1	7	5	US-10-728-028-18
83	83	27	93.1	7	US-10-825-958-10
84	84	27	93.1	7	US-10-825-958-10
85	85	27	93.1	7	US-10-825-958-25
86	86	27	93.1	7	US-10-825-958-26
87	87	27	93.1	7	US-10-810-881A-128
88	27	93.1	8	3	US-10-505-313-269
89	89	27	93.1	8	US-09-850-061A-44
90	90	27	93.1	8	US-09-972-475-5
91	91	27	93.1	8	US-10-235-483-1
92	27	93.1	8	4	US-10-463-729-5
93	93	27	93.1	8	US-10-281-092-42
94	27	93.1	8	4	US-10-721-774-44
95	95	27	93.1	8	US-10-810-881A-125
96	96	27	93.1	8	US-10-817-979-73
97	97	27	93.1	9	US-09-867-847-9
98	27	93.1	9	3	US-09-899-815-2
99	98	27	93.1	9	US-09-747-408-20
100	100	27	93.1	9	US-10-235-483-64
		27	93.1	9	US-10-619-454-3

101	27	93.1	9	4	US-10-619-454-25	Sequence 25, Appl	174	27	93.1	13	4	US-10-281-458-1	Sequence 1, Appl
102	27	93.1	9	4	US-10-619-454-28	Sequence 28, Appl	175	27	93.1	13	5	US-10-625-854-127	Sequence 127, App
103	27	93.1	9	4	US-10-619-454-57	Sequence 57, Appl	176	27	93.1	13	5	US-10-625-854-140	Sequence 140, App
104	27	93.1	9	4	US-10-619-454-157	Sequence 157, Appl	177	27	93.1	14	3	US-09-992-800-5	Sequence 5, Appl
105	27	93.1	10	3	US-09-867-847-29	Sequence 29, Appl	178	27	93.1	14	3	US-09-992-994-5	Sequence 5, Appl
106	27	93.1	10	3	US-09-915-082-19	Sequence 19, Appl	179	27	93.1	14	4	US-10-385-065-5	Sequence 5, Appl
107	27	93.1	10	3	US-10-889-999-20	Sequence 20, Appl	180	27	93.1	14	5	US-10-810-881A-114	Sequence 114, App
108	27	93.1	10	5	US-10-889-999-21	Sequence 21, Appl	181	27	93.1	14	5	US-10-505-313-2	Sequence 2, Appl
109	27	93.1	10	5	US-10-889-999-22	Sequence 22, Appl	182	27	93.1	14	5	US-10-625-854-115	Sequence 115, App
110	27	93.1	10	5	US-10-889-999-23	Sequence 23, Appl	183	27	93.1	14	5	US-10-625-854-128	Sequence 128, App
111	27	93.1	10	5	US-10-889-999-24	Sequence 24, Appl	184	27	93.1	14	5	US-10-625-854-141	Sequence 141, App
112	27	93.1	10	5	US-10-890-070-20	Sequence 20, Appl	185	27	93.1	14	6	US-11-063-350-5	Sequence 5, Appl
113	27	93.1	10	5	US-10-890-070-21	Sequence 21, Appl	186	27	93.1	15	3	US-09-972-475-14	Sequence 14, Appl
114	27	93.1	10	5	US-10-890-070-22	Sequence 22, Appl	187	27	93.1	15	3	US-09-996-357-9	Sequence 9, Appl
115	27	93.1	10	5	US-10-890-070-23	Sequence 23, Appl	188	27	93.1	15	4	US-10-235-483-56	Sequence 56, Appl
116	27	93.1	10	5	US-10-890-070-24	Sequence 24, Appl	189	27	93.1	15	4	US-10-235-483-57	Sequence 57, Appl
117	27	93.1	10	5	US-10-890-000-20	Sequence 20, Appl	190	27	93.1	15	4	US-10-235-483-58	Sequence 58, Appl
118	27	93.1	10	5	US-10-890-000-21	Sequence 21, Appl	191	27	93.1	15	4	US-10-235-483-60	Sequence 60, Appl
119	27	93.1	10	5	US-10-890-000-22	Sequence 22, Appl	192	27	93.1	15	4	US-10-235-483-61	Sequence 61, Appl
120	27	93.1	10	5	US-10-890-000-23	Sequence 23, Appl	193	27	93.1	15	4	US-10-235-483-63	Sequence 63, Appl
121	27	93.1	10	5	US-10-890-000-24	Sequence 24, Appl	194	27	93.1	15	4	US-10-235-483-65	Sequence 65, Appl
122	27	93.1	10	5	US-10-823-463-20	Sequence 20, Appl	195	27	93.1	15	4	US-10-463-729-14	Sequence 14, Appl
123	27	93.1	10	5	US-10-823-463-21	Sequence 21, Appl	196	27	93.1	15	5	US-10-625-854-103	Sequence 103, App
124	27	93.1	10	5	US-10-823-463-22	Sequence 22, Appl	197	27	93.1	15	5	US-10-625-854-116	Sequence 116, App
125	27	93.1	10	5	US-10-823-463-23	Sequence 23, Appl	198	27	93.1	15	5	US-10-625-854-129	Sequence 129, App
126	27	93.1	10	5	US-10-823-463-24	Sequence 24, Appl	199	27	93.1	15	5	US-10-625-854-142	Sequence 142, App
127	27	93.1	10	5	US-10-728-028-19	Sequence 19, Appl	200	27	93.1	16	5	US-10-625-854-91	Sequence 91, Appl
128	27	93.1	10	5	US-10-823-968-20	Sequence 20, Appl	201	27	93.1	16	5	US-10-625-854-104	Sequence 104, App
129	27	93.1	10	5	US-10-823-968-21	Sequence 21, Appl	202	27	93.1	16	5	US-10-625-854-117	Sequence 117, App
130	27	93.1	10	5	US-10-823-968-22	Sequence 22, Appl	203	27	93.1	16	5	US-10-625-854-130	Sequence 130, App
131	27	93.1	10	5	US-10-823-968-23	Sequence 23, Appl	204	27	93.1	16	5	US-10-625-854-143	Sequence 143, App
132	27	93.1	10	5	US-10-823-968-24	Sequence 24, Appl	205	27	93.1	17	3	US-09-992-800-3	Sequence 3, Appl
133	27	93.1	10	5	US-10-777-792-20	Sequence 20, Appl	206	27	93.1	17	3	US-09-992-994-3	Sequence 3, Appl
134	27	93.1	10	5	US-10-777-792-21	Sequence 21, Appl	207	27	93.1	17	3	US-09-998-491-8	Sequence 8, Appl
135	27	93.1	10	5	US-10-777-792-22	Sequence 22, Appl	208	27	93.1	17	4	US-10-385-065-3	Sequence 3, Appl
136	27	93.1	10	5	US-10-777-792-23	Sequence 23, Appl	209	27	93.1	17	4	US-10-451-367-26	Sequence 26, Appl
137	27	93.1	10	5	US-10-777-792-24	Sequence 24, Appl	210	27	93.1	17	4	US-10-475-281-8	Sequence 8, Appl
138	27	93.1	10	5	US-10-825-958-27	Sequence 27, Appl	211	27	93.1	17	4	US-10-810-919-3	Sequence 3, Appl
139	27	93.1	10	5	US-10-890-071-20	Sequence 20, Appl	212	27	93.1	17	5	US-10-684-346-24	Sequence 24, Appl
140	27	93.1	10	5	US-10-890-071-21	Sequence 21, Appl	213	27	93.1	17	5	US-10-997-078-46	Sequence 46, Appl
141	27	93.1	10	5	US-10-890-071-22	Sequence 22, Appl	214	27	93.1	17	5	US-10-997-700-19	Sequence 19, Appl
142	27	93.1	10	5	US-10-890-071-23	Sequence 23, Appl	215	27	93.1	17	6	US-11-063-350-3	Sequence 3, Appl
143	27	93.1	10	5	US-10-890-071-24	Sequence 24, Appl	216	27	93.1	17	6	US-11-066-697-950	Sequence 950, App
144	27	93.1	10	5	US-10-890-024-20	Sequence 20, Appl	217	27	93.1	17	6	US-11-066-697-983	Sequence 983, App
145	27	93.1	10	5	US-10-890-024-21	Sequence 21, Appl	218	27	93.1	19	3	US-09-825-242-5	Sequence 5, Appl
146	27	93.1	10	5	US-10-890-024-22	Sequence 22, Appl	219	27	93.1	19	4	US-10-439-216-5	Sequence 5, Appl
147	27	93.1	10	5	US-10-890-024-23	Sequence 23, Appl	220	27	93.1	19	4	US-10-816-022-5	Sequence 5, Appl
148	27	93.1	10	5	US-10-890-024-24	Sequence 24, Appl	221	27	93.1	19	4	US-10-816-529-5	Sequence 5, Appl
149	27	93.1	10	5	US-10-928-926-20	Sequence 20, Appl	222	27	93.1	19	4	US-10-815-353-5	Sequence 5, Appl
150	27	93.1	10	5	US-10-928-926-21	Sequence 21, Appl	223	27	93.1	19	4	US-10-815-391-5	Sequence 5, Appl
151	27	93.1	10	5	US-10-928-926-22	Sequence 22, Appl	224	27	93.1	19	5	US-10-828-548-5	Sequence 5, Appl
152	27	93.1	10	5	US-10-928-926-23	Sequence 23, Appl	225	27	93.1	19	5	US-10-816-380-5	Sequence 5, Appl
153	27	93.1	10	5	US-10-928-926-24	Sequence 24, Appl	226	27	93.1	19	5	US-10-889-999-75	Sequence 75, Appl
154	27	93.1	10	6	US-11-058-757-20	Sequence 20, Appl	227	27	93.1	19	5	US-10-890-070-75	Sequence 75, Appl
155	27	93.1	10	6	US-11-058-757-21	Sequence 21, Appl	228	27	93.1	19	5	US-10-890-000-75	Sequence 75, Appl
156	27	93.1	10	6	US-11-058-757-22	Sequence 22, Appl	229	27	93.1	19	5	US-10-788-666-5	Sequence 5, Appl
157	27	93.1	10	6	US-11-058-757-23	Sequence 23, Appl	230	27	93.1	19	5	US-10-923-471-5	Sequence 5, Appl
158	27	93.1	10	6	US-11-058-757-24	Sequence 24, Appl	231	27	93.1	19	5	US-10-823-463-75	Sequence 75, Appl
159	27	93.1	11	3	US-09-988-842-9	Sequence 9, Appl	232	27	93.1	19	5	US-10-923-469-5	Sequence 5, Appl
160	27	93.1	11	3	US-09-988-842-25	Sequence 25, Appl	233	27	93.1	19	5	US-10-933-559-5	Sequence 5, Appl
161	27	93.1	11	4	US-10-235-483-14	Sequence 14, Appl	234	27	93.1	19	5	US-10-815-404-5	Sequence 5, Appl
162	27	93.1	11	4	US-10-050-200-33	Sequence 33, Appl	235	27	93.1	19	5	US-10-934-609-5	Sequence 5, Appl
163	27	93.1	11	4	US-10-237-673-20	Sequence 20, Appl	236	27	93.1	19	5	US-10-923-474-5	Sequence 5, Appl
164	27	93.1	11	5	US-10-464-117-13	Sequence 13, Appl	237	27	93.1	19	5	US-10-884-892-5	Sequence 5, Appl
165	27	93.1	11	5	US-10-772-230-9	Sequence 9, Appl	238	27	93.1	19	5	US-10-822-968-75	Sequence 75, Appl
166	27	93.1	11	5	US-10-772-230-25	Sequence 25, Appl	239	27	93.1	19	5	US-10-777-792-75	Sequence 75, Appl
167	27	93.1	12	3	US-09-867-847-8	Sequence 8, Appl	240	27	93.1	19	5	US-10-890-071-75	Sequence 75, Appl
168	27	93.1	12	5	US-10-810-881A-115	Sequence 115, App	241	27	93.1	19	5	US-10-890-024-75	Sequence 75, Appl
169	27	93.1	12	5	US-10-810-881A-117	Sequence 117, App	242	27	93.1	19	5	US-10-934-819-5	Sequence 5, Appl
170	27	93.1	12	5	US-10-508-586-2	Sequence 2, Appl	243	27	93.1	19	5	US-10-923-267-5	Sequence 5, Appl
171	27	93.1	12	5	US-10-508-586-3	Sequence 3, Appl	244	27	93.1	19	5	US-10-928-526-75	Sequence 75, Appl
172	27	93.1	12	5	US-10-625-854-139	Sequence 139, App	245	27	93.1	19	6	US-11-058-757-75	Sequence 75, Appl
173	27	93.1	12	6	US-11-012-797A-33	Sequence 33, Appl	246	27	93.1	19	6	US-11-108-102-5	Sequence 5, Appl

Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 5, Appl
Sequence 6, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 4, Appl
Sequence 66, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 2, Appl
Sequence 7, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 66, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 3, Appl
Sequence 959, Appl
Sequence 965, Appl
Sequence 976, Appl
Sequence 992, Appl
Sequence 1003, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 9, Appl
Sequence 24, Appl
Sequence 5, Appl
Sequence 99, Appl
Sequence 295, Appl
Sequence 84, Appl
Sequence 85, Appl
Sequence 98, Appl
Sequence 99, Appl
Sequence 85, Appl
Sequence 295, Appl
Sequence 3, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 3, Appl
Sequence 979, Appl
Sequence 1006, Appl
Sequence 6, Appl
Sequence 11, Appl
Sequence 6, Appl
Sequence 11, Appl

247 27 93.1 20 3 US-09-908-943A-25
248 27 93.1 20 5 US-10-801-487-25
249 27 93.1 20 5 US-10-801-938-25
250 27 93.1 20 5 US-10-801-509-25
251 27 93.1 20 5 US-10-801-486-25
252 27 93.1 20 5 US-10-801-493-25
253 27 93.1 24 5 US-10-728-246-5
254 27 93.1 24 5 US-10-728-246-6
255 27 93.1 26 3 US-09-792-079-11
256 27 93.1 26 4 US-10-159-279-11
257 27 93.1 28 3 US-09-867-847-4
258 27 93.1 28 3 US-09-865-294-66
259 27 93.1 28 3 US-09-792-079-5
260 27 93.1 28 4 US-10-159-279-5
261 27 93.1 28 4 US-10-363-082-2
262 27 93.1 28 4 US-10-433-385-7
263 27 93.1 28 4 US-10-390-472-4
264 27 93.1 28 4 US-10-741-205-36
265 27 93.1 28 4 US-10-416-2628-7
266 27 93.1 28 4 US-10-478-308-4
267 27 93.1 28 4 US-10-478-307-4
268 27 93.1 28 5 US-10-861-614-66
269 27 93.1 28 5 US-10-825-958-4
270 27 93.1 28 6 US-11-091-309-3
271 27 93.1 28 6 US-11-066-697-959
272 27 93.1 28 6 US-11-066-697-965
273 27 93.1 28 6 US-11-066-697-976
274 27 93.1 28 6 US-11-066-697-992
275 27 93.1 28 6 US-11-066-697-1003
276 27 93.1 30 3 US-09-861-847-1
277 27 93.1 30 4 US-10-301-488A-1
278 27 93.1 30 4 US-10-666-423-1
279 27 93.1 30 4 US-10-617-876-9
280 27 93.1 30 4 US-10-619-454-24
281 27 93.1 30 4 US-10-301-448-1
282 27 93.1 30 5 US-10-775-562-5
283 27 93.1 32 4 US-10-732-862A-99
284 27 93.1 33 3 US-09-930-915A-295
285 27 93.1 33 4 US-10-082-014-84
286 27 93.1 33 4 US-10-372-076-85
287 27 93.1 33 4 US-10-732-862A-98
288 27 93.1 33 4 US-10-806-006-295
289 27 93.1 33 4 US-10-677-074-85
290 27 93.1 33 4 US-10-805-913-295
291 27 93.1 35 3 US-09-867-847-3
292 27 93.1 35 3 US-09-972-475-16
293 27 93.1 35 4 US-10-463-729-16
294 27 93.1 35 5 US-10-825-958-3
295 27 93.1 35 6 US-11-066-697-979
296 27 93.1 35 6 US-11-066-697-1006
297 27 93.1 36 3 US-09-861-847-6
298 27 93.1 36 3 US-09-861-847-11
299 27 93.1 36 4 US-10-301-488A-6
300 27 93.1 36 4 US-10-301-488A-11

ALIGNMENTS

RESULT 1
US-09-867-847-11
; Sequence 11, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-11

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 2

US-09-867-847-19
; Sequence 19, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-19

Query Match 100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 3

US-09-915-092-1
; Sequence 1, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert

```
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 2001-07-24
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-1

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 4
US-09-915-092-9
; Sequence 9, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 2001-07-24
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-9

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 5
US-09-747-408-1
; Sequence 1, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 6
US-09-747-408-10
; Sequence 10, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match      100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
      |||||
Db      1 KIVFFA 6

RESULT 7
US-10-728-028-1
; Sequence 1, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
;
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-1

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6

RESULT 8
US-10-728-028-9
; Sequence 9, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: KONG, Xianqi
; APPLICANT: GONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-9

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6

RESULT 9
US-10-825-958-9
; Sequence 9, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-9

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6

RESULT 10
US-10-825-958-17
; Sequence 17, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-17

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6

RESULT 11
US-10-425-115-280164
; Sequence 280164, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
```

```

; NUMBER OF SEQ ID NOS: 369326
;
; SEQ ID NO 280164
;   LENGTH: 58
;   TYPE: PRM
;   ORGANISM: Zea mays
;   FEATURE:
;
;   OTHER INFORMATION: clone ID
US-10-425-115-280164

```

Query Match 100.0%; Score 29; DB 4; Length 58;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 12
US-10-424-599-165325
; Sequence 165325, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285604
; SEQ ID NO 165325
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120303C.1.pap
US-10-424-599-165325

```

Query Match 100.0%; Score 29; DB 4; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 13
US-10-424-599-240310
; Sequence 240310, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240310
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59027C.1.pep
US-10-424-599-240310

```

```

Query Match      100.0%; Score 29; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. NO. 1.re+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
        |||||
Db      34 KIVFFA 39

```

```

RESULT 14
US-10-450-763-56957
; Sequence 56957, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hveseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)...(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 dom
; OTHER INFORMATION: eMATRIX, accession number DN013542,
; OTHER INFORMATION: 9.06
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-56957

```

```

Query Match      100.0%; Score 29; DB 5; Length 99;
Best Local Similarity 100.0%; Pred. NO. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVEFFA 6
        |||||
Db      63 KIVEFFA 68

```

RESULT 15
US-09-867-847-18
; Sequence 18, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-18

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 1 KVVFFA 6

RESULT 16
US-09-867-847-26
; Sequence 26, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-26

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 1 KVVFFA 6

RESULT 17
US-09-915-092-8
; Sequence 8, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808

; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-8

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 1 KVVFFA 6

RESULT 18
US-09-915-092-16
; Sequence 16, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-16

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 1 KVVFFA 6

RESULT 19
US-09-747-408-9
; Sequence 9, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 20
US-09-747-408-17
; Sequence 17, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match 96.6%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 21
US-10-728-028-8
; Sequence 8, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-8

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 22
US-10-728-028-16
; Sequence 16, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-16

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 23
US-10-825-958-16
; Sequence 16, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-16

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 1 KVVFFA 6

RESULT 24
US-10-825-958-24
; Sequence 24, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lisa
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-24

Query Match 96.6%; Score 28; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 1 KVVFFA 6

RESULT 25
US-10-641-924-7
; Sequence 7, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 53035AUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-924-7

Query Match 96.6%; Score 28; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 18 KVVFFA 23

RESULT 26
US-10-642-255-7
; Sequence 7, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyl, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; FILE REFERENCE: 52339AUSM1
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-255-7

Query Match 96.6%; Score 28; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 73;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 18 KVVFFA 23

RESULT 27
US-10-437-963-173619
; Sequence 173619, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173619
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71639C.1.pap
US-10-437-963-173619

Query Match 96.6%; Score 28; DB 4; Length 60;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 28

US-10-437-963-133986
; Sequence 133986, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133986
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35803C.1.pep
US-10-437-963-133986

Query Match 96.6%; Score 28; DB 4; Length 87;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 6 KVVFFA 11

RESULT 29

US-10-437-963-105773
; Sequence 105773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105773
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102988C.1.pep
US-10-437-963-105773

Query Match 96.6%; Score 28; DB 4; Length 109;
Best Local Similarity 83.3%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 30

US-10-437-963-141578
; Sequence 141578, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141578
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42668C.1.pep
US-10-437-963-141578

Query Match 96.6%; Score 28; DB 4; Length 135;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 31

US-10-437-963-122124
; Sequence 122124, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122124
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(175)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25081C.1.pep
US-10-437-963-122124

Query Match 96.6%; Score 28; DB 4; Length 175;

Best Local Similarity 83.3%; Pred. No. 3.3e+02; Mismatches 1; Gaps 0; Indels 0; Mismatches 0; Gaps 0; Indels 0;

QY 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 32
US-10-481-032A-214
; Sequence 214, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wenqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: Patentin Ver. 2.2
; SEQ ID NO 214
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-214

Query Match 96.6%; Score 28; DB 5; Length 186;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 33
US-10-481-032A-228
; Sequence 228, Application US/10481032A
; Publication No. US20050177901A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wenqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16

; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: Patentin Ver. 2.2
; SEQ ID NO 228
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-228

Query Match 96.6%; Score 28; DB 5; Length 186;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 34
US-10-437-963-172476
; Sequence 172476, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172476
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(188)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70608C.1.pap
US-10-437-963-172476

Query Match 96.6%; Score 28; DB 4; Length 188;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 35
US-10-437-963-172452
; Sequence 172452, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua

```
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172452
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Oryza sativa
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70587C.1.pep
US-10-437-963-172452

Query Match          96.6%; Score 28; DB 4; Length 198;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 36
US-10-055-475-14
; Sequence 14, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalkrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-055-475-14

Query Match          96.6%; Score 28; DB 4; Length 416;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 57 KVVFFA 62

RESULT 37
US-11-042-922-14
; Sequence 14, Application US/11042922
; Publication No. US20050186211A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalkrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
```

```
; APPLICANT: Gopalkrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: 10/055,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 416
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-042-922-14

Query Match          96.6%; Score 28; DB 6; Length 416;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 57 KVVFFA 62

RESULT 38
US-10-055-475-13
; Sequence 13, Application US/10055475
; Publication No. US20030022855A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalkrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
; FILE REFERENCE: A34614-A-PCT-USA-A (070050.1921)
; CURRENT APPLICATION NUMBER: US/10/055,475
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-10-055-475-13

Query Match          96.6%; Score 28; DB 4; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 57 KVVFFA 62

RESULT 39
US-11-042-922-13
; Sequence 13, Application US/11042922
; Publication No. US20050186211A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Paul B.
; APPLICANT: Kang, Dong-Chul
; APPLICANT: Gopalkrishnan, Rahul V.
; TITLE OF INVENTION: USE OF MDA-5 AS AN ANTIVIRAL AND
; TITLE OF INVENTION: ANTIPROLIFERATIVE AGENT
```

FILE REFERENCE: A34614-A-PCT-USA-A-A (070050.2689)
; CURRENT APPLICATION NUMBER: US/11/042,922
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 10/055,475
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/06960
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 09/515,363
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 514
; TYPE: PRT
; ORGANISM: sus scrofa
US-11-042-922-13

Query Match 96.6%; Score 28; DB 6; Length 514;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 57 KVVFFA 62

RESULT 40

US-11-097-143-12723
; Sequence 12723, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CLO00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12723
; LENGTH: 564
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-12723

Query Match 96.6%; Score 28; DB 6; Length 564;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 53 KIVFFA 58

RESULT 41

US-10-408-765A-2031
; Sequence 2031, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Bojin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2031
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2031

Query Match 96.6%; Score 28; DB 4; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 42

US-10-755-889-234
; Sequence 234, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 234
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-234

Query Match 96.6%; Score 28; DB 4; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 292 KVVFFA 297

RESULT 43

US-10-370-715B-8
; Sequence 8, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY

```
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 8
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-370-715B-8

Query Match          96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      292 KVVFFA 297

RESULT 44
US-10-631-467-680
; Sequence 680, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-680

Query Match          96.6%; Score 28; DB 5; Length 925,
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      292 KVVFFA 297

RESULT 45
US-10-631-467-747
; Sequence 747, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
```

```
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 747
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-631-467-747

Query Match          96.6%; Score 28; DB 5; Length 925;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      292 KVVFFA 297

RESULT 46
US-09-870-759-124
; Sequence 124, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-870-759-124

Query Match          96.6%; Score 28; DB 3; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      514 KVVFFA 519

RESULT 47
US-09-751-708A-124
; Sequence 124, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-751-708A-124

Query Match          96.6%; Score 28; DB 3; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      514 KVVFFA 519
```

Db 514 KVVFFA 519

RESULT 48

US-10-428-817A-120
; Sequence 120, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-428-817A-120

Query Match 96.6%; Score 28; DB 4; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 49

US-10-937-758A-101
; Sequence 101, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-937-758A-101

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 50

US-10-631-467-1388
; Sequence 1388, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive p
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1388
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1388

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 51

US-10-631-467-1464
; Sequence 1464, Application US/10631467
; Publication No. US20050208496A1
; GENERAL INFORMATION:
; APPLICANT: Genox Research Inc.
; TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructive i
; FILE REFERENCE: 3462.1005-000
; CURRENT APPLICATION NUMBER: US/10/631,467
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: JP 2003-077212
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2002-229312
; PRIOR FILING DATE: 2002-08-06
; NUMBER OF SEQ ID NOS: 2086
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1464
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-631-467-1464

Query Match 96.6%; Score 28; DB 5; Length 1144;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 514 KVVFFA 519

RESULT 52

US-11-097-143-32208
; Sequence 32208, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

```

; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32208
; LENGTH: 1443
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-32208

Query Match          96.6%; Score 28; DB 6; Length 1443;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   ||:||||
Db 1204 KIIFFA 1209

RESULT 53
US-10-437-963-109646
; Sequence 109646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109646
; LENGTH: 1640
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_13784C.1.pep
US-10-437-963-109646

Query Match          96.6%; Score 28; DB 4; Length 1640;
Best Local Similarity 83.3%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   ||:||||
Db 1596 KVVFFA 1601

; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-7

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   ||:||||
Db 1 KLVFFA 6

RESULT 54
US-09-867-847-7
; Sequence 7, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-7

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   ||:||||
Db 1 KLVFFA 6

RESULT 55
US-09-867-847-20
; Sequence 20, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-20

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 56
US-09-972-475-9
; Sequence 9, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US98/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US98/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-972-475-9

Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 57
US-09-915-092-10
; Sequence 10, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139

; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-10

Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 58
US-09-915-092-28
; Sequence 28, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(6)
; OTHER INFORMATION: D-amino acids
US-09-915-092-28

Query Match 93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 59
US-09-956-625-25
; Sequence 25, Application US/09956625
; Patent No. US20020119926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; CURRENT FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25

```
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence:Antifibrillogenic agents
US-09-956-625-25

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 60
US-09-747-408-3
; Sequence 3, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-3

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 61
US-09-747-408-11
; Sequence 11, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match          93.1%; Score 27; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 62
US-10-463-729-9
; Sequence 9, Application US/10463729
; Publication No. US20040005307A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/463,729
; FILING DATE: 17-JUNE-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-10-463-729-9

Query Match          93.1%; Score 27; DB 4; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:|
Db 1 KLVFFA 6

RESULT 63
US-10-728-028-10
; Sequence 10, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
```



```
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-10
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db       1 KLVFFA 6
```

```
RESULT 64
US-10-728-028-27
; Sequence 27, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-27
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db       1 KLVFFA 6
```

```
RESULT 65
US-10-728-028-28
; Sequence 28, Application US/10728028
```

```
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-28
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db       1 KLVFFA 6
```

```
RESULT 66
US-10-825-958-7
; Sequence 7, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D. peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-7
```

```
Query Match          93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db       1 KLVFFA 6
```

```
RESULT 67
US-10-825-958-18
; Sequence 18, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-18

Query Match      93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db      1 KLVFFA 6

RESULT 68
US-10-666-095-3
; Sequence 3, Application US/10666095
; Publication No. US20050119187A1
; GENERAL INFORMATION:
; APPLICANT: Hammer, Robert P.
; APPLICANT: Fu, Yanwen
; APPLICANT: Aucoin, Jed P.
; APPLICANT: Miller, Tod J.
; APPLICANT: McLaughlin, Mark L.
; APPLICANT: McCarley, Robin L.
; TITLE OF INVENTION: Anti-Fibril Peptides
; FILE REFERENCE: 0212.1 Hammer
; CURRENT APPLICATION NUMBER: US/10/666,095
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,081
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-666-095-3

Query Match      93.1%; Score 27; DB 5; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db      1 KLVFFA 6

RESULT 69
US-09-867-847-12
; Sequence 12, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-12

Query Match      93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db      2 KLVFFA 7

RESULT 70
US-09-867-847-27
; Sequence 27, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-27

Query Match      93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
       |:||||
Db      2 KLVFFA 7
```

```
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 71
US-09-867-847-28
; Sequence 28, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; NAME/KEY: MOD_RES
; LOCATION: (7)
; OTHER INFORMATION: AMIDATION
US-09-867-847-28

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 72
US-09-972-475-7
; Sequence 7, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
```

```
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-972-475-7

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 73
US-09-915-092-2
; Sequence 2, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-2

Query Match 93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLVFFA 6
Db 2 KLVFFA 7

RESULT 74
US-09-915-092-17
; Sequence 17, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangi
; APPLICANT: Chalfour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
```

```

; TITLE OF INVENTION:  USES THEREOF
; FILE REFERENCE:  NBI-139
; CURRENT APPLICATION NUMBER:  US/09/915,092
; CURRENT FILING DATE:  2001-07-24
; PRIOR APPLICATION NUMBER:  60/220,808
; PRIOR FILING DATE:  2000-07-25
; NUMBER OF SEQ ID NOS:  28
; SOFTWARE:  FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH:  7
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-915-092-17

Query Match      93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |:||||
Db      1 KLVFFA 6

RESULT 75
US-09-915-092-18
; Sequence 18, Application US/09915092
; Publication No. US20020115717A1
; GENERAL INFORMATION:
; APPLICANT:  Gervais, Francine
; APPLICANT:  Kong, Xianqi
; APPLICANT:  Chalifour, Robert
; APPLICANT:  Migneault, David
; TITLE OF INVENTION:  AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION:  USES THEREOF
; FILE REFERENCE:  NBI-139
; CURRENT APPLICATION NUMBER:  US/09/915,092
; CURRENT FILING DATE:  2001-07-24
; PRIOR APPLICATION NUMBER:  60/220,808
; PRIOR FILING DATE:  2000-07-25
; NUMBER OF SEQ ID NOS:  28
; SOFTWARE:  FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH:  7
; TYPE:  PRT
; ORGANISM:  Homo sapiens
US-09-915-092-18

Query Match      93.1%; Score 27; DB 3; Length 7;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
      |:||||
Db      1 KLVFFA 6

Search completed:  December 29, 2005, 18:49:45
Job time : 66.2903 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-10

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

: Maximum Match 100%

: Listing first 300 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/prodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/PCUTS_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/baCkfilea1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	2	US-09-747-408-1
2	29	100.0	6	2	US-09-747-408-10
3	28	96.6	6	2	US-09-747-408-9
4	28	96.6	6	2	US-09-747-408-17
5	28	96.6	77	2	US-09-513-999C-6921
6	28	96.6	1144	1	US-08-147-812-5
7	28	96.6	1144	1	US-08-319-866-12
8	28	96.6	1144	2	US-09-123-708-2
9	28	96.6	1144	2	US-09-123-624-2
10	28	96.6	1144	2	US-09-661-258-5
11	28	96.6	1144	2	US-08-809-917-12
12	28	96.6	1144	2	US-09-419-371-12
13	27	93.1	6	1	US-08-612-785B-9
14	27	93.1	6	2	US-08-703-675C-32
15	27	93.1	6	2	US-08-617-267C-9
16	27	93.1	6	2	US-09-747-408-3
17	27	93.1	6	2	US-09-747-408-11
18	27	93.1	7	1	US-08-127-904-14
19	27	93.1	7	1	US-08-612-785B-7
20	27	93.1	7	2	US-08-703-675C-30
21	27	93.1	7	2	US-08-617-267C-7
22	27	93.1	7	2	US-09-264-709A-13
23	27	93.1	7	2	US-09-747-408-2
24	27	93.1	7	2	US-09-747-408-18
25	27	93.1	7	2	US-09-747-408-19
26	27	93.1	7	4	PCT-US94-10475-14
27	27	93.1	8	1	US-08-612-785B-5

28	27	93.1	8	1	US-08-630-645-1	Sequence 1, Appli
29	27	93.1	8	2	US-08-703-675C-28	Sequence 28, Appl
30	27	93.1	8	2	US-08-617-267C-5	Sequence 5, Appli
31	27	93.1	8	2	US-09-095-106A-44	Sequence 44, Appl
32	27	93.1	8	2	US-08-766-596A-1	Sequence 1, Appli
33	27	93.1	8	2	US-09-668-314C-73	Sequence 73, Appl
34	27	93.1	8	4	PCT-US96-10220-1	Sequence 1, Appli
35	27	93.1	9	2	US-08-766-596A-64	Sequence 64, Appl
36	27	93.1	9	2	US-09-747-408-20	Sequence 20, Appl
37	27	93.1	10	2	US-08-970-833-3	Sequence 3, Appli
38	27	93.1	10	2	US-09-724-961-20	Sequence 20, Appl
39	27	93.1	10	2	US-09-724-961-21	Sequence 21, Appl
40	27	93.1	10	2	US-09-724-961-22	Sequence 22, Appl
41	27	93.1	10	2	US-09-724-961-23	Sequence 23, Appl
42	27	93.1	10	2	US-09-724-961-24	Sequence 24, Appl
43	27	93.1	10	2	US-09-580-018-20	Sequence 20, Appl
44	27	93.1	10	2	US-09-580-018-21	Sequence 21, Appl
45	27	93.1	10	2	US-09-580-018-22	Sequence 22, Appl
46	27	93.1	10	2	US-09-580-018-23	Sequence 23, Appl
47	27	93.1	10	2	US-09-580-018-24	Sequence 24, Appl
48	27	93.1	10	2	US-09-724-551-20	Sequence 20, Appl
49	27	93.1	10	2	US-09-724-551-21	Sequence 21, Appl
50	27	93.1	10	2	US-09-724-551-22	Sequence 22, Appl
51	27	93.1	10	2	US-09-724-551-23	Sequence 23, Appl
52	27	93.1	10	2	US-09-724-551-24	Sequence 24, Appl
53	27	93.1	10	2	US-09-724-940-20	Sequence 20, Appl
54	27	93.1	10	2	US-09-724-940-21	Sequence 21, Appl
55	27	93.1	10	2	US-09-724-940-22	Sequence 22, Appl
56	27	93.1	10	2	US-09-724-940-23	Sequence 23, Appl
57	27	93.1	10	2	US-09-724-940-24	Sequence 24, Appl
58	27	93.1	11	1	US-08-630-645-14	Sequence 14, Appl
59	27	93.1	11	1	US-08-766-596A-14	Sequence 14, Appl
60	27	93.1	11	2	US-09-988-842-9	Sequence 9, Appli
61	27	93.1	11	2	US-09-988-842-25	Sequence 25, Appl
62	27	93.1	11	4	PCT-US96-10220-14	Sequence 14, Appl
63	27	93.1	14	2	US-09-594-366-5	Sequence 5, Appli
64	27	93.1	14	2	US-09-992-800-5	Sequence 5, Appli
65	27	93.1	15	1	US-08-612-785B-14	Sequence 14, Appl
66	27	93.1	15	1	US-08-612-785B-37	Sequence 37, Appl
67	27	93.1	15	2	US-08-617-267C-17	Sequence 17, Appl
68	27	93.1	15	2	US-08-766-596A-56	Sequence 56, Appl
69	27	93.1	15	2	US-08-766-596A-57	Sequence 57, Appl
70	27	93.1	15	2	US-08-766-596A-58	Sequence 58, Appl
71	27	93.1	15	2	US-08-766-596A-60	Sequence 60, Appl
72	27	93.1	15	2	US-08-766-596A-61	Sequence 61, Appl
73	27	93.1	15	2	US-08-766-596A-63	Sequence 63, Appl
74	27	93.1	15	2	US-08-766-596A-65	Sequence 65, Appl
75	27	93.1	17	2	US-09-264-709A-2	Sequence 2, Appli
76	27	93.1	17	2	US-09-594-366-3	Sequence 3, Appli
77	27	93.1	17	2	US-09-623-548A-950	Sequence 950, App
78	27	93.1	17	2	US-09-623-548A-983	Sequence 983, App
79	27	93.1	17	2	US-09-992-800-3	Sequence 3, Appli
80	27	93.1	17	2	US-09-657-276-950	Sequence 950, App
81	27	93.1	17	2	US-09-657-276-983	Sequence 983, App
82	27	93.1	19	2	US-08-970-833-11	Sequence 11, Appl
83	27	93.1	19	2	US-09-723-384-5	Sequence 5, Appli
84	27	93.1	19	2	US-09-724-961-75	Sequence 75, Appl
85	27	93.1	19	2	US-09-724-552-5	Sequence 5, Appli
86	27	93.1	19	2	US-09-580-018-75	Sequence 75, Appl
87	27	93.1	19	2	US-09-723-927-5	Sequence 5, Appli
88	27	93.1	19	2	US-09-724-489-5	Sequence 5, Appli
89	27	93.1	19	2	US-09-723-477-5	Sequence 5, Appli
90	27	93.1	19	2	US-09-723-762-5	Sequence 5, Appli
91	27	93.1	19	2	US-09-201-430-5	Sequence 5, Appli
92	27	93.1	19	2	US-09-724-551-75	Sequence 75, Appl
93	27	93.1	19	2	US-10-815-353-5	Sequence 5, Appli
94	27	93.1	19	2	US-10-816-529-5	Sequence 5, Appli
95	27	93.1	19	2	US-10-815-391-5	Sequence 5, Appli
96	27	93.1	19	2	US-10-816-022-5	Sequence 5, Appli
97	27	93.1	19	2	US-09-724-940-75	Sequence 75, Appl
98	27	93.1	19	2	US-10-934-609-5	Sequence 5, Appli
99	27	93.1	19	2	US-10-884-892-5	Sequence 5, Appli
100	27	93.1	20	2	US-08-970-833-10	Sequence 10, Appl

101	27	93.1	20	2	US-09-724-953-33	Sequence 33, Appl	174	27	93.1	38	2	US-09-657-276-1002	Sequence 1002, Ap
102	27	93.1	20	2	US-09-724-567-33	Sequence 33, Appl	175	27	93.1	39	1	US-08-304-585-5	Sequence 5, Appl
103	27	93.1	20	2	US-09-979-952-33	Sequence 33, Appl	176	27	93.1	39	1	US-08-302-808-2	Sequence 2, Appl
104	27	93.1	20	2	US-09-585-817-33	Sequence 33, Appl	177	27	93.1	39	1	US-08-609-090-7	Sequence 7, Appl
105	27	93.1	26	1	US-08-304-585-7	Sequence 7, Appl	178	27	93.1	39	1	US-08-682-245A-1	Sequence 1, Appl
106	27	93.1	28	1	US-08-346-849-4	Sequence 4, Appl	179	27	93.1	39	1	US-08-986-948-2	Sequence 2, Appl
107	27	93.1	28	1	US-08-303-808-7	Sequence 7, Appl	180	27	93.1	40	1	US-07-744-767A-1	Sequence 1, Appl
108	27	93.1	28	1	US-08-609-090-2	Sequence 2, Appl	181	27	93.1	40	1	US-08-235-400-2	Sequence 2, Appl
109	27	93.1	28	1	US-08-986-948-7	Sequence 7, Appl	182	27	93.1	40	1	US-08-476-464A-2	Sequence 2, Appl
110	27	93.1	28	1	US-08-293-284A-4	Sequence 4, Appl	183	27	93.1	40	1	US-08-304-585-1	Sequence 1, Appl
111	27	93.1	28	1	US-08-461-216-2	Sequence 2, Appl	184	27	93.1	40	1	US-08-304-585-8	Sequence 8, Appl
112	27	93.1	28	2	US-09-388-890-2	Sequence 2, Appl	185	27	93.1	40	1	US-08-302-808-3	Sequence 3, Appl
113	27	93.1	28	2	US-09-388-890-3	Sequence 3, Appl	186	27	93.1	40	1	US-08-433-734-1	Sequence 1, Appl
114	27	93.1	28	2	US-09-388-890-4	Sequence 4, Appl	187	27	93.1	40	1	US-08-609-090-8	Sequence 8, Appl
115	27	93.1	28	2	US-09-388-890-5	Sequence 5, Appl	188	27	93.1	40	1	US-07-737-371E-69	Sequence 69, Appl
116	27	93.1	28	2	US-09-388-890-6	Sequence 6, Appl	189	27	93.1	40	1	US-08-682-245A-2	Sequence 2, Appl
117	27	93.1	28	2	US-09-388-890-7	Sequence 7, Appl	190	27	93.1	40	1	US-08-986-948-3	Sequence 3, Appl
118	27	93.1	28	2	US-09-388-890-8	Sequence 8, Appl	191	27	93.1	40	1	US-08-461-216-1	Sequence 1, Appl
119	27	93.1	28	2	US-09-388-890-9	Sequence 9, Appl	192	27	93.1	40	2	US-08-959-148-1	Sequence 1, Appl
120	27	93.1	28	2	US-09-388-890-10	Sequence 10, Appl	193	27	93.1	40	2	US-09-242-724-22	Sequence 22, Appl
121	27	93.1	28	2	US-09-388-890-12	Sequence 12, Appl	194	27	93.1	40	2	US-08-723-661B-1	Sequence 1, Appl
122	27	93.1	28	2	US-09-388-890-13	Sequence 13, Appl	195	27	93.1	40	2	US-09-062-365-3	Sequence 3, Appl
123	27	93.1	28	2	US-09-388-890-14	Sequence 14, Appl	196	27	93.1	40	2	US-09-133-866-1	Sequence 1, Appl
124	27	93.1	28	2	US-09-264-709A-1	Sequence 1, Appl	197	27	93.1	40	2	US-09-861-847A-7	Sequence 7, Appl
125	27	93.1	28	2	US-08-723-661B-2	Sequence 2, Appl	198	27	93.1	40	2	US-09-861-847A-8	Sequence 8, Appl
126	27	93.1	28	2	US-09-660-954-2	Sequence 2, Appl	199	27	93.1	40	2	US-09-988-842-3	Sequence 3, Appl
127	27	93.1	28	2	US-09-660-954-3	Sequence 3, Appl	200	27	93.1	40	2	US-10-455-218-1	Sequence 1, Appl
128	27	93.1	28	2	US-09-660-954-4	Sequence 4, Appl	201	27	93.1	40	2	US-10-151-614-1	Sequence 1, Appl
129	27	93.1	28	2	US-09-660-954-5	Sequence 5, Appl	202	27	93.1	40	2	US-09-623-548A-956	Sequence 956, App
130	27	93.1	28	2	US-09-660-954-6	Sequence 6, Appl	203	27	93.1	40	2	US-09-623-548A-962	Sequence 962, App
131	27	93.1	28	2	US-09-660-954-7	Sequence 7, Appl	204	27	93.1	40	2	US-09-623-548A-968	Sequence 968, App
132	27	93.1	28	2	US-09-660-954-8	Sequence 8, Appl	205	27	93.1	40	2	US-09-623-548A-978	Sequence 978, App
133	27	93.1	28	2	US-09-660-954-9	Sequence 9, Appl	206	27	93.1	40	2	US-09-623-548A-989	Sequence 989, App
134	27	93.1	28	2	US-09-660-954-10	Sequence 10, Appl	207	27	93.1	40	2	US-09-623-548A-995	Sequence 995, App
135	27	93.1	28	2	US-09-660-954-12	Sequence 12, Appl	208	27	93.1	40	2	US-09-623-548A-1005	Sequence 1005, Ap
136	27	93.1	28	2	US-09-660-954-13	Sequence 13, Appl	209	27	93.1	40	2	US-09-657-276-956	Sequence 956, App
137	27	93.1	28	2	US-09-660-954-14	Sequence 14, Appl	210	27	93.1	40	2	US-09-657-276-962	Sequence 962, App
138	27	93.1	28	2	US-08-898-300-4	Sequence 4, Appl	211	27	93.1	40	2	US-09-657-276-968	Sequence 968, App
139	27	93.1	28	2	US-08-824-513-4	Sequence 4, Appl	212	27	93.1	40	2	US-09-657-276-978	Sequence 978, App
140	27	93.1	28	2	US-09-623-548A-959	Sequence 959, App	213	27	93.1	40	2	US-09-657-276-989	Sequence 989, App
141	27	93.1	28	2	US-09-623-548A-965	Sequence 965, App	214	27	93.1	40	2	US-09-657-276-995	Sequence 995, App
142	27	93.1	28	2	US-09-623-548A-976	Sequence 976, App	215	27	93.1	40	2	US-09-657-276-1005	Sequence 1005, Ap
143	27	93.1	28	2	US-09-623-548A-992	Sequence 992, App	216	27	93.1	40	2	US-09-962-955D-36	Sequence 36, Appl
144	27	93.1	28	2	US-09-623-548A-1003	Sequence 1003, App	217	27	93.1	40	4	PCT-US92-06700-1	Sequence 1, Appl
145	27	93.1	28	2	US-09-657-276-959	Sequence 959, App	218	27	93.1	41	1	US-07-819-361-1	Sequence 1, Appl
146	27	93.1	28	2	US-09-657-276-965	Sequence 965, App	219	27	93.1	41	1	US-08-302-808-4	Sequence 4, Appl
147	27	93.1	28	2	US-09-657-276-976	Sequence 976, App	220	27	93.1	41	1	US-08-682-245A-3	Sequence 3, Appl
148	27	93.1	28	2	US-09-657-276-992	Sequence 992, App	221	27	93.1	41	1	US-08-986-948-4	Sequence 4, Appl
149	27	93.1	28	2	US-09-657-276-1003	Sequence 992, App	222	27	93.1	41	1	US-08-986-948-4	Sequence 4, Appl
150	27	93.1	28	2	US-09-657-276-1003	Sequence 1003, Ap	223	27	93.1	42	1	US-07-744-767A-2	Sequence 2, Appl
151	27	93.1	30	1	US-08-609-090-3	Sequence 3, Appl	224	27	93.1	42	1	US-08-179-574-1	Sequence 1, Appl
152	27	93.1	30	1	US-08-861-847A-1	Sequence 1, Appl	225	27	93.1	42	1	US-08-271-162-5	Sequence 5, Appl
153	27	93.1	34	1	US-08-609-090-4	Sequence 4, Appl	226	27	93.1	42	1	US-08-347-144-1	Sequence 1, Appl
154	27	93.1	34	1	US-08-475-579A-4	Sequence 4, Appl	227	27	93.1	42	1	US-08-462-859A-19	Sequence 19, Appl
155	27	93.1	35	1	US-08-304-585-6	Sequence 6, Appl	228	27	93.1	42	1	US-08-123-659A-19	Sequence 19, Appl
156	27	93.1	35	1	US-08-612-785B-16	Sequence 16, Appl	229	27	93.1	42	1	US-08-464-247A-19	Sequence 19, Appl
157	27	93.1	35	1	US-08-612-785B-36	Sequence 36, Appl	230	27	93.1	42	1	US-08-464-248A-19	Sequence 19, Appl
158	27	93.1	35	1	US-08-612-785B-38	Sequence 38, Appl	231	27	93.1	42	1	US-08-476-464A-1	Sequence 1, Appl
159	27	93.1	35	1	US-08-612-785B-48	Sequence 48, Appl	232	27	93.1	42	1	US-08-304-585-2	Sequence 2, Appl
160	27	93.1	35	2	US-08-617-267C-16	Sequence 16, Appl	233	27	93.1	42	1	US-08-302-808-5	Sequence 5, Appl
161	27	93.1	35	2	US-09-623-548A-979	Sequence 979, App	234	27	93.1	42	1	US-08-268-348A-1	Sequence 1, Appl
162	27	93.1	35	2	US-09-623-548A-1006	Sequence 1006, Ap	235	27	93.1	42	1	US-08-268-348A-3	Sequence 3, Appl
163	27	93.1	35	2	US-09-657-276-979	Sequence 979, App	236	27	93.1	42	1	US-08-268-348A-4	Sequence 4, Appl
164	27	93.1	35	2	US-09-657-276-1006	Sequence 1006, Ap	237	27	93.1	42	1	US-08-268-348A-5	Sequence 5, Appl
165	27	93.1	36	1	US-08-609-090-6	Sequence 6, Appl	238	27	93.1	42	1	US-08-288-348A-6	Sequence 6, Appl
166	27	93.1	36	2	US-09-861-847A-6	Sequence 6, Appl	239	27	93.1	42	1	US-08-433-734-2	Sequence 2, Appl
167	27	93.1	36	2	US-09-861-847A-11	Sequence 11, Appl	240	27	93.1	42	1	US-08-609-090-9	Sequence 9, Appl
168	27	93.1	38	1	US-08-302-808-1	Sequence 1, Appl	241	27	93.1	42	1	US-07-737-371E-72	Sequence 72, Appl
169	27	93.1	38	1	US-07-737-371E-68	Sequence 68, Appl	242	27	93.1	42	1	US-08-422-333-4	Sequence 4, Appl
170	27	93.1	38	1	US-08-986-948-1	Sequence 1, Appl	243	27	93.1	42	1	US-08-682-245A-4	Sequence 4, Appl
171	27	93.1	38	2	US-09-623-548A-975	Sequence 975, App	244	27	93.1	42	1	US-08-986-948-5	Sequence 5, Appl
172	27	93.1	38	2	US-09-623-548A-1002	Sequence 1002, Ap	245	27	93.1	42	2	US-08-717-551A-2	Sequence 2, Appl
173	27	93.1	38	2	US-09-657-276-975	Sequence 975, App	246	27	93.1	42	2	US-09-388-890-1	Sequence 1, Appl

```
247 27 93.1 42 2 US-09-005-215-20
248 27 93.1 42 2 US-09-242-724-23
249 27 93.1 42 2 US-08-922-930-2
250 27 93.1 42 2 US-09-660-954-1
251 27 93.1 42 2 US-08-923-055-2
252 27 93.1 42 2 US-08-922-889-2
253 27 93.1 42 2 US-09-731-460-1
254 27 93.1 42 2 US-09-133-866-2
255 27 93.1 42 2 US-09-723-384-1
256 27 93.1 42 2 US-09-724-961-42
257 27 93.1 42 2 US-09-724-552-1
258 27 93.1 42 2 US-10-455-018-2
259 27 93.1 42 2 US-09-580-018-42
260 27 93.1 42 2 US-09-723-927-1
261 27 93.1 42 2 US-09-724-489-1
262 27 93.1 42 2 US-09-724-477-1
263 27 93.1 42 2 US-09-723-762-1
264 27 93.1 42 2 US-09-201-430-1
265 27 93.1 42 2 US-09-724-551-42
266 27 93.1 42 2 US-10-815-353-1
267 27 93.1 42 2 US-10-278-181-1
268 27 93.1 42 2 US-10-816-529-1
269 27 93.1 42 2 US-09-623-548A-955
270 27 93.1 42 2 US-09-623-548A-961
271 27 93.1 42 2 US-09-623-548A-967
272 27 93.1 42 2 US-09-623-548A-988
273 27 93.1 42 2 US-09-623-548A-994
274 27 93.1 42 2 US-10-815-391-1
275 27 93.1 42 2 US-10-816-022-1
276 27 93.1 42 2 US-09-724-953-34
277 27 93.1 42 2 US-09-657-276-955
278 27 93.1 42 2 US-09-657-276-961
279 27 93.1 42 2 US-09-657-276-967
280 27 93.1 42 2 US-09-657-276-988
281 27 93.1 42 2 US-09-657-276-994
282 27 93.1 42 2 US-09-724-567-34
283 27 93.1 42 2 US-09-724-940-42
284 27 93.1 42 2 US-09-865-294A-65
285 27 93.1 42 2 US-09-979-952-34
286 27 93.1 42 2 US-09-585-817-34
287 27 93.1 42 2 US-09-962-955D-37
288 27 93.1 42 2 US-09-706-574A-20
289 27 93.1 42 2 US-10-934-609-1
290 27 93.1 42 2 US-10-884-892-1
291 27 93.1 42 4 PCT-US92-06700-2
292 27 93.1 42 4 PCT-US93-00325-1
293 27 93.1 42 4 PCT-US95-08302-5
294 27 93.1 42 6 5220013-12
295 27 93.1 42 6 5220013-14
296 27 93.1 42 6 5223482-12
297 27 93.1 43 1 US-08-235-400-1
298 27 93.1 43 1 US-08-437-067-1
299 27 93.1 43 1 US-08-302-808-6
300 27 93.1 43 1 US-08-079-511-1

ALIGNMENTS

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-1

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 2
US-09-747-408-10
; Sequence 10, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-10

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 3
US-09-747-408-9
; Sequence 9, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match 96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
;
;
; GENERAL INFORMATION:
; APPLICANT: Xie, Qiao-wen
; APPLICANT: Nathan, Carl F.
; APPLICANT: Mumford, Richard A.
; APPLICANT: Calaycay, Jimmy Ramos
; TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 East Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: Macintosh Centris650
; OPERATING SYSTEM: Macintosh 7.0.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,812
; FILING DATE: No. 5766909 Available
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/841,641
; FILING DATE: 02-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W III
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 186581A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; TELEX: 138825
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-147-812-5

Query Match 96.6%; Score 28; DB 1; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 7
US-08-319-866-12
; Sequence 12, Application US/08319866
; Patent No. 5929223
; GENERAL INFORMATION:
; APPLICANT: Tully, Timothy P.
; APPLICANT: Yin, Jerry C.
; APPLICANT: Regulski, Michael
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;
;
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-747-408-17

Query Match 96.6%; Score 28; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 5
US-09-513-999C-6921
; Sequence 6921, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6921
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-513-999C-6921

Query Match 96.6%; Score 28; DB 2; Length 77;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 38 KVVFFA 43

RESULT 6
US-08-147-812-5
; Sequence 5, Application US/08147812
; Patent No. 5766909
```



```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/319,866
; FILING DATE: 7-OCT-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1144 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-319-866-12

Query Match 96.6%; Score 28; DB 1; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 8
US-09-123-708-2
; Sequence 2, Application US/09123708
; Patent No. 6146887
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2003
; CURRENT APPLICATION NUMBER: US/09/123,708
; CURRENT FILING DATE: 1998-07-28
; EARLIER APPLICATION NUMBER: 08/553,503
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: P4411402.8
; EARLIER FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Cytomegalovirus
US-09-123-708-2

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 9
US-09-123-624-2
; Sequence 2, Application US/09123624
; Patent No. 6149936
; GENERAL INFORMATION:
; APPLICANT: SCHRADER, Juergen
; APPLICANT: GODECKE, Axel
; TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC

; TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
; FILE REFERENCE: 511169-2004
; CURRENT APPLICATION NUMBER: US/09/123,624
; CURRENT FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 08/553,503
; PRIOR FILING DATE: 1996-03-01
; PRIOR APPLICATION NUMBER: 4411402.8
; PRIOR FILING DATE: 1994-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-123-624-2

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 10
US-09-661-258-5
; Sequence 5, Application US/09661258
; Patent No. 6620616
; GENERAL INFORMATION:
; APPLICANT: Stuehr, Dennis J.
; APPLICANT: Adak, Subrata
; TITLE OF INVENTION: Nucleic Acids Encoding Nitric Oxide Synthase Variants
; FILE REFERENCE: 26473/04028
; CURRENT APPLICATION NUMBER: US/09/661,258
; CURRENT FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1144
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-661-258-5

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 514 KVVFFA 519

RESULT 11
US-08-809-917-12
; Sequence 12, Application US/08809917
; Patent No. 6689557
; GENERAL INFORMATION:
; APPLICANT: APPLICANT
; APPLICANT: APPLICANT
; TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
; TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,917
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13198
FILING DATE:
APPLICATION NUMBER: US 08/361,063
FILING DATE: 21-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/319,866
FILING DATE: 07-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-03A2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1144 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-917-12

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 514 KVVFFA 519

RESULT 12
US-09-419-371-12
Sequence 12, Application US/09419371
Patent No. 6890516
GENERAL INFORMATION:
APPLICANT: Tully, Timothy P.
TITLE OF INVENTION: Cloning and Characterizing of Genes
TITLE OF INVENTION: Associated With Long-Term Memory
FILE REFERENCE: CSHL94-03A32
CURRENT APPLICATION NUMBER: US/09/419,371
CURRENT FILING DATE: 1999-10-14
PRIOR APPLICATION NUMBER: 08/809,917
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: PCT/US95/13198
PRIOR FILING DATE: 1995-10-06
PRIOR APPLICATION NUMBER: 08/361,063
PRIOR FILING DATE: 1994-12-21
PRIOR APPLICATION NUMBER: 08/319,866
PRIOR FILING DATE: 1994-10-07
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 12
LENGTH: 1144
TYPE: PRT
ORGANISM: mouse
US-09-419-371-12

Query Match 96.6%; Score 28; DB 2; Length 1144;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||

Db 514 KVVFFA 519
RESULT 13
US-08-612-785B-9
Sequence 9, Application US/08612785B
Patent No. 5854204
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
TITLE OF INVENTION: Aggregation
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-612-785B-9

Query Match 93.1%; Score 27; DB 1; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 1 KVVFFA 6

RESULT 14
US-08-703-675C-32
Sequence 32, Application US/08703675C
Patent No. 6303567
GENERAL INFORMATION:
APPLICANT: Findeis, Mark A. et al.
TITLE OF INVENTION: Modulators of -Amyloid Peptide
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston

```

; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/703,675C
; FILING DATE: 27-AUG-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-617-267C-32

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 15
US-08-617-267C-9
; Sequence 9, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/617,267C
; FILING DATE: 14-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831

```

```

; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Gaudio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-617-267C-9

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 16
US-09-747-408-3
; Sequence 3, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-747-408-3

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 1 KLVFFA 6

RESULT 17
US-09-747-408-11
; Sequence 11, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408

```

; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-11

Query Match 93.1%; Score 27; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 18
US-08-127-904-14
; Sequence 14, Application US/08127904
; Patent No. 5470951
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For Antagonizing
; TITLE OF INVENTION: Amesic Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving the
; TITLE OF INVENTION: Quality of Life in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4" diskette
; COMPUTER: Wang PC MS DOS Version 3.20
; OPERATING SYSTEM: Microsoft
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; FILING DATE: 29 September 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5470951e
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: No. 5470951e
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; TELEX: No. 5470951e
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
US-08-127-904-14

Query Match 93.1%; Score 27; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 19
US-08-612-785B-7
; Sequence 7, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: AB Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-7

Query Match 93.1%; Score 27; DB 1; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 20
US-08-703-675C-30
; Sequence 30, Application US/08703675C
; Patent No. 6303567
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Modulators of -Amyloid Peptide
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,675C
FILING DATE: 27-AUG-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kara, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-30

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 21
US-08-617-267C-7
; Sequence 7, Application US/08617267C
; Patent No. 6319498
; GENERAL INFORMATION:
; APPLICANT: Fintelis, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-7

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 22
US-09-264-709A-13
; Sequence 13, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR FILING DATE: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-13

Query Match 93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 23
US-09-747-408-2
; Sequence 2, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23

```
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-2

Query Match          93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 2 KLVFFA 7

RESULT 24
US-09-747-408-18
; Sequence 18, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-18

Query Match          93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 2 KLVFFA 7

RESULT 25
US-09-747-408-19
; Sequence 19, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-19

Query Match          93.1%; Score 27; DB 2; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 26
PCT-US94-10475-14
; Sequence 14, Application PC/TUS9410475
; GENERAL INFORMATION:
; APPLICANT: Eugene Roberts
; TITLE OF INVENTION: Method For
; TITLE OF INVENTION: Antagonizing Amnestic
; TITLE OF INVENTION: Effects of Amyloid n
; TITLE OF INVENTION: Protein and Improving
; TITLE OF INVENTION: the Quality of Life
; TITLE OF INVENTION: in Individuals
; TITLE OF INVENTION: With Alzheimer Disease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: City of Hope
; STREET: 1500 East Duarte Road
; CITY: Duarte
; STATE: California
; COUNTRY: United States of America
; ZIP: 91010-0269
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3M Double Density 5 1/4"
; MEDIUM TYPE: diskette
; COMPUTER: Wang PC
; OPERATING SYSTEM: MS DOS Version 3.20
; SOFTWARE: Microsoft
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10475
; FILING DATE: 16 September 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA: U. S. Application
; PRIOR APPLICATION DATA: Serial No.
; PRIOR APPLICATION DATA: 08/127,904; filed
; PRIOR APPLICATION DATA: 29 September 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Irons, Edward S.
; REGISTRATION NUMBER: 16,541
; REFERENCE/DOCKET NUMBER: None
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 626-3564 or 783-6030
; TELEFAX: (202) 783-6031
; TELEX: None
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: Amino Acid
; STRANDEDNESS:
; TOPOLOGY: Unknown
PCT-US94-10475-14

Query Match          93.1%; Score 27; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 27
US-08-612-785B-5
; Sequence 5, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; TITLE OF INVENTION: Aggregation
```

;/ NUMBER OF SEQUENCES: 40
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: LAHIVE & COCKFIELD
;/ STREET: 28 State Street, Suite 510
;/ CITY: Boston
;/ STATE: Massachusetts
;/ COUNTRY: USA
;/ ZIP: 02109-1875
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/612,785B
;/ FILING DATE: Herewith
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/404,831
;/ FILING DATE: 14-MAR-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/475,579
;/ FILING DATE: 07-JUN-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/548,998
;/ FILING DATE: 27-OCT-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: DeConti, Giulio A.
;/ REGISTRATION NUMBER: 31,503
;/ REFERENCE/DOCKET NUMBER: PPI-002CP3
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (617)227-7400
;/ TELEFAX: (617)742-4214
;/ INFORMATION FOR SEQ ID NO: 5:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 8 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-612-785B-5

Query Match 93.1%; Score 27; DB 1; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 28
US-08-630-645-1
;/ Sequence 1, Application US/08630645
;/ Patent No. 5948763
;/ GENERAL INFORMATION:
;/ APPLICANT: SOTO-JARA, Claudio
;/ APPLICANT: BAUMANN, Marc
;/ APPLICANT: FRANGIONE, Blas
;/ TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;/ TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
;/ WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
;/ NUMBER OF SEQUENCES: 26
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: BROWDY AND NEIMARK
;/ STREET: 419 Seventh Street, N.W., Suite 400
;/ CITY: Washington
;/ STATE: D.C.
;/ COUNTRY: USA
;/ ZIP: 20004
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS

;/ SOFTWARE: PatentIn Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA: US/08/630,645
;/ FILING DATE:
;/ CLASSIFICATION: 530
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/478,326
;/ FILING DATE: 06-JUN-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: YUN, Allen C.
;/ REGISTRATION NUMBER: 37,971
;/ REFERENCE/DOCKET NUMBER: SOTO-JARA=1
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 202-628-5197
;/ TELEFAX: 202-737-3528
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 8 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-630-645-1

Query Match 93.1%; Score 27; DB 1; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 29
US-08-703-675C-28
;/ Sequence 28, Application US/08703675C
;/ Patent No. 6303567
;/ GENERAL INFORMATION:
;/ APPLICANT: Findels, Mark A. et al.
;/ TITLE OF INVENTION: Modulators of -Amyloid Peptide
;/ NUMBER OF SEQUENCES: 46
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: LAHIVE & COCKFIELD, LLP
;/ STREET: 28 State Street
;/ CITY: Boston
;/ STATE: Massachusetts
;/ COUNTRY: USA
;/ ZIP: 02109-1875
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/703,675C
;/ FILING DATE: 27-AUG-1996
;/ CLASSIFICATION: 514
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/404,831
;/ FILING DATE: 14-MAR-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/475,579
;/ FILING DATE: 07-JUN-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/548,998
;/ FILING DATE: 27-OCT-1995
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: USSN 08/616,081
;/ FILING DATE: 14-MAR-1996
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Kara, Catherine J.
;/ REGISTRATION NUMBER: 41,106
;/ REFERENCE/DOCKET NUMBER: PPI-016CP2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-703-675C-28

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 30

US-08-617-267C-5
Sequence 5, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-617-267C-5

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||

Db 3 KLVFFA 8

RESULT 31

US-09-095-106A-44
Sequence 44, Application US/09095106A
Patent No. 6331440
GENERAL INFORMATION:
APPLICANT: NORDSTEDT, Christer
APPLICANT: NASLUND, Jan
APPLICANT: THYBERG, Johan
APPLICANT: TERNERBERG, Lars O.
APPLICANT: TERNIUS, Lars
TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
FILE REFERENCE: 000500-124
CURRENT APPLICATION NUMBER: US/09/095,106A
CURRENT FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: US 60/009,386
PRIOR FILING DATE: 1995-12-29
PRIOR APPLICATION NUMBER: PCT/SE96/01621
PRIOR FILING DATE: 1996-12-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44
LENGTH: 8
TYPE: PPT
ORGANISM: Amyloidosis
US-09-095-106A-44

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 32

US-08-766-596A-1
Sequence 1, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-1

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 33
US-09-668-314C-73
Sequence 73, Application US/09668314C
Patent No. 6844148
GENERAL INFORMATION:
APPLICANT: Gurney, et al
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND USES
FILE REFERENCE: 28341/6280NCP
CURRENT APPLICATION NUMBER: US/09/668,314C
CURRENT FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US 60/169,232
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US 09/416,901
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn version 3.1
SEQ ID NO 73
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-668-314C-73

Query Match 93.1%; Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 34
PCT-US96-10220-1
Sequence 1, Application PC/TUS9610220
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS

TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10220
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-10220-1
Query Match 93.1%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 35
US-08-766-596A-64
Sequence 64, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-766-596A-64
```

```
Query Match      93.1%; Score 27; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
        |:||||
Db      2 KLVFFA 7
```

```
RESULT 36
US-09-747-408-20
; Sequence 20, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-747-408-20
```

```
Query Match      93.1%; Score 27; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
        |:||||
Db      4 KLVFFA 9
```

```
RESULT 37
US-08-970-833-3
; Sequence 3, Application US/08970833
; Patent No. 6022859
; GENERAL INFORMATION:
; APPLICANT: Kiessling, Laura L.
```

```
; APPLICANT: Murphy, Regina M.
; TITLE OF INVENTION: INHIBITORS OF BETA-AMYLOID TOXICITY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 411 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: U.S.A.
; ZIP: 53202-4497
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,833
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Jean C.
; REGISTRATION NUMBER: 35,433
; REFERENCE/DOCKET NUMBER: 960296.94291
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (414) 277-5709
; TELEFAX: (414) 271-3552
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-970-833-3
```

```
Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
        |:||||
Db      1 KLVFFA 6
```

```
RESULT 38
US-09-724-961-20
; Sequence 20, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
```

```
;
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-20

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFA 6
Db      5 KLVFFA 10
|:|||||

RESULT 39
US-09-724-961-21
; Sequence 21, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-21

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFA 6
Db      4 KLVFFA 9
|:|||||

RESULT 40
US-09-724-961-22
; Sequence 22, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
```

```
;
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-22

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFA 6
Db      3 KLVFFA 8
|:|||||

RESULT 41
US-09-724-961-23
; Sequence 23, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-23
```

```
Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      2 KLVFFA 7

RESULT 42
US-09-724-961-24
; Sequence 24, Application US/09724961
; Patent No. 6743427
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vaquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,961
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-961-24

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1 KLVFFA 6

RESULT 43
US-09-580-018-20
; Sequence 20, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-20

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1 KLVFFA 6

RESULT 44
US-09-580-018-21
; Sequence 21, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-21

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      4 KLVFFA 9

RESULT 45
US-09-580-018-22
; Sequence 22, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-22
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-20

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      5 KLVFFA 10

RESULT 44
US-09-580-018-21
; Sequence 21, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-21

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      4 KLVFFA 9

RESULT 45
US-09-580-018-22
; Sequence 22, Application US/09580018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-580-018-22
```

; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
peptide)
US-09-580-018-22

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 3 KLVFFA 8

RESULT 46
US-09-580-018-23
; Sequence 23, Application US/095800018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
peptide)
US-09-580-018-23

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 47
US-09-580-018-24
; Sequence 24, Application US/095800018
; Patent No. 6761888
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
peptide)
US-09-580-018-24

US-09-580-018-24
Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 48
US-09-724-551-20
; Sequence 20, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
peptide)
US-09-724-551-20

Query Match 93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 49
US-09-724-551-21
; Sequence 21, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
peptide)
US-09-724-551-21

```
; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 4 KLVFFA 9

RESULT 50
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 3 KLVFFA 8

RESULT 51
US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-21

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 4 KLVFFA 9

RESULT 50
US-09-724-551-22
; Sequence 22, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-22

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 3 KLVFFA 8

RESULT 51
US-09-724-551-23
; Sequence 23, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004760US
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 52
US-09-724-551-24
; Sequence 24, Application US/09724551
; Patent No. 6787637
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004760US
; CURRENT APPLICATION NUMBER: US/09/724,551
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,018
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from ANI792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-551-24

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFFA 6
   |:||||
Db 1 KLVFFA 6

RESULT 53
US-09-724-940-20
; Sequence 20, Application US/09724940
; Patent No. 6905886
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
```

```
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-20

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:||||
Db 5 KLVFFA 10

RESULT 54
US-09-724-940-21
; Sequence 21, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-21

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:||||
Db 4 KLVFFA 9

RESULT 55
US-09-724-940-22
; Sequence 22, Application US/09724940
; Patent No. 6905686
```

```
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/724,940
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-22

Query Match          93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
   |:||||
Db 3 KLVFFA 8

RESULT 56
US-09-724-940-23
; Sequence 23, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Vednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
;
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-23

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
        |:||||
Db      2 KLVFFA 7

RESULT 57
US-09-724-940-24
; Sequence 24, Application US/09724940
; Patent No. 6905686
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Bard, Frederique
; APPLICANT: Vasquez, Nicki
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004750UC
; CURRENT APPLICATION NUMBER: US/09/724,940
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US/09/580,015
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/322,289
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: US 09/201,430
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: WO PCT/US00/14810
; PRIOR FILING DATE: 1998-11-30
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:10-mer peptide
; OTHER INFORMATION: from AN1792 sequence (human Abeta42, beta-amyloid
; OTHER INFORMATION: peptide)
US-09-724-940-24

Query Match      93.1%; Score 27; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 5.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
        |:||||
Db      1 KLVFFA 6

RESULT 58
US-08-630-645-14
; Sequence 14, Application US/08630645
; Patent No. 5948763
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
; TITLE OF INVENTION: WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; NUMBER OF SEQUENCES: 26
```

```
;
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,645
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-630-645-14

Query Match      93.1%; Score 27; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
        |:||||
Db      2 KLVFFA 7

RESULT 59
US-08-766-596A-14
; Sequence 14, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
; CLASSIFICATION: 435
```


;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: YUN, Allen C.
;; REGISTRATION NUMBER: 37,971
;; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-766-596A-14

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 60
US-09-988-842-9
;; Sequence 9, Application US/09988842
;; Patent No. 6716589
;; GENERAL INFORMATION:
;; APPLICANT: Johansson, Jan
;; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
;; TITLE OF INVENTION: OF AMYLOID FORMATION
;; FILE REFERENCE: 12125-002001
;; CURRENT APPLICATION NUMBER: US/09/988,842
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: US 60/251,662
;; PRIOR FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: US 60/253,695
;; PRIOR FILING DATE: 2000-11-20
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-9

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 61
US-09-988-842-25
;; Sequence 25, Application US/09988842
;; Patent No. 6716589
;; GENERAL INFORMATION:
;; APPLICANT: Johansson, Jan
;; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
;; TITLE OF INVENTION: OF AMYLOID FORMATION

;; FILE REFERENCE: 12125-002001
;; CURRENT APPLICATION NUMBER: US/09/988,842
;; CURRENT FILING DATE: 2001-11-19
;; PRIOR APPLICATION NUMBER: US 60/251,662
;; PRIOR FILING DATE: 2000-12-06
;; PRIOR APPLICATION NUMBER: US 60/253,695
;; PRIOR FILING DATE: 2000-11-20
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 25
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-25

Query Match 93.1%; Score 27; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 62
PCT-US96-10220-14
;; Sequence 14, Application PC/TUS9610220
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL COMPOSITIONS
;; TITLE OF INVENTION: THEREOF FOR TREATMENT OF DISORDERS OR DISEASES ASSOCIATED
;; WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE DEPOSITS
;; NUMBER OF SEQUENCES: 26
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: BROWDY AND NEIMARK
;; STREET: 419 Seventh Street, N.W., Suite 400
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20004
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/10220
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/478,326
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/630,645
;; FILING DATE: 10-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROWDY, Roger L.
;; REGISTRATION NUMBER: 25,618
;; REFERENCE/DOCKET NUMBER: SOTO-JARA=1 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-628-5197
;; TELEFAX: 202-737-3528
;; INFORMATION FOR SEQ ID NO: 14:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
PCT-US96-10220-14

Query Match 93.1%; Score 27; DB 4; Length 11;

Best Local Similarity 83.3%; Pred. No. 6.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 2 KLVFFA 7

RESULT 63
US-09-594-366-5
; Sequence 5, Application US/09594366
; Patent No. 6582945
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2004
; CURRENT APPLICATION NUMBER: US/09/594,366
; CURRENT FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-594-366-5

Query Match 93.1%; Score 27; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 64
US-09-992-800-5
; Sequence 5, Application US/09992800
; Patent No. 6872554
; GENERAL INFORMATION:
; APPLICANT: Raso, Victor
; TITLE OF INVENTION: IMMUNOLOGICAL CONTROL OF BETA-AMYLOID LEVELS IN VIVO
; FILE REFERENCE: BBRI-2006
; CURRENT APPLICATION NUMBER: US/09/992,800
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 09/594,366
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/139,408
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-800-5

Query Match 93.1%; Score 27; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 7.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 4 KLVFFA 9

RESULT 65
US-08-612-785B-14
; Sequence 14, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:

; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-612-785B-14

Query Match 93.1%; Score 27; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 66
US-08-612-785B-37
; Sequence 37, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/612,785B
FILING DATE: Herewith
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-37

Query Match 93.1%; Score 27; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 6 KLVFFA 11

RESULT 67
US-08-617-267C-14
Sequence 14, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Finkelstein, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-617-267C-14

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
Db 1 KLVFFA 6

RESULT 68
US-08-766-596A-56
Sequence 56, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-766-596A-56

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 69

US-08-766-596A-57
; Sequence 57, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766.596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-57

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 70

US-08-766-596A-58

; Sequence 58, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766.596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-58

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 5 KLVFFA 10

RESULT 71

US-08-766-596A-60
; Sequence 60, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-60

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVPFA 6
|:||||
Db 5 KLVFFA 10

RESULT 72
US-08-766-596A-61
; Sequence 61, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-61

Query Match 93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVPFA 6
|:||||
Db 5 KLVFFA 10

RESULT 73
US-08-766-596A-63
; Sequence 63, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,596A
; FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197

```
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-63

Query Match          93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      5 KLVEFA 10

RESULT 74
US-08-766-596A-65
; Sequence 65, Application US/08766596A
; Patent No. 6462171
; GENERAL INFORMATION:
; APPLICANT: SOTO-JARA, Claudio
; APPLICANT: BAUMANN, Marc
; APPLICANT: FRANGIONE, Blas
; TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
; TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
; TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
; TITLE OF INVENTION: DEPOSITS
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 400
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766.596A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/630,645
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/478,326
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: SOTO-JARA=1A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-766-596A-65

Query Match          93.1%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 8.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
Db      5 KLVEFA 10

RESULT 75
US-09-264-709A-2
; Sequence 2, Application US/09264709A
; Patent No. 6320024
; GENERAL INFORMATION:
; APPLICANT: Roberts, Eugene
; TITLE OF INVENTION: Method for Design of Substances that Enhance Memory and
; TITLE OF INVENTION: Improve the Quality of Life
; FILE REFERENCE: 2124-310
; CURRENT APPLICATION NUMBER: US/09/264,709A
; CURRENT FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: 08/797,782
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-264-709A-2

Query Match          93.1%; Score 27; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      5 KLVEFA 10

Search completed: December 29, 2005, 17:52:37
Job time : 21.1323 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:33:58 ; Search time 3.58065 Seconds
(without alignments)
18.497 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KIVPFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 65735 seqs, 11038596 residues

Total number of hits satisfying chosen parameters: 65735

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Pending Patents AA New.*

1: /cgn2_6/prodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/prodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/prodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/prodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/prodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/prodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/prodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	93.1	7	7	US-11-269-857-6
2	27	93.1	11	7	US-11-291-770-20
3	27	93.1	24	1	PCT-US05-32135-5
4	27	93.1	24	1	PCT-US05-32135-6
5	27	93.1	28	7	US-11-297-316-2
6	27	93.1	39	7	US-11-194-989-19
7	27	93.1	39	7	US-11-195-207-19
8	27	93.1	40	1	PCT-US05-32135-4
9	27	93.1	40	6	US-10-966-919B-2
10	27	93.1	40	7	US-11-269-857-3
11	27	93.1	40	7	US-11-194-989-15
12	27	93.1	40	7	US-11-194-989-20
13	27	93.1	40	7	US-11-194-989-21
14	27	93.1	40	7	US-11-194-989-22
15	27	93.1	40	7	US-11-194-989-23
16	27	93.1	40	7	US-11-194-989-24
17	27	93.1	40	7	US-11-194-989-25
18	27	93.1	40	7	US-11-195-207-15
19	27	93.1	40	7	US-11-195-207-20
20	27	93.1	40	7	US-11-195-207-21
21	27	93.1	40	7	US-11-195-207-22
22	27	93.1	40	7	US-11-195-207-23
23	27	93.1	40	7	US-11-195-207-24
24	27	93.1	40	7	US-11-195-207-25
25	27	93.1	40	7	US-11-087-102A-18
26	27	93.1	40	7	US-11-087-102A-19
27	27	93.1	40	7	US-11-087-102A-20
28	27	93.1	40	7	US-11-087-102A-21
29	27	93.1	40	7	US-11-087-102A-22
30	27	93.1	40	7	US-11-087-102A-23
31	27	93.1	40	7	US-11-087-102A-24
32	27	93.1	40	7	US-11-087-102A-25
33	27	93.1	40	7	US-11-087-102A-26
34	27	93.1	40	7	US-11-087-102A-27
35	27	93.1	40	7	US-11-087-102A-28
36	27	93.1	40	7	US-11-087-102A-29
37	27	93.1	40	7	US-11-087-102A-30
38	27	93.1	40	7	US-11-087-102A-31
39	27	93.1	40	7	US-11-087-102A-32
40	27	93.1	40	7	US-11-087-102A-33
41	27	93.1	40	7	US-11-087-102A-34
42	27	93.1	40	7	US-11-087-102A-35
43	27	93.1	40	7	US-11-087-102A-36
44	27	93.1	40	7	US-11-087-102A-37
45	27	93.1	40	7	US-11-087-102A-38
46	27	93.1	40	7	US-11-087-102A-39
47	27	93.1	40	7	US-11-087-102A-40
48	27	93.1	40	7	US-11-087-102A-41
49	27	93.1	40	7	US-11-087-102A-42
50	27	93.1	40	7	US-11-087-102A-43
51	27	93.1	40	7	US-11-087-102A-44
52	27	93.1	40	7	US-11-087-102A-45
53	27	93.1	40	7	US-11-087-102A-46
54	27	93.1	40	7	US-11-087-102A-47
55	27	93.1	40	7	US-11-087-102A-48
56	27	93.1	40	7	US-11-087-102A-49
57	27	93.1	40	7	US-11-087-102A-50
58	27	93.1	40	7	US-11-087-102A-51
59	27	93.1	40	7	US-11-087-102A-52
60	27	93.1	40	7	US-11-087-102A-53
61	27	93.1	40	7	US-11-087-102A-54
62	27	93.1	40	7	US-11-087-102A-55
63	27	93.1	40	7	US-11-087-102A-56
64	27	93.1	40	7	US-11-087-102A-57
65	27	93.1	40	7	US-11-087-102A-58
66	27	93.1	40	7	US-11-087-102A-59
67	27	93.1	40	7	US-11-087-102A-60
68	27	93.1	40	7	US-11-087-102A-61
69	27	93.1	40	7	US-11-087-102A-62
70	27	93.1	40	7	US-11-087-102A-63
71	27	93.1	40	7	US-11-087-102A-64
72	27	93.1	40	7	US-11-087-102A-65
73	27	93.1	40	7	US-11-087-102A-66
74	27	93.1	40	7	US-11-087-102A-67
75	27	93.1	40	7	US-11-087-102A-68
76	27	93.1	40	7	US-11-087-102A-69
77	27	93.1	40	7	US-11-087-102A-70
78	27	93.1	40	7	US-11-087-102A-71
79	27	93.1	40	7	US-11-087-102A-72
80	27	93.1	40	7	US-11-087-102A-73
81	27	93.1	40	7	US-11-087-102A-74
82	27	93.1	40	7	US-11-087-102A-75
83	27	93.1	40	7	US-11-087-102A-76
84	27	93.1	40	7	US-11-087-102A-77
85	27	93.1	40	7	US-11-087-102A-78
86	27	93.1	40	7	US-11-087-102A-79
87	27	93.1	40	7	US-11-087-102A-80
88	27	93.1	40	7	US-11-087-102A-81
89	27	93.1	40	7	US-11-087-102A-82
90	27	93.1	40	7	US-11-087-102A-83
91	27	93.1	40	7	US-11-087-102A-84
92	27	93.1	40	7	US-11-087-102A-85
93	27	93.1	40	7	US-11-087-102A-86
94	27	93.1	40	7	US-11-087-102A-87
95	27	93.1	40	7	US-11-087-102A-88
96	27	93.1	40	7	US-11-087-102A-89
97	27	93.1	40	7	US-11-087-102A-90
98	27	93.1	40	7	US-11-087-102A-91
99	27	93.1	40	7	US-11-087-102A-92
100	27	93.1	40	7	US-11-087-102A-93
101	27	93.1	40	7	US-11-087-102A-94
102	27	93.1	40	7	US-11-087-102A-95
103	27	93.1	40	7	US-11-087-102A-96
104	27	93.1	40	7	US-11-087-102A-97
105	27	93.1	40	7	US-11-087-102A-98
106	27	93.1	40	7	US-11-087-102A-99
107	27	93.1	40	7	US-11-087-102A-100
108	27	93.1	40	7	US-11-087-102A-101
109	27	93.1	40	7	US-11-087-102A-102
110	27	93.1	40	7	US-11-087-102A-103
111	27	93.1	40	7	US-11-087-102A-104
112	27	93.1	40	7	US-11-087-102A-105
113	27	93.1	40	7	US-11-087-102A-106
114	27	93.1	40	7	US-11-087-102A-107
115	27	93.1	40	7	US-11-087-102A-108
116	27	93.1	40	7	US-11-087-102A-109
117	27	93.1	40	7	US-11-087-102A-110
118	27	93.1	40	7	US-11-087-102A-111
119	27	93.1	40	7	US-11-087-102A-112
120	27	93.1	40	7	US-11-087-102A-113
121	27	93.1	40	7	US-11-087-102A-114
122	27	93.1	40	7	US-11-087-102A-115
123	27	93.1	40	7	US-11-087-102A-116
124	27	93.1	40	7	US-11-087-102A-117
125	27	93.1	40	7	US-11-087-102A-118
126	27	93.1	40	7	US-11-087-102A-119
127	27	93.1	40	7	US-11-087-102A-120
128	27	93.1	40	7	US-11-087-102A-121
129	27	93.1	40	7	US-11-087-102A-122
130	27	93.1	40	7	US-11-087-102A-123
131	27	93.1	40	7	US-11-087-102A-124
132	27	93.1	40	7	US-11-087-102A-125
133	27	93.1	40	7	US-11-087-102A-126
134	27	93.1	40	7	US-11-087-102A-127
135	27	93.1	40	7	US-11-087-102A-128
136	27	93.1	40	7	US-11-087-102A-129
137	27	93.1	40	7	US-11-087-102A-130
138	27	93.1	40	7	US-11-087-102A-131
139	27	93.1	40	7	US-11-087-102A-132
140	27	93.1	40	7	US-11-087-102A-133
141	27	93.1	40	7	US-11-087-102A-134
142	27	93.1	40	7	US-11-087-102A-135
143	27	93.1	40	7	US-11-087-102A-136
144	27	93.1	40	7	US-11-087-102A-137
145	27	93.1	40	7	US-11-087-102A-138
146	27	93.1	40	7	US-11-087-102A-139
147	27	93.1	40	7	US-11-087-102A-140
148	27	93.1	40	7	US-11-087-102A-141
149	27	93.1	40	7	US-11-087-102A-142
150	27	93.1	40	7	US-11-087-102A-143
151	27	93.1	40	7	US-11-087-102A-144
152	27	93.1	40	7	US-11-087-102A-145
153	27	93.1	40	7	US-11-087-102A-146
154	27	93.1	40	7	US-11-087-102A-147
155	27	93.1	40	7	US-11-087-102A-148
156	27	93.1	40	7	US-11-087-102A-149
157	27	93.1	40	7	US-11-087-102A-150
158	27	93.1	40	7	US-11-087-102A-151
159	27	93.1	40	7	US-11-087-102A-152
160	27	93.1	40	7	US-11-087-102A-153
161	27	93.1	40	7	US-11-087-102A-154
162	27	93.1	40	7	US-11-087-102A-155
163	27	93.1	40	7	US-11-087-102A-156
164	27	93.1	40	7	US-11-087-102A-157
165	27	93.1	40	7	US-11-087-102A-158
166	27	93.1	40	7	US-11-087-102A-159
167	27	93.1	40	7	US-11-087-102A-160
168	27	93.1	40	7	US-11-087-102A-161
169	27	93.1	40	7	US-11-087-102A-162
170	27	93.1	40	7	US-11-087-102A-163
171	27	93.1	40	7	US-11-087-102A-164
172	27	93.1	40	7	US-11-087-102A-165
173	27	93.1	40	7	US-11-087-102A-166

99	22	75.9	306	7	US-11-045-004-2097	Sequence 2097, Ap	172	20	69.0	99	7	US-11-264-096-1972	Sequence 1972, Ap
100	22	75.9	316	7	US-11-045-004-1254	Sequence 1254, Ap	173	20	69.0	104	6	US-10-395-463A-28	Sequence 28, Appl
101	22	75.9	335	6	US-10-556-060-357	Sequence 357, App	174	20	69.0	109	7	US-11-264-096-1507	Sequence 1507, Ap
102	22	75.9	344	6	US-10-964-241B-376	Sequence 376, App	175	20	69.0	109	7	US-11-264-096-1509	Sequence 1509, Ap
103	22	75.9	344	7	US-11-290-153-376	Sequence 376, App	176	20	69.0	111	6	US-10-031-158B-15	Sequence 15, Appl
104	22	75.9	347	8	US-60-742-219-2754	Sequence 2754, Ap	177	20	69.0	115	8	US-60-742-219-524	Sequence 524, App
105	22	75.9	370	7	US-11-268-745-7	Sequence 7, Appli	178	20	69.0	123	6	US-10-868-184C-2907	Sequence 2907, Ap
106	22	75.9	412	7	US-11-264-096-1676	Sequence 1676, Ap	179	20	69.0	153	6	US-10-206-921A-232	Sequence 232, App
107	22	75.9	463	7	US-11-045-004-1257	Sequence 1257, Ap	180	20	69.0	155	7	US-11-122-396-23	Sequence 23, Appl
108	22	75.9	517	7	US-11-296-657-20	Sequence 20, Appl	181	20	69.0	158	7	US-11-266-446-54	Sequence 54, Appl
109	22	75.9	576	7	US-11-292-951-18	Sequence 18, Appl	182	20	69.0	177	6	US-10-018-470B-65	Sequence 65, Appl
110	22	75.9	589	7	US-11-296-657-40	Sequence 40, Appl	183	20	69.0	184	7	US-11-123-692-109	Sequence 109, App
111	22	75.9	599	7	US-11-302-678-5	Sequence 5, Appli	184	20	69.0	187	6	US-10-018-470B-85	Sequence 85, Appl
112	22	75.9	1475	7	US-11-045-004-1602	Sequence 1602, Ap	185	20	69.0	187	7	US-11-045-004-2114	Sequence 2114, Ap
113	22	75.9	2014	8	US-60-742-219-1856	Sequence 1856, Ap	186	20	69.0	190	6	US-10-395-463A-26	Sequence 26, Appl
114	22	75.9	3906	8	US-60-748-312-1	Sequence 1, Appli	187	20	69.0	214	7	US-11-284-236-213	Sequence 213, App
115	21	72.4	26	7	US-11-264-096-151	Sequence 151, App	188	20	69.0	217	7	US-11-144-347A-570	Sequence 570, App
116	21	72.4	50	6	US-10-868-184C-3203	Sequence 3203, Ap	189	20	69.0	226	7	US-11-045-004-608	Sequence 608, App
117	21	72.4	50	6	US-10-868-184C-3204	Sequence 3204, Ap	190	20	69.0	233	7	US-11-197-712-306	Sequence 306, App
118	21	72.4	57	6	US-10-868-184C-2645	Sequence 2645, Ap	191	20	69.0	236	7	US-11-045-004-1559	Sequence 1559, Ap
119	21	72.4	74	6	US-10-868-184C-4553	Sequence 4553, Ap	192	20	69.0	239	7	US-11-045-004-1828	Sequence 1828, Ap
120	21	72.4	125	7	US-11-045-004-2558	Sequence 2558, Ap	193	20	69.0	248	8	US-60-742-219-2486	Sequence 2486, Ap
121	21	72.4	144	7	US-11-301-554-327	Sequence 327, App	194	20	69.0	252	6	US-10-703-799B-66	Sequence 66, Appl
122	21	72.4	160	7	US-11-197-712-316	Sequence 316, App	195	20	69.0	252	7	US-11-199-489A-142	Sequence 142, App
123	21	72.4	259	7	US-60-742-871-341	Sequence 341, App	196	20	69.0	257	6	US-10-206-921A-304	Sequence 304, App
124	21	72.4	259	7	US-11-045-004-2552	Sequence 2552, Ap	197	20	69.0	257	7	US-11-264-096-198	Sequence 198, App
125	21	72.4	271	8	US-60-732-162-610	Sequence 610, App	198	20	69.0	257	7	US-11-264-096-199	Sequence 199, App
126	21	72.4	275	7	US-11-045-004-2089	Sequence 2089, Ap	199	20	69.0	257	7	US-11-045-004-1339	Sequence 1339, Ap
127	21	72.4	276	7	US-11-045-004-950	Sequence 950, App	200	20	69.0	257	8	US-60-742-219-826	Sequence 826, App
128	21	72.4	277	7	US-11-045-004-2845	Sequence 2845, Ap	201	20	69.0	258	8	US-60-742-219-16	Sequence 16, Appl
129	21	72.4	282	8	US-60-732-162-1078	Sequence 1078, Ap	202	20	69.0	277	7	US-11-264-096-1270	Sequence 1270, Ap
130	21	72.4	348	6	US-10-206-921A-94	Sequence 94, Appl	203	20	69.0	282	1	PCT-US05-40306-72	Sequence 72, Appl
131	21	72.4	348	7	US-11-045-004-602	Sequence 602, App	204	20	69.0	282	1	PCT-US05-40142-46	Sequence 46, Appl
132	21	72.4	350	8	US-60-732-162-612	Sequence 612, App	205	20	69.0	282	1	PCT-US05-40255-85	Sequence 85, Appl
133	21	72.4	388	7	US-11-045-004-36	Sequence 36, Appl	206	20	69.0	282	1	PCT-US05-40256-113	Sequence 113, App
134	21	72.4	398	6	US-10-703-799B-256	Sequence 256, App	207	20	69.0	282	7	US-11-264-737-113	Sequence 113, App
135	21	72.4	415	8	US-60-742-219-196	Sequence 196, App	208	20	69.0	282	7	US-11-265-761-85	Sequence 85, Appl
136	21	72.4	417	5	US-09-155-676C-5	Sequence 5, Appli	209	20	69.0	282	7	US-11-264-784-72	Sequence 72, Appl
137	21	72.4	431	7	US-11-045-004-790	Sequence 790, App	210	20	69.0	286	7	US-11-045-004-2832	Sequence 2832, Ap
138	21	72.4	439	7	US-11-296-657-80	Sequence 80, Appl	211	20	69.0	291	7	US-11-217-995-10	Sequence 10, Appl
139	21	72.4	453	7	US-11-296-657-74	Sequence 74, Appl	212	20	69.0	294	7	US-11-045-004-1428	Sequence 1428, Ap
140	21	72.4	457	7	US-11-045-004-111	Sequence 111, App	213	20	69.0	301	6	US-10-080-960-11	Sequence 11, Appl
141	21	72.4	502	6	US-10-779-251A-13	Sequence 13, Appl	214	20	69.0	301	6	US-10-080-960-11	Sequence 11, Appl
142	21	72.4	525	6	US-10-779-251A-12	Sequence 12, Appl	215	20	69.0	301	8	US-60-732-162-1162	Sequence 1162, Ap
143	21	72.4	544	6	US-10-703-799B-254	Sequence 254, App	216	20	69.0	310	7	US-11-217-995-11	Sequence 11, Appl
144	21	72.4	555	8	US-60-732-162-1330	Sequence 1330, Ap	217	20	69.0	310	7	US-11-045-004-1579	Sequence 1579, Ap
145	21	72.4	584	7	US-11-296-657-141	Sequence 141, Appl	218	20	69.0	314	7	US-11-045-004-136	Sequence 136, App
146	21	72.4	642	8	US-60-732-162-1414	Sequence 1414, Ap	219	20	69.0	317	7	US-11-217-995-9	Sequence 9, Appli
147	21	72.4	747	7	US-11-077-664-1	Sequence 1, Appli	220	20	69.0	317	7	US-11-217-995-30	Sequence 30, Appl
148	21	72.4	772	6	US-10-556-060-486	Sequence 486, App	221	20	69.0	321	7	US-11-045-004-1924	Sequence 1924, Ap
149	21	72.4	943	8	US-60-732-162-1420	Sequence 1420, Ap	222	20	69.0	321	7	US-11-045-004-1959	Sequence 1959, Ap
150	21	72.4	1077	6	US-10-556-060-265	Sequence 265, App	223	20	69.0	339	7	US-11-264-096-2185	Sequence 2185, Ap
151	21	72.4	1201	7	US-11-045-004-689	Sequence 689, App	224	20	69.0	339	7	US-11-264-096-2186	Sequence 2186, Ap
152	20	69.0	17	6	US-10-868-184C-4095	Sequence 4095, Ap	225	20	69.0	346	7	US-11-045-004-2385	Sequence 2385, Ap
153	20	69.0	24	7	US-11-264-096-403	Sequence 403, App	226	20	69.0	347	7	US-11-045-004-1121	Sequence 1121, Ap
154	20	69.0	28	6	US-10-250-581-14	Sequence 14, Appl	227	20	69.0	349	7	US-11-264-096-1591	Sequence 1591, Ap
155	20	69.0	28	6	US-10-250-581-17	Sequence 17, Appl	228	20	69.0	350	6	US-10-511-455-32	Sequence 32, Appl
156	20	69.0	29	6	US-10-868-184C-4775	Sequence 4775, Ap	229	20	69.0	357	7	US-11-045-004-1663	Sequence 1663, Ap
157	20	69.0	375	6	US-10-868-184C-2753	Sequence 2753, Ap	230	20	69.0	361	8	US-60-736-600-10	Sequence 10, Appl
158	20	69.0	36	6	US-10-868-184C-4759	Sequence 4759, Ap	231	20	69.0	370	7	US-11-197-712-456	Sequence 456, App
159	20	69.0	40	6	US-10-250-581-15	Sequence 15, Appl	232	20	69.0	376	8	US-60-741-048-7	Sequence 7, Appli
160	20	69.0	40	6	US-10-250-581-18	Sequence 18, Appl	233	20	69.0	376	8	US-60-742-871-202	Sequence 202, App
161	20	69.0	42	6	US-10-250-581-16	Sequence 16, Appl	234	20	69.0	377	8	US-60-732-162-322	Sequence 322, App
162	20	69.0	42	6	US-10-250-581-19	Sequence 19, Appl	235	20	69.0	382	6	US-10-206-921A-20	Sequence 20, Appl
163	20	69.0	50	6	US-10-868-184C-4304	Sequence 4304, Ap	236	20	69.0	386	7	US-11-045-004-769	Sequence 769, App
164	20	69.0	56	7	US-11-121-566A-26	Sequence 26, Appl	237	20	69.0	389	7	US-11-197-712-414	Sequence 414, App
165	20	69.0	56	7	US-11-223-699A-26	Sequence 26, Appl	238	20	69.0	389	7	US-11-077-664-2	Sequence 2, Appli
166	20	69.0	75	7	US-11-199-489A-110	Sequence 110, App	239	20	69.0	395	8	US-60-742-219-520	Sequence 520, App
167	20	69.0	88	8	US-60-742-219-1430	Sequence 1430, Ap	240	20	69.0	397	7	US-11-045-004-2019	Sequence 2019, App
168	20	69.0	89	7	US-11-264-096-1938	Sequence 1938, Ap	241	20	69.0	399	7	US-11-077-664-3	Sequence 3, Appli
169	20	69.0	89	7	US-11-264-096-1939	Sequence 1939, Ap	242	20	69.0	406	7	US-11-045-004-245	Sequence 245, App
170	20	69.0	97	7	US-11-264-096-2145	Sequence 2145, Ap	243	20	69.0	420	7	US-11-045-004-1329	Sequence 1329, Ap
171	20	69.0	99	7	US-11-264-096-1971	Sequence 1971, Ap	244	20	69.0	429	7	US-11-127-877A-51	Sequence 51, Appl


```

245 20 69.0 432 6 US-10-206-921A-74
246 20 69.0 432 6 US-10-501-841-45
247 20 69.0 436 7 US-11-296-657-68
248 20 69.0 436 7 US-11-296-657-69
249 20 69.0 436 7 US-11-296-657-70
250 20 69.0 442 7 US-11-296-657-67
251 20 69.0 442 7 US-11-296-657-77
252 20 69.0 450 7 US-11-045-004-2808
253 20 69.0 450 7 US-11-296-657-78
254 20 69.0 451 7 US-11-045-004-84
255 20 69.0 453 8 US-60-732-162-656
256 20 69.0 457 1 PCT-US05-43141-19
257 20 69.0 459 7 US-11-045-004-289
258 20 69.0 463 7 US-11-045-004-2865
259 20 69.0 463 8 US-60-741-048-420
260 20 69.0 465 8 US-60-742-219-522
261 20 69.0 466 6 US-10-206-921A-316
262 20 69.0 466 6 US-10-558-119-434
263 20 69.0 466 7 US-11-127-877A-50
264 20 69.0 466 8 US-60-742-872-59
265 20 69.0 466 8 US-60-742-872-60
266 20 69.0 466 8 US-60-742-873-19
267 20 69.0 466 8 US-60-742-873-20
268 20 69.0 470 1 PCT-US05-26647A-141
269 20 69.0 470 8 US-60-732-162-1714
270 20 69.0 472 7 US-11-191-274A-3
271 20 69.0 472 7 US-11-191-274A-5
272 20 69.0 475 6 US-10-206-921A-260
273 20 69.0 475 8 US-60-732-162-1676
274 20 69.0 477 6 US-10-964-241B-452
275 20 69.0 477 7 US-11-290-153-452
276 20 69.0 481 8 US-60-742-219-518
277 20 69.0 482 7 US-11-045-004-2698
278 20 69.0 486 7 US-11-045-004-971
279 20 69.0 493 7 US-11-045-004-828
280 20 69.0 496 6 US-10-503-253A-6
281 20 69.0 497 7 US-11-264-096-1593
282 20 69.0 497 7 US-11-264-096-1594
283 20 69.0 499 8 US-60-741-048-425
284 20 69.0 499 8 US-60-741-048-425
285 20 69.0 501 6 US-10-395-463A-24
286 20 69.0 506 1 PCT-US05-38623-2
287 20 69.0 508 7 US-11-296-657-3
288 20 69.0 509 7 US-11-264-096-2187
289 20 69.0 530 7 US-11-296-657-6
290 20 69.0 530 7 US-11-296-657-11
291 20 69.0 530 7 US-11-296-657-12
292 20 69.0 530 7 US-11-296-657-13
293 20 69.0 539 7 US-11-226-554-126
294 20 69.0 548 7 US-11-045-004-1058
295 20 69.0 562 7 US-11-045-004-2022
296 20 69.0 568 8 US-60-732-162-792
297 20 69.0 574 6 US-10-556-747-18
298 20 69.0 584 7 US-11-292-951-16
299 20 69.0 585 7 US-10-503-836-18
300 20 69.0 585 7 US-11-264-096-18

```

ALIGNMENTS

```

RESULT 1
US-11-269-857-6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (2)...(2)
; OTHER INFORMATION: methylated leucine
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)...(4)
; OTHER INFORMATION: methylated phenylalanine
; NAME/KEY: MOD_RES
; LOCATION: (6)...(6)
; OTHER INFORMATION: methylated alanine
; FEATURE:
; OTHER INFORMATION: synthetic
US-11-269-857-6
Query Match 93.1%; Score 27; DB 7; Length 7;
Best Local Similarity 83.3%; Pred. NO. 5.4e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
DB 1 KLVFFA 6

RESULT 2
US-11-291-770-20
; Sequence 20, Application US/11291770
; GENERAL INFORMATION:
; APPLICANT: FUJITSU LIMITED
; TITLE OF INVENTION: Method for predicting protein-protein interactions
; FILE REFERENCE: GP01-1001PCT
; CURRENT FILING DATE: 2005-12-02
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: JP P2000-72485
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-291-770-20
Query Match 93.1%; Score 27; DB 7; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
|:||||
DB 1 KLVFFA 6

RESULT 3
PCT-US05-32135-5
; Sequence 5, Application PC/TUS0532135
; GENERAL INFORMATION:
; APPLICANT: ORSER, CINDY S.
; APPLICANT: PAN, TAO
; TITLE OF INVENTION: IMMOBILIZED PROBES AND METHODS OF DETECTING
; FILE REFERENCE: ADL-102-PCT
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: PCT/US05/32135
; PRIOR FILING DATE: 2004-11-08

```

```
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 5
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-32135-5

Query Match          93.1%; Score 27; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.2; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KIVFFA 6
   |:||||
Db 6 KLVFFA 11

RESULT 4
PCT-US05-32135-6
; Sequence 6, Application PC/TUS0532135
; GENERAL INFORMATION:
; APPLICANT: ORSER, CINDY S.
; APPLICANT: PAN, TAO
; TITLE OF INVENTION: IMMOBILIZED PROBES AND METHODS OF DETECTING
; FILE REFERENCE: ADL-102-PCT
; CURRENT APPLICATION NUMBER: PCT/US05/32135
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: 60/608,541
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-32135-6

Query Match          93.1%; Score 27; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 3.2; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KIVFFA 6
   |:||||
Db 6 KLVFFA 11

RESULT 5
US-11-297-316-2
; Sequence 2, Application US/11297316
; GENERAL INFORMATION:
; APPLICANT: American Cyanamid Company
; TITLE OF INVENTION: Packaging of positive-strand RNA virus replicon
; FILE REFERENCE: 01142-0200-00304
; CURRENT APPLICATION NUMBER: US/11/297,316
; CURRENT FILING DATE: 2005-12-08
; PRIOR APPLICATION NUMBER: 60/228,906
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-297-316-2

Query Match          93.1%; Score 27; DB 7; Length 28;
Best Local Similarity 83.3%; Pred. No. 3.7; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KIVFFA 6
   |:||||
```

```
Db 16 KLVFFA 21

RESULT 6
US-11-194-989-19
; Sequence 19, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-194-989-19

Query Match          93.1%; Score 27; DB 7; Length 39;
Best Local Similarity 83.3%; Pred. No. 4.9; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KIVFFA 6
   |:||||
Db 16 KLVFFA 21

RESULT 7
US-11-195-207-19
; Sequence 19, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-195-207-19

Query Match          93.1%; Score 27; DB 7; Length 39;
Best Local Similarity 83.3%; Pred. No. 4.9; 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

Qy 1 KIVFFA 6
   |:||||
```

```
Db          16 KLVFFA 21

RESULT 8
PCT-US05-32135-4
; Sequence 4, Application PC/TUS0532135
; GENERAL INFORMATION:
; APPLICANT: ORSER, CINDY S.
; APPLICANT: PAN, TAO
; TITLE OF INVENTION: IMMOBILIZED PROBES AND METHODS OF DETECTING
; FILE OF INVENTION: CONFORMATIONALLY ALTERED PRION PROTEINS
; FILE REFERENCE: ADL-102-PCT
; CURRENT APPLICATION NUMBER: PCT/US05/32135
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: 60/608,541
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 4
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-32135-4

Query Match          93.1%; Score 27; DB 1; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 KIVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 9
US-10-966-919B-2
; Sequence 2, Application US/10966919B
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; APPLICANT: Sundaram, Pazhani
; APPLICANT: Kasinathan, Chinnaswamy
; TITLE OF INVENTION: Detoxification Depot for Alzheimer's Disease
; FILE REFERENCE: 7628-0001
; CURRENT APPLICATION NUMBER: US/10/966,919B
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,674
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-919B-2

Query Match          93.1%; Score 27; DB 6; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 KIVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 10
US-11-269-857-3
; Sequence 3, Application US/11269857
; GENERAL INFORMATION:
; APPLICANT: Ponara, Nunzio
; TITLE OF INVENTION: Methods and Compositions for Treatment
; FILE OF INVENTION: and Prevention of Major Depressive Disorder
; FILE REFERENCE: 1049-1-052N
; CURRENT APPLICATION NUMBER: US/11/269,857
; CURRENT FILING DATE: 2005-11-08
; PRIOR APPLICATION NUMBER: 60/625,824

; PRIOR FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/676,093
; CURRENT FILING DATE: 2005-08-01
; CURRENT APPLICATION NUMBER: US/11/194,989
; FILE REFERENCE: 514712002300
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; APPLICANT: GRIMM, Jan Markus
; APPLICANT: HO, Wei-Hsien
; APPLICANT: PONS, Jaume
; APPLICANT: ROSENTHAL, Arnon
; GENERAL INFORMATION:
; Sequence 20, Application US/11194989
US-11-194-989-20

Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 KIVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 11
US-11-194-989-15
; Sequence 15, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-194-989-15

Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          1 KIVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 12
US-11-194-989-20
; Sequence 20, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
```

```
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-20
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
        |:||||
Db      16 KLVFFA 21
```

```
RESULT 13
US-11-194-989-21
; Sequence 21, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-21
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
        |:||||
Db      16 KLVFFA 21
```

```
RESULT 14
US-11-194-989-22
; Sequence 22, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
```

```
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-22
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
        |:||||
Db      16 KLVFFA 21
```

```
RESULT 15
US-11-194-989-23
; Sequence 23, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-23
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KIVFFA 6
        |:||||
Db      16 KLVFFA 21
```

```
RESULT 16
US-11-194-989-24
; Sequence 24, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
```

```
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-24
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db      16 KLVFFA 21
```

```
RESULT 17
US-11-194-989-25
; Sequence 25, Application US/11/194,989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-194-989-25
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db      16 KLVFFA 21
```

```
RESULT 18
US-11-195-207-15
; Sequence 15, Application US/11/195,207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
```

```
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-195-207-15
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db      16 KLVFFA 21
```

```
RESULT 19
US-11-195-207-20
; Sequence 20, Application US/11/195,207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-20
```

```
Query Match          93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KLVFFA 6
        |:||||
Db      16 KLVFFA 21
```

```
RESULT 20
US-11-195-207-21
; Sequence 21, Application US/11/195,207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
```

```
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-21

Query Match      93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFA 6
Db      16 KLVFFA 21

RESULT 21
US-11-195-207-22
; Sequence 22, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-22

Query Match      93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFA 6
Db      16 KLVFFA 21

RESULT 22
US-11-195-207-23
; Sequence 23, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-23

Query Match      93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFA 6
Db      16 KLVFFA 21

RESULT 23
US-11-195-207-24
; Sequence 24, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-24

Query Match      93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KLVFFA 6
Db      16 KLVFFA 21

RESULT 24
US-11-195-207-25
; Sequence 25, Application US/11195207
```

GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-11-195-207-25

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 25
US-11-087-102A-18
; Sequence 18, Application US/11087102A
; GENERAL INFORMATION:
; APPLICANT: Vereenigde
; APPLICANT: Gebbink, Martijn F. B. G.
; APPLICANT: Bouma, Barend
; APPLICANT: Kranenburg, Onno W.
; APPLICANT: Kroon, Louise M. J.
; TITLE OF INVENTION: Cross-Beta Structure Comprising Amyloid Binding Proteins and Meth
; TITLE OF INVENTION: for Detection of the Cross-Beta Structure, for Modulating Cross-
; TITLE OF INVENTION: Structures Fibril Formation and for Modulating Cross-Beta
; TITLE OF INVENTION: Structure-Mediated Toxicity and Method for Interfering with Bloc
; TITLE OF INVENTION: Coagulation
; FILE REFERENCE: 2183-6874US
; CURRENT APPLICATION NUMBER: US/11/087,102A
; CURRENT FILING DATE: 2005-03-21
; PRIOR APPLICATION NUMBER: US 11/033,105
; PRIOR FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: PCT/NL03/00501
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: EP 02077797.5
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Peptide A Beta (1-40) from Homo sapiens
US-11-087-102A-18

Query Match 93.1%; Score 27; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 5;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||

Db 16 KLVFFA 21
|:||||

RESULT 26
US-11-194-989-18
; Sequence 18, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-194-989-18

Query Match 93.1%; Score 27; DB 7; Length 41;
Best Local Similarity 83.3%; Pred. No. 5.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 16 KLVFFA 21

RESULT 27
US-11-195-207-18
; Sequence 18, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-195-207-18

Query Match 93.1%; Score 27; DB 7; Length 41;
Best Local Similarity 83.3%; Pred. No. 5.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||

```
Db          16 KLVFFA 21

RESULT 28
US-10-966-919B-3
; Sequence 3, Application US/10966919B
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; APPLICANT: Sundaram, Pazhani
; APPLICANT: Kasinathan, Chinnaswamy
; TITLE OF INVENTION: Detoxification Depot for Alzheimer's Disease
; FILE REFERENCE: 7628-0001
; CURRENT APPLICATION NUMBER: US/10/966,919B
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,674
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-919B-3

Query Match          93.1%; Score 27; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KLVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 29
US-11-270-774-174
; Sequence 174, Application US/11270774
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/11/270,774
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/09/848,616
; PRIOR FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 174
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amyloid Beta Peptide
US-11-270-774-174

Query Match          93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KLVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 30
US-11-269-857-5
; Sequence 5, Application US/11269857
; GENERAL INFORMATION:
; APPLICANT: Pomara, Nunzio
; TITLE OF INVENTION: Methods and Compositions for Treatment
; TITLE OF INVENTION: and Prevention of Major Depressive Disorder

; FILE REFERENCE: 1049-1-052N
; CURRENT APPLICATION NUMBER: US/11/269,857
; CURRENT FILING DATE: 2005-11-08
; PRIOR APPLICATION NUMBER: 60/625,824
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-269-857-5

Query Match          93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KLVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 31
US-11-194-989-16
; Sequence 16, Application US/11194989
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002300
; CURRENT APPLICATION NUMBER: US/11/194,989
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: US 60/653,197
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/592,494
; PRIOR FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-194-989-16

Query Match          93.1%; Score 27; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy          1 KLVFFA 6
           |:||||
Db          16 KLVFFA 21

RESULT 32
US-11-195-207-16
; Sequence 16, Application US/11195207
; GENERAL INFORMATION:
; APPLICANT: ROSENTHAL, Arnon
; APPLICANT: PONS, Jaume
; APPLICANT: HO, Wei-Hsien
; APPLICANT: GRIMM, Jan Markus
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
; TITLE OF INVENTION: PEPTIDE AND METHODS USING SAME
; FILE REFERENCE: 514712002301
; CURRENT APPLICATION NUMBER: US/11/195,207
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US 60/676,093
; PRIOR FILING DATE: 2005-04-29
```



```
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION NUMBER: USN 08/548,998  
; FILING DATE: 27-OCT-1995  
; APPLICATION NUMBER: USSN 08/616,081  
; FILING DATE: 14-MAR-1996  
; APPLICATION NUMBER: USSN 08/703,675  
; FILING DATE: 27-AUG-1996  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: 21-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KARA, Catherine J.  
; REGISTRATION NUMBER: 41,106  
; REFERENCE/DOCKET NUMBER: PFI-016CP4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617)227-7400  
; TELEFAX: (617)227-5941  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 43 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
  
US-08-920-162A-1  
  
Query Match          93.1%; Score 27; DB 4; Length 43;  
Best Local Similarity 83.3%; Pred. No. 5.3;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY      1 KIVFFFA 6  
        |:||||  
DB      16 KLVFVFA 21  
  
RESULT 35  
US-10-677-076-1  
; Sequence 1, Application US/10677076  
; GENERAL INFORMATION:  
; APPLICANT: Findeis, M. et al.  
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide Aggregation Comprising D-Amino Acids  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02109-1875  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/677,076  
; FILING DATE: 30-Sep-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/920,162  
; FILING DATE: 27-AUG-1997  
; APPLICATION NUMBER: USSN 08/548,998  
; FILING DATE: 27-OCT-1995  
; APPLICATION NUMBER: USSN 08/616,081  
; FILING DATE: 14-MAR-1996  
; APPLICATION NUMBER: USSN 08/703,675  
; FILING DATE: 27-AUG-1996  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: 21-JUL-1997  
; ATTORNEY/AGENT INFORMATION:
```

```
/ NAME: KARA, Catherine J.
/ REGISTRATION NUMBER: 41,106
/ REFERENCE/DOCKET NUMBER: PPI-016CP4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617)227-7400
/ TELEFAX: (617)227-5941
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 43 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: internal
/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-677-076-1

Query Match          93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 16 KLVFFA 21

RESULT 36
US-10-966-919B-1
/ Sequence 1, Application US/10966919B
/ GENERAL INFORMATION:
/ APPLICANT: Sundaram, Stanley
/ APPLICANT: Stein, Stanley
/ APPLICANT: Sundaram, Fazhani
/ APPLICANT: Kasinathan, Chinnaswamy
/ TITLE OF INVENTION: Detoxification Depot for Alzheimer's Disease
/ FILE REFERENCE: 7628-0001
/ CURRENT APPLICATION NUMBER: US/10/966,919B
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: US 60/511,674
/ PRIOR FILING DATE: 2003-10-17
/ NUMBER OF SEQ ID NOS: 4
/ SEQ ID NO 1
/ LENGTH: 43
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-966-919B-1

Query Match          93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 16 KLVFFA 21

RESULT 37
US-10-250-581-1
/ Sequence 1, Application US/10250581
/ GENERAL INFORMATION:
/ APPLICANT: Fraunhofer Society for Promotion of Applied ...
/ TITLE OF INVENTION: Soluble cyclic analogs....
/ FILE REFERENCE: 16069
/ CURRENT APPLICATION NUMBER: US/10/250,581
/ CURRENT FILING DATE: 2004-01-14
/ NUMBER OF SEQ ID NOS: 19
/ SOFTWARE: Patent In Version 2.1
/ SEQ ID NO 1
/ LENGTH: 43
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-250-581-1

Query Match          93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

NAME: KARA, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-677-076-1

Query Match          93.1%; Score 27; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 16 KLVFFA 21

RESULT 38
US-11-194-989-17
/ Sequence 17, Application US/11194989
/ GENERAL INFORMATION:
/ APPLICANT: ROSENTHAL, Arnon
/ APPLICANT: PONS, Jaume
/ APPLICANT: HO, Wei-Hsien
/ APPLICANT: GRIMM, Jan Markus
/ TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
/ FILE REFERENCE: 514712002300
/ CURRENT APPLICATION NUMBER: US/11/194,989
/ CURRENT FILING DATE: 2005-08-01
/ PRIOR APPLICATION NUMBER: US 60/676,093
/ PRIOR FILING DATE: 2005-04-29
/ PRIOR APPLICATION NUMBER: US 60/653,197
/ PRIOR FILING DATE: 2005-02-14
/ PRIOR APPLICATION NUMBER: US 60/592,494
/ PRIOR FILING DATE: 2004-07-30
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 43
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-194-989-17

Query Match          93.1%; Score 27; DB 7; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
   |:||||
Db 16 KLVFFA 21

RESULT 39
US-11-195-207-17
/ Sequence 17, Application US/11195207
/ GENERAL INFORMATION:
/ APPLICANT: ROSENTHAL, Arnon
/ APPLICANT: PONS, Jaume
/ APPLICANT: HO, Wei-Hsien
/ APPLICANT: GRIMM, Jan Markus
/ TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST AMYLOID-BETA
/ FILE REFERENCE: 514712002301
/ CURRENT APPLICATION NUMBER: US/11/195,207
/ CURRENT FILING DATE: 2005-08-01
/ PRIOR APPLICATION NUMBER: US 60/676,093
/ PRIOR FILING DATE: 2005-04-29
/ PRIOR APPLICATION NUMBER: US 60/653,197
/ PRIOR FILING DATE: 2005-02-14
/ PRIOR APPLICATION NUMBER: US 60/592,494
/ PRIOR FILING DATE: 2004-07-30
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 43
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-195-207-17

Query Match          93.1%; Score 27; DB 7; Length 43;
Best Local Similarity 83.3%; Pred. No. 5.3;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 KLVFFA 6
Db 16 KLVFFA 21

RESULT 40
US-10-721-297-12
; Sequence 12, Application US/10721297
; GENERAL INFORMATION:
; APPLICANT: Suchof, Thomas C.
; APPLICANT: Li, Qiming
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND ASSAYS RELATED TO SECRETASE CLEAVAGE
; TITLE OF INVENTION: SPECIFICITY
; FILE REFERENCE: UN1919/4-006US
; CURRENT APPLICATION NUMBER: US/10/721,297
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 12
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homosapiens
US-10-721-297-12

Query Match 93.1%; Score 27; DB 6; Length 62;
Best Local Similarity 83.3%; Pred. No. 7.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 24 KLVFFA 29

RESULT 41
US-11-270-774-173
; Sequence 173, Application US/11270774
; GENERAL INFORMATION:
; APPLICANT: Sebbel, Peter
; APPLICANT: Dunant, Nicolas
; APPLICANT: Bachmann, Martin
; APPLICANT: Tissot, Alain
; APPLICANT: Lechner, Franziska
; TITLE OF INVENTION: Molecular Antigen Array
; FILE REFERENCE: 1700.0180002
; CURRENT APPLICATION NUMBER: US/11/270,774
; CURRENT FILING DATE: 2005-11-10
; PRIOR APPLICATION NUMBER: US/09/848,616
; PRIOR FILING DATE: 2001-05-05
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 173
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-270-774-173

Query Match 93.1%; Score 27; DB 7; Length 82;
Best Local Similarity 83.3%; Pred. No. 9.4;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 33 KLVFFA 38

RESULT 42
US-08-920-162A-2
; Sequence 2, Application US/08920162A
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide
Aggregation Comprising D-Amino Acids

NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/920,162A
FILING DATE: 27-Aug-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/548,998
FILING DATE: 27-OCT-1995
APPLICATION NUMBER: USSN 08/616,081
FILING DATE: 14-MAR-1996
APPLICATION NUMBER: USSN 08/703,675
FILING DATE: 27-AUG-1996
APPLICATION NUMBER: <Unknown>
FILING DATE: 21-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: KARA, Catherine J.
REGISTRATION NUMBER: 41,106
REFERENCE/DOCKET NUMBER: PPI-016CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-920-162A-2

Query Match 93.1%; Score 27; DB 4; Length 103;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLVFFA 6
Db 20 KLVFFA 25

RESULT 43
US-10-677-076-2
; Sequence 2, Application US/10677076
; GENERAL INFORMATION:
; APPLICANT: Findeis, M. et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid
Peptide
Aggregation Comprising D-Amino Acids
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/677,076
; FILING DATE: 30-Sep-2003
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,162
; FILING DATE: 27-AUG-1997
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; APPLICATION NUMBER: USSN 08/616,081
; FILING DATE: 14-MAR-1996
; APPLICATION NUMBER: USSN 08/703,675
; FILING DATE: 27-AUG-1996
; APPLICATION NUMBER: <Unknown>
; FILING DATE: 21-JUL-1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: KARA, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: PPI-016CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-677-076-2

Query Match      93.1%; Score 27; DB 6; Length 103;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      20 KLVFFA 25

RESULT 44
US-60-742-871-82
; Sequence 82, Application US/60742871
; GENERAL INFORMATION:
; APPLICANT: Steve RUBEN et al.
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001652
; CURRENT APPLICATION NUMBER: US/60/742,871
; CURRENT FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-742-871-82

Query Match      93.1%; Score 27; DB 8; Length 639;
Best Local Similarity 83.3%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      556 KLVFFA 561

RESULT 45
US-60-742-871-80
; Sequence 80, Application US/60742871
; GENERAL INFORMATION:
; APPLICANT: Steve RUBEN et al.
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001652
; CURRENT APPLICATION NUMBER: US/60/742,871
; CURRENT FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-742-871-80

Query Match      93.1%; Score 27; DB 8; Length 695;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      612 KLVFFA 617

RESULT 46
US-11-220-372-313
; Sequence 313, Application US/11220372
; GENERAL INFORMATION:
; APPLICANT: BERTHET, FRANCOIS XAVIER
; APPLICANT: CASADEVALI, FRANCESC VAYREDA
; APPLICANT: SANZ MARIA, MARIA CRUZ
; APPLICANT: GARCIA, TERESA LLOP
; APPLICANT: OLLE, ANGELS MOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN INFECTION
; FILE REFERENCE: INL-084CP
; CURRENT APPLICATION NUMBER: US/11/220,372
; CURRENT FILING DATE: 2005-09-06
; PRIOR APPLICATION NUMBER: PCT/ES05/00355
; PRIOR FILING DATE: 2005-06-23
; PRIOR APPLICATION NUMBER: US 11/116,144
; PRIOR FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: PCT/ES04/00581
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: EP 03 380 307.3
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 313
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-220-372-313

Query Match      93.1%; Score 27; DB 7; Length 751;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      668 KLVFFA 673

RESULT 47
US-60-742-871-81
; Sequence 81, Application US/60742871
; GENERAL INFORMATION:
; APPLICANT: Steve RUBEN et al.
; TITLE OF INVENTION: BREAST DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL001652
; CURRENT APPLICATION NUMBER: US/60/742,871
; CURRENT FILING DATE: 2005-12-07
; NUMBER OF SEQ ID NOS: 1274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-742-871-81
```

US-60-742-871-81

Query Match 93.1%; Score 27; DB 8; Length 751;
Best Local Similarity 83.3%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

Db 668 KLVFFA 673

RESULT 48

US-11-270-774-172
Sequence 172, Application US/11270774

GENERAL INFORMATION:

APPLICANT: Sebbel, Peter
APPLICANT: Dunant, Nicolas
APPLICANT: Bachmann, Martin
APPLICANT: Tissot, Alain
APPLICANT: Lechner, Franziska
TITLE OF INVENTION: Molecular Antigen Array
FILE REFERENCE: 1700.0180002
CURRENT APPLICATION NUMBER: US/11/270,774
CURRENT FILING DATE: 2005-11-10
PRIOR APPLICATION NUMBER: US/09/848,616
PRIOR FILING DATE: 2001-05-05
NUMBER OF SEQ ID NOS: 186
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 172
LENGTH: 770
TYPE: PRT
ORGANISM: Homo Sapiens
US-11-270-774-172

Query Match 93.1%; Score 27; DB 7; Length 770;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

Db 687 KLVFFA 692

RESULT 49

US-10-868-184C-4923
Sequence 4923, Application US/10868184C
GENERAL INFORMATION:
APPLICANT: Rosen, et. al
TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS805
CURRENT APPLICATION NUMBER: US/10/868,184C
CURRENT FILING DATE: 2004-06-16
PRIOR APPLICATION NUMBER: 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/833,245
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: PCT/US01/11988
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: PCT/US00/06043
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: PCT/US00/06012
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: PCT/US00/06058
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: PCT/US00/06044
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: PCT/US00/06059
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: PCT/US00/06042
PRIOR FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: PCT/US00/06014
PRIOR FILING DATE: 2000-03-09
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 13046
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4923
LENGTH: 34
TYPE: PRT
ORGANISM: Homo sapiens
US-10-868-184C-4923

Query Match 86.2%; Score 25; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5

Db 7 KIVFF 11

RESULT 50

US-11-045-004-1961
Sequence 1961, Application US/11045004

GENERAL INFORMATION:
APPLICANT: BUCHRIEGER, CARMEN
APPLICANT: FRANGEUL, LIONEL
APPLICANT: COUVE, ELISABETH
APPLICANT: RUSNIOK, CHRISTOPHE
APPLICANT: PSYHI, HAFIDA
APPLICANT: DEHOUC, PIERRE
APPLICANT: DUSURGET, OLIVIER
APPLICANT: CHETOUANI, FARID
APPLICANT: NEDJARI, HAFED
APPLICANT: GLASER, PHILIPPE
APPLICANT: KUNST, FRANCK
APPLICANT: COSSART, PASCALE
APPLICANT: DANIELS, JUSTIN
APPLICANT: GOEBEL, WERNER
APPLICANT: KREFT, JURGEN
APPLICANT: KUHN, MICHAEL
APPLICANT: NG, EVA
APPLICANT: VAZQUEZ-BOLAND, ANTONIO
APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
APPLICANT: GARRIDO-GARCIA, PATRICIA
APPLICANT: TIERREZ-MARTINEZ, ALBERTO
APPLICANT: AMEND, ALEXANDRA
APPLICANT: CHAKRABORTY, TRINAD
APPLICANT: DOMANN, EUGEN
APPLICANT: HAIN, THORSTEN
APPLICANT: BERCHE, PATRICK
APPLICANT: CHARBIT, ALAIN
APPLICANT: DURANT, LIONEL
APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
APPLICANT: BAQUERO, FERNANDO
APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
APPLICANT: GOMEZ-LOPEZ, NURIA
APPLICANT: MADUENIO, ENCARN
APPLICANT: PABLOS, BETRIZ DE
APPLICANT: WEHLAND, JURGEN
APPLICANT: KARST, UWE
APPLICANT: ENTIAN, KARL-DIETER
APPLICANT: HAUF, JORG
APPLICANT: ROSE, MATTHIAS
APPLICANT: VOSS, HAMUT
TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
FILE REFERENCE: 05394.0018-02
CURRENT APPLICATION NUMBER: US/11/045,004
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: 10/637,657
PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: 10/257,023
PRIOR FILING DATE: 2002-10-08
PRIOR APPLICATION NUMBER: PCT/FR01/01118
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: FR 00/04,629
PRIOR FILING DATE: 2000-04-11

```
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1961
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1961

Query Match      86.2%; Score 25; DB 7; Length 256;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFF 5
Db      3 KIVFF 7

RESULT 51
US-10-018-105A-6
; Sequence 6, Application US/10018105A
; GENERAL INFORMATION:
; APPLICANT: MYCOTA BIOSCIENCES INC.
; APPLICANT: ROEMER, Terry
; APPLICANT: BUSSEY, Howard
; APPLICANT: DAVISON, John
; TITLE OF INVENTION: IDENTIFICATION OF CANDIDA ALBICANS ESSENTIAL FUNGAL
; TITLE OF INVENTION: SPECIFIC GENES AND USE THEREOF IN ANTIFUNGAL DRUG
; FILE REFERENCE: 10182-015-999 (originally 12875.3)
; CURRENT APPLICATION NUMBER: US/10/018,105A
; CURRENT FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/132,878
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 844
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-018-105A-6

Query Match      86.2%; Score 25; DB 6; Length 844;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFF 5
Db      517 KIVFF 521

RESULT 52
US-11-144-947A-659
; Sequence 659, Application US/11144947A
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947A
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 353
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (234)
; OTHER INFORMATION: Xaa equals stop translation
US-11-144-947A-353

Query Match      82.8%; Score 24; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      176 IVFFA 180
```

```
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 659
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-947A-659

Query Match      82.8%; Score 24; DB 7; Length 60;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      56 IVFFA 60

RESULT 53
US-11-144-947A-353
; Sequence 353, Application US/11144947A
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947A
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 353
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (234)
; OTHER INFORMATION: Xaa equals stop translation
US-11-144-947A-353

Query Match      82.8%; Score 24; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 IVFFA 6
Db      176 IVFFA 180
```

RESULT 54

US-10-868-184C-3591
 ; Sequence 3591, Application US/10868184C
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen, et. al
 ; TITLE OF INVENTION: Human Secreted Proteins
 ; FILE REFERENCE: PS805
 ; CURRENT APPLICATION NUMBER: US/10/868,184C
 ; CURRENT FILING DATE: 2004-06-16
 ; PRIOR APPLICATION NUMBER: 60/278,650
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: 09/833,245
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: PCT/US01/11988
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: PCT/US00/06043
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06012
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06058
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06044
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06059
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06042
 ; PRIOR FILING DATE: 2000-03-09
 ; PRIOR APPLICATION NUMBER: PCT/US00/06014
 ; PRIOR FILING DATE: 2000-03-09
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 13046
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3591
 ; LENGTH: 399
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-868-184C-3591

Query Match 82.8%; Score 24; DB 6; Length 399;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
 |||||
 Db 279 IVFFA 283

RESULT 55

US-11-045-004-728
 ; Sequence 728, Application US/11045004
 ; GENERAL INFORMATION:
 ; APPLICANT: BUCHRIESEN, CARMEN
 ; APPLICANT: FRANGEUL, LIONEL
 ; APPLICANT: COUVE, ELISABETH
 ; APPLICANT: RUSNIOK, CHRISTOPHE
 ; APPLICANT: FSIHI, HAFIDA
 ; APPLICANT: DEHOUX, PIERRE
 ; APPLICANT: DUSSURGET, OLIVIER
 ; APPLICANT: CHETOUANI, FARID
 ; APPLICANT: NEDJARI, HAFED
 ; APPLICANT: GLASER, PHILIPPE
 ; APPLICANT: KUNST, FRANK
 ; APPLICANT: COSSART, PASCALE
 ; APPLICANT: DANIELS, JUSTIN
 ; APPLICANT: GOEBEL, WERNER
 ; APPLICANT: KREFT, JURGEN
 ; APPLICANT: KUHN, MICHAEL
 ; APPLICANT: NG, EVA
 ; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
 ; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
 ; APPLICANT: GARRIDO-GARCIA, PATRICIA

APPLICANT: TIERREZ-MARTINEZ, ALBERTO
 APPLICANT: AMEND, ALEXANDRA
 APPLICANT: CHAKRABORTY, TRINAD
 APPLICANT: DOMANN, EUGEN
 APPLICANT: HAIN, THORSTEN
 APPLICANT: BERCHE, PATRICK
 APPLICANT: CHARBIT, ALAIN
 APPLICANT: DURANT, LIONEL
 APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
 APPLICANT: BAQUERO, FERNANDO
 APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
 APPLICANT: GOMEZ-LOPEZ, NURIA
 APPLICANT: MADUENIO, ENCARNIA
 APPLICANT: PABLOS, BETRIZ DE
 APPLICANT: WEHLAND, JURGEN
 APPLICANT: KARST, UWE
 APPLICANT: ENTIAN, KARL-DIETER
 APPLICANT: HAUF, JORG
 APPLICANT: ROSE, MATTHIAS
 APPLICANT: VOSS, HAMUT
 ; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
 ; FILE REFERENCE: 05394.0018-02
 ; CURRENT APPLICATION NUMBER: US/11/045,004
 ; CURRENT FILING DATE: 2005-01-28
 ; PRIOR APPLICATION NUMBER: 10/637,657
 ; PRIOR FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: 10/257,023
 ; PRIOR FILING DATE: 2002-10-08
 ; PRIOR APPLICATION NUMBER: PCT/FR01/01118
 ; PRIOR FILING DATE: 2001-04-11
 ; PRIOR APPLICATION NUMBER: FR 00/04,629
 ; PRIOR FILING DATE: 2000-04-11
 ; NUMBER OF SEQ ID NOS: 2854
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 728
 ; LENGTH: 435
 ; TYPE: PRT
 ; ORGANISM: Listeria monocytogenes
 US-11-045-004-728

Query Match 82.8%; Score 24; DB 7; Length 435;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
 |||||
 Db 35 IVFFA 39

RESULT 56

US-11-045-004-1192
 ; Sequence 1192, Application US/11045004
 ; GENERAL INFORMATION:
 ; APPLICANT: BUCHRIESEN, CARMEN
 ; APPLICANT: FRANGEUL, LIONEL
 ; APPLICANT: COUVE, ELISABETH
 ; APPLICANT: RUSNIOK, CHRISTOPHE
 ; APPLICANT: FSIHI, HAFIDA
 ; APPLICANT: DEHOUX, PIERRE
 ; APPLICANT: DUSSURGET, OLIVIER
 ; APPLICANT: CHETOUANI, FARID
 ; APPLICANT: NEDJARI, HAFED
 ; APPLICANT: GLASER, PHILIPPE
 ; APPLICANT: KUNST, FRANK
 ; APPLICANT: COSSART, PASCALE
 ; APPLICANT: DANIELS, JUSTIN
 ; APPLICANT: GOEBEL, WERNER
 ; APPLICANT: KREFT, JURGEN
 ; APPLICANT: KUHN, MICHAEL
 ; APPLICANT: NG, EVA
 ; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
 ; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
 ; APPLICANT: GARRIDO-GARCIA, PATRICIA

; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARNIA
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUP, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1192
; LENGTH: 574
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-11-045-004-1192

Query Match 82.8%; Score 24; DB 7; Length 574;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:|||||
Db 521 RLVFFA 526

RESULT 57
US-11-302-994-13
; Sequence 13, Application US/11302994
; GENERAL INFORMATION:
; APPLICANT: BOGA, RAMESH BABU
; APPLICANT: MALIK, SOHAIL
; APPLICANT: QUIRK, STEPHEN
; TITLE OF INVENTION: MATERIALS FOR INHIBITING COMPLEXATION OF C-REACTIVE
; FILE REFERENCE: KCX-1105
; CURRENT APPLICATION NUMBER: US/11/302,994
; CURRENT FILING DATE: 2005-12-14
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 13
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-302-994-13

Query Match 82.8%; Score 24; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
:|||||
Db 531 KAVFFA 536

RESULT 58
US-10-964-241B-230
; Sequence 230, Application US/10964241B
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary B.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C33
; CURRENT APPLICATION NUMBER: US/10/964,241B
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US/10/123,236
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 230
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-964-241B-230

Query Match 82.8%; Score 24; DB 6; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IVFFA 6
:|||||
Db 557 IVFFA 561

RESULT 59
US-11-290-153-230
; Sequence 230, Application US/11290153
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C321
; CURRENT APPLICATION NUMBER: US/11/290,153
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: US/10/146,728
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 230
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-290-153-230

Query Match 82.8%; Score 24; DB 7; Length 677;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
| | | | |
DB 557 IVFFA 561

RESULT 60
US-10-556-060-220
; Sequence 220, Application US/10556060
; GENERAL INFORMATION:
; APPLICANT: MEINKE, ANDREAS
; APPLICANT: NAGY, ESZTER
; APPLICANT: HANNER, MARKUS
; APPLICANT: HORKY, MARKUS
; APPLICANT: KALLEND, SABINE
; APPLICANT: FRUSTOMERSKY, SONJA
; TITLE OF INVENTION: S. AGALACTIAE ANTIGENS I + II
; FILE REFERENCE: SONN:080US
; CURRENT APPLICATION NUMBER: US/10/556,060
; CURRENT FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: PCT/EP2004/004856

; PRIOR FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 03450112.2
; PRIOR FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: 03450266.6
; PRIOR FILING DATE: 2003-11-28
; NUMBER OF SEQ ID NOS: 514
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 220
; LENGTH: 1241
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-556-060-220

Query Match 82.8%; Score 24; DB 6; Length 1241;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KIVFFA 6
| | | | |
DB 80 KVFFA 85

RESULT 61
US-10-966-919B-4
; Sequence 4, Application US/10966919B
; GENERAL INFORMATION:
; APPLICANT: Stein, Stanley
; APPLICANT: Sundaram, Pazhani
; APPLICANT: Kasinathan, Chinnaswamy
; TITLE OF INVENTION: Detoxification Depot for Alzheimer's Disease
; FILE REFERENCE: 7628-0001
; CURRENT APPLICATION NUMBER: US/10/966,919B
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/511,674
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-919B-4

Query Match 79.3%; Score 23; DB 6; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.4e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
| | | | |
DB 1 KLVFF 5

RESULT 62
US-11-269-857-7
; Sequence 7, Application US/11269857
; GENERAL INFORMATION:
; APPLICANT: Pomara, Nunzio
; TITLE OF INVENTION: Methods and Compositions for Treatment
; FILE REFERENCE: 1049-1-052N
; CURRENT APPLICATION NUMBER: US/11/269,857
; CURRENT FILING DATE: 2005-11-08
; PRIOR APPLICATION NUMBER: 60/625,824
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-11-269-857-7

```
Query Match          79.3%; Score 23; DB 7; Length 5;
Best Local Similarity 80.0%; Pred. No. 5.4e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFF 5
Db 1 KLVFF 5

RESULT 63
PCT-US05-12482A-5
; Sequence 5, Application PC/TUS0512482A
; GENERAL INFORMATION:
; APPLICANT: THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK
; APPLICANT: CORNELL RESEARCH FOUNDATION, INC.
; APPLICANT: YAN, SHI DU
; APPLICANT: STERN, DAVID M
; APPLICANT: LUSTBADER, JOYCE W
; APPLICANT: HAO, WU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING ABAD/aa PROTEIN INTERACTI
; FILE REFERENCE: 68545-PCT/JPW/JW
; CURRENT APPLICATION NUMBER: PCT/US05/12482A
; CURRENT FILING DATE: 2005-04-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human
PCT-US05-12482A-5

Query Match          79.3%; Score 23; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 20;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFF 5
Db 16 KLVFF 20

RESULT 64
US-10-868-184C-4123
; Sequence 4123, Application US/10868184C
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS805
; CURRENT APPLICATION NUMBER: US/10/868,184C
; CURRENT FILING DATE: 2004-06-16
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: PCT/US01/11988
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06043
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06059
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06042
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: PCT/US00/06014
; PRIOR FILING DATE: 2000-03-09
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13046
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4123
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-184C-3208

Query Match          79.3%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 43;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLVFF 5
Db 5 KLVFF 9

RESULT 66
US-11-045-004-2209
; Sequence 2209, Application US/11045004
; GENERAL INFORMATION:
; APPLICANT: BUCHRIEGER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSTHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
```

```
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCAL
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAGABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHE, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; APPLICANT: TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2209
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; US-11-045-004-2209

Query Match 79.3%; Score 23; DB 7; Length 77;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVFFA 6
Db 63 VVFFA 67

RESULT 67
US-11-144-947A-503
; Sequence 503, Application US/11144947A
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2C2
; CURRENT APPLICATION NUMBER: US/11/144,947A
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 09/882,171
; PRIOR FILING DATE: 2005-06-03
; PRIOR APPLICATION NUMBER: 09/809,391
```

```
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/190,068
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 10/164,861
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
; PRIOR FILING DATE: 1997-03-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 503
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: Xaa equals stop translation
; US-11-144-947A-503

Query Match 79.3%; Score 23; DB 7; Length 147;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
Db 34 KVIFP 38

RESULT 68
US-11-268-554-406
; Sequence 406, Application US/11268554
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno et al.
; TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND USES
; FILE REFERENCE: CL001557
; CURRENT APPLICATION NUMBER: US/11/268,554
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 1004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 406
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-268-554-406

Query Match 79.3%; Score 23; DB 7; Length 166;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFF 5
Db 130 KVIFP 134

RESULT 69
US-60-741-051-80
; Sequence 80, Application US/60741051
; GENERAL INFORMATION:
; APPLICANT: BIRSE, Charles et al.
; TITLE OF INVENTION: BREAST CANCER SECRETED TARGETS AND USES
; THEREOF
```

```
; FILE REFERENCE: CL001625
; CURRENT APPLICATION NUMBER: US/60/741,051
; CURRENT FILING DATE: 2005-12-01
; NUMBER OF SEQ ID NOS: 526
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-741-051-80

Query Match      79.3%; Score 23; DB 8; Length 166;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFF 5
Db 130 KIVFF 134

RESULT 70
US-11-264-096-399
; Sequence 399, Application US/11264096
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 399
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-399

Query Match      79.3%; Score 23; DB 7; Length 183;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 6 KISFFA 11

RESULT 71
US-11-264-096-1048
; Sequence 1048, Application US/11264096
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1

; FILE REFERENCE: CL001625
; CURRENT APPLICATION NUMBER: US/60/741,051
; CURRENT FILING DATE: 2005-12-01
; NUMBER OF SEQ ID NOS: 526
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1048
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1048

Query Match      79.3%; Score 23; DB 7; Length 183;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 6 KISFFA 11

RESULT 72
US-11-264-096-1049
; Sequence 1049, Application US/11264096
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF546D1
; CURRENT APPLICATION NUMBER: US/11/264,096
; CURRENT FILING DATE: 2005-11-02
; PRIOR APPLICATION NUMBER: 09/833,245
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/229, 358
; PRIOR FILING DATE: 2000-04-12
; PRIOR APPLICATION NUMBER: 60/256, 931
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/199, 384
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 2267
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1049
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-264-096-1049

Query Match      79.3%; Score 23; DB 7; Length 183;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 6 KISFFA 11

RESULT 73
US-10-964-241B-410
; Sequence 410, Application US/10964241B
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Deanovers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC33
```

```

; CURRENT APPLICATION NUMBER: US/10/964, 241B
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US/10/123, 236
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 410
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-964-241B-410

Query Match          79.3%; Score 23; DB 6; Length 229;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVVF 5
Db      118 KVIFF 122

RESULT 74
US-11-290-153-410
; Sequence 410, Application US/11290153
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: DeNovo, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C321
; CURRENT APPLICATION NUMBER: US/11/290,153
; CURRENT FILING DATE: 2005-11-30
; PRIOR APPLICATION NUMBER: US/10/146,728
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17

```

```

; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 410
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-290-153-410

Query Match          79.3%; Score 23; DB 7; Length 229;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVVF 5
Db      118 KVIFF 122

RESULT 75
US-11-289-102-222
; Sequence 222, Application US/11289102
; GENERAL INFORMATION:
; APPLICANT: Lee, Hyerim
; APPLICANT: Shaw, Peter M.
; APPLICANT: Clark, Edwin
; TITLE OF INVENTION: BIOMARKERS AND METHODS FOR DETERMINING SENSITIVITY TO
; FILE REFERENCE: 10338 NP
; CURRENT APPLICATION NUMBER: US/11/289,102
; CURRENT FILING DATE: 2005-11-29
; PRIOR APPLICATION NUMBER: US 60/631,993
; PRIOR FILING DATE: 2004-11-30
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: Patentih version 3.3
; SEQ ID NO 222
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-289-102-222

Query Match          79.3%; Score 23; DB 7; Length 229;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVVF 5
Db      118 KVIFF 122

Search completed: December 29, 2005, 18:38:05
Job time : 13.5806 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:19:12 ; Search time 258.871 Seconds
(without alignments)
32.030 Million cell updates/sec

Title: US-10-009-122-1

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Pending Patents AA Main:*

1: /cgn2_6/ptodata/1/paa/US080 COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US081 COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US082 COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US083 COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US084 COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US085 COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US086 COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US087 COMB.pep:*

9: /cgn2_6/ptodata/1/paa/US088 COMB.pep:*

10: /cgn2_6/ptodata/1/paa/US089 COMB.pep:*

11: /cgn2_6/ptodata/1/paa/US090 COMB.pep:*

12: /cgn2_6/ptodata/1/paa/US091 COMB.pep:*

13: /cgn2_6/ptodata/1/paa/US092 COMB.pep:*

14: /cgn2_6/ptodata/1/paa/US093 COMB.pep:*

15: /cgn2_6/ptodata/1/paa/US094 COMB.pep:*

16: /cgn2_6/ptodata/1/paa/US095 COMB.pep:*

17: /cgn2_6/ptodata/1/paa/US096 COMB.pep:*

18: /cgn2_6/ptodata/1/paa/US097 COMB.pep:*

19: /cgn2_6/ptodata/1/paa/US098 COMB.pep:*

20: /cgn2_6/ptodata/1/paa/US099 COMB.pep:*

21: /cgn2_6/ptodata/1/paa/US100 COMB.pep:*

22: /cgn2_6/ptodata/1/paa/US101 COMB.pep:*

23: /cgn2_6/ptodata/1/paa/US102 COMB.pep:*

24: /cgn2_6/ptodata/1/paa/US103 COMB.pep:*

25: /cgn2_6/ptodata/1/paa/US104 COMB.pep:*

26: /cgn2_6/ptodata/1/paa/US105 COMB.pep:*

27: /cgn2_6/ptodata/1/paa/US106 COMB.pep:*

28: /cgn2_6/ptodata/1/paa/US107 COMB.pep:*

29: /cgn2_6/ptodata/1/paa/US108 COMB.pep:*

30: /cgn2_6/ptodata/1/paa/US109 COMB.pep:*

31: /cgn2_6/ptodata/1/paa/US110 COMB.pep:*

32: /cgn2_6/ptodata/1/paa/US111 COMB.pep:*

33: /cgn2_6/ptodata/1/paa/US112 COMB.pep:*

34: /cgn2_6/ptodata/1/paa/US113 COMB.pep:*

35: /cgn2_6/ptodata/1/paa/US114 COMB.pep:*

36: /cgn2_6/ptodata/1/paa/US115 COMB.pep:*

37: /cgn2_6/ptodata/1/paa/US116 COMB.pep:*

38: /cgn2_6/ptodata/1/paa/US117 COMB.pep:*

39: /cgn2_6/ptodata/1/paa/US118 COMB.pep:*

40: /cgn2_6/ptodata/1/paa/US119 COMB.pep:*

41: /cgn2_6/ptodata/1/paa/US120 COMB.pep:*

42: /cgn2_6/ptodata/1/paa/US121 COMB.pep:*

43: /cgn2_6/ptodata/1/paa/US122 COMB.pep:*

44: /cgn2_6/ptodata/1/paa/US600 COMB.pep:*

45: /cgn2_6/ptodata/1/paa/US601 COMB.pep:*

46: /cgn2_6/ptodata/1/paa/US602 COMB.pep:*

47: /cgn2_6/ptodata/1/paa/US603 COMB.pep:*

48: /cgn2_6/ptodata/1/paa/US604 COMB.pep:*

49: /cgn2_6/ptodata/1/paa/US605 COMB.pep:*

50: /cgn2_6/ptodata/1/paa/US606 COMB.pep:*

51: /cgn2_6/ptodata/1/paa/US607 COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	27	US-09-724-842-9 Sequence 9, Appl
2	29	100.0	6	27	US-09-724-842-17 Sequence 17, Appl
3	29	100.0	6	27	US-09-724-842A-9 Sequence 9, Appl
4	29	100.0	6	27	US-09-724-842A-17 Sequence 17, Appl
5	29	100.0	6	28	US-09-867-847-11 Sequence 11, Appl
6	29	100.0	6	28	US-09-867-847-19 Sequence 19, Appl
7	29	100.0	6	28	US-09-867-847A-11 Sequence 11, Appl
8	29	100.0	6	28	US-09-867-847A-19 Sequence 19, Appl
9	29	100.0	6	29	US-09-915-092-1 Sequence 1, Appl
10	29	100.0	6	29	US-09-915-092-9 Sequence 9, Appl
11	29	100.0	6	30	US-10-009-122-1 Sequence 1, Appl
12	29	100.0	6	30	US-10-009-122-10 Sequence 10, Appl
13	29	100.0	6	37	US-10-705-028-1 Sequence 1, Appl
14	29	100.0	6	37	US-10-705-028-10 Sequence 10, Appl
15	29	100.0	6	37	US-10-728-028-1 Sequence 1, Appl
16	29	100.0	6	37	US-10-728-028-9 Sequence 9, Appl
17	29	100.0	6	38	US-10-825-958-9 Sequence 9, Appl
18	29	100.0	6	38	US-10-825-958-17 Sequence 17, Appl
19	29	100.0	58	34	US-10-425-115-280164 Sequence 280164, Ap
20	29	100.0	90	34	US-10-424-599-165325 Sequence 165325, Ap
21	29	100.0	93	34	US-10-424-599-240310 Sequence 240310, Ap
22	29	100.0	99	1	PCT-US01-08631-56957 Sequence 56957, A
23	29	100.0	99	34	US-10-450-763-56957 Sequence 56957, A
24	29	100.0	690	49	US-60-581-351-2850 Sequence 2850, Ap
25	29	100.0	698	49	US-60-581-351-2835 Sequence 2835, Ap
26	29	96.6	6	27	US-09-724-842-16 Sequence 16, Appl
27	28	96.6	6	27	US-09-724-842-24 Sequence 24, Appl
28	28	96.6	6	27	US-09-724-842A-16 Sequence 16, Appl
29	28	96.6	6	27	US-09-724-842A-24 Sequence 24, Appl
30	28	96.6	6	28	US-09-867-847-18 Sequence 18, Appl
31	28	96.6	6	28	US-09-867-847-26 Sequence 26, Appl
32	28	96.6	6	28	US-09-867-847A-18 Sequence 18, Appl
33	28	96.6	6	28	US-09-867-847A-26 Sequence 26, Appl
34	28	96.6	6	29	US-09-915-092-8 Sequence 8, Appl
35	28	96.6	6	29	US-09-915-092-16 Sequence 16, Appl
36	28	96.6	6	30	US-10-009-122-9 Sequence 9, Appl
37	28	96.6	6	30	US-10-009-122-17 Sequence 17, Appl
38	28	96.6	6	37	US-10-705-028-9 Sequence 9, Appl
39	28	96.6	6	37	US-10-705-028-17 Sequence 17, Appl
40	28	96.6	6	37	US-10-728-028-8 Sequence 8, Appl
41	28	96.6	6	37	US-10-728-028-16 Sequence 16, Appl
42	28	96.6	6	38	US-10-825-958-16 Sequence 16, Appl
43	28	96.6	6	38	US-10-825-958-24 Sequence 24, Appl
44	28	96.6	37	1	PCT-US03-25626-7 Sequence 7, Appl
45	28	96.6	37	28	US-09-807-877-16 Sequence 16, Appl
46	28	96.6	37	36	US-10-641-924-7 Sequence 7, Appl
47	28	96.6	37	36	US-10-642-255-7 Sequence 7, Appl
48	28	96.6	60	34	US-10-437-963-173619 Sequence 173619, Ap
49	28	96.6	77	37	US-10-793-479-6921 Sequence 6921, Ap
50	28	96.6	87	34	US-10-437-963-133986 Sequence 133986, A
51	28	96.6	88	27	US-09-708-427-14352 Sequence 14352, A
52	28	96.6	91	27	US-09-708-427-14351 Sequence 14351, A
53	28	96.6	109	34	US-10-437-963-105773 Sequence 105773, A
54	28	96.6	112	27	US-09-733-089-9030 Sequence 9030, Ap
55	28	96.6	112	28	US-09-816-660-9030 Sequence 9030, Ap

56	28	96.6	135	34	US-10-437-363-141578	Sequence 141578,	129	28	96.6	1144	36	US-10-631-467-1388	Sequence 1388, Ap
57	28	96.6	140	27	US-09-733-089-23062	Sequence 23062, A	130	28	96.6	1144	36	US-10-631-467-1454	Sequence 1454, Ap
58	28	96.6	146	28	US-09-816-660-23062	Sequence 23062, A	131	28	96.6	1144	39	US-10-937-758A-101	Sequence 101, App
59	28	96.6	150	24	US-09-417-507-41853	Sequence 41853, A	132	28	96.6	1196	11	US-08-132-372-5	Sequence 5, Appli
60	28	96.6	158	27	US-09-733-089-23064	Sequence 23064, A	133	28	96.6	1443	26	US-09-614-150-32208	Sequence 32208, A
61	28	96.6	165	28	US-09-816-660-23064	Sequence 23064, A	134	28	96.6	1443	26	US-09-614-150A-32208	Sequence 32208, A
62	28	96.6	165	27	US-09-733-089-23060	Sequence 23060, A	135	28	96.6	1443	40	US-11-097-143-32208	Sequence 32208, A
63	28	96.6	165	28	US-09-816-660-23060	Sequence 23060, A	136	28	96.6	1443	40	US-11-097-143-32208	Sequence 32208, A
64	28	96.6	175	32	US-10-220-366A-25111	Sequence 25111, A	137	28	96.6	1640	34	US-10-437-963-109646	Sequence 109646,
65	28	96.6	175	34	US-10-437-963-122124	Sequence 122124,	138	28	96.6	1640	34	US-10-438-246-24934	Sequence 24934, A
66	28	96.6	181	27	US-09-733-089-23063	Sequence 23063, A	139	28	96.6	1764	31	US-10-155-881-25401	Sequence 25401, A
67	28	96.6	181	28	US-09-816-660-23063	Sequence 23063, A	140	28	96.6	1764	31	US-10-155-881-28754	Sequence 28754, A
68	28	96.6	186	34	US-10-481-032A-214	Sequence 214, App	141	28	96.6	1764	34	US-10-438-246-17664	Sequence 17664, A
69	28	96.6	186	34	US-10-481-032A-228	Sequence 228, App	142	28	93.1	6	15	US-08-548-998A-8	Sequence 8, Appli
70	28	96.6	188	34	US-10-437-963-172476	Sequence 172476,	143	27	93.1	6	15	US-08-548-998A-8	Sequence 8, Appli
71	28	96.6	190	1	PCT-US01-01354-11385	Sequence 11385, A	144	27	93.1	6	16	US-08-612-785-9	Sequence 9, Appli
72	28	96.6	190	27	US-09-764-905-11385	Sequence 11385, A	145	27	93.1	6	16	US-08-616-081-9	Sequence 9, Appli
73	28	96.6	190	30	US-10-092-399-11385	Sequence 11385, A	146	27	93.1	6	16	US-08-616-081A-9	Sequence 9, Appli
74	28	96.6	198	34	US-10-437-963-172452	Sequence 172452,	147	27	93.1	6	27	US-09-724-842-7	Sequence 7, Appli
75	28	96.6	199	27	US-09-733-089-23065	Sequence 23065, A	148	27	93.1	6	27	US-09-724-842-18	Sequence 18, Appl
76	28	96.6	199	28	US-09-816-660-23065	Sequence 23065, A	149	27	93.1	6	27	US-09-724-842A-7	Sequence 7, Appli
77	28	96.6	214	50	US-60-655-875-150287	Sequence 150287,	150	27	93.1	6	27	US-09-724-842A-18	Sequence 18, Appl
78	28	96.6	268	50	US-60-655-875-151925	Sequence 151925,	151	27	93.1	6	28	US-09-867-847-7	Sequence 7, Appli
79	28	96.6	416	30	US-10-055-475-14	Sequence 14, Appl	152	27	93.1	6	28	US-09-867-847-20	Sequence 20, Appl
80	28	96.6	416	40	US-11-042-922-14	Sequence 14, Appl	153	27	93.1	6	28	US-09-867-847A-7	Sequence 7, Appli
81	28	96.6	514	30	US-10-055-475-13	Sequence 13, Appl	154	27	93.1	6	28	US-09-867-847A-20	Sequence 20, Appl
82	28	96.6	514	40	US-11-042-922-13	Sequence 13, Appl	155	27	93.1	6	29	US-09-915-092-10	Sequence 10, Appl
83	28	96.6	564	26	US-09-614-150-12723	Sequence 12723, A	156	27	93.1	6	29	US-09-915-092-28	Sequence 28, Appl
84	28	96.6	564	26	US-09-614-150A-12723	Sequence 12723, A	157	27	93.1	6	29	US-09-956-625-25	Sequence 25, Appl
85	28	96.6	564	40	US-11-097-143-12723	Sequence 12723, A	158	27	93.1	6	29	US-09-972-475-9	Sequence 9, Appli
86	28	96.6	564	45	US-60-167-217-12757	Sequence 12757, A	159	27	93.1	6	29	US-09-972-475A-9	Sequence 9, Appli
87	28	96.6	564	45	US-60-173-464-10379	Sequence 10379, A	160	27	93.1	6	30	US-10-009-122-3	Sequence 3, Appli
88	28	96.6	564	45	US-60-191-637-12761	Sequence 12761, A	161	27	93.1	6	30	US-10-009-122-11	Sequence 11, Appl
89	28	96.6	564	45	US-60-191-681-10037	Sequence 10037, A	162	27	93.1	6	34	US-10-463-729-9	Sequence 9, Appli
90	28	96.6	647	27	US-09-724-676-88682	Sequence 88682, A	163	27	93.1	6	36	US-10-666-095-3	Sequence 3, Appli
91	28	96.6	647	27	US-09-724-676A-88682	Sequence 88682, A	164	27	93.1	6	36	US-10-666-095-3	Sequence 3, Appli
92	28	96.6	666	40	US-11-087-099-8103	Sequence 8103, Ap	165	27	93.1	6	37	US-10-705-028-11	Sequence 11, Appl
93	28	96.6	666	41	US-11-188-298-7496	Sequence 7496, Ap	166	27	93.1	6	37	US-10-705-028-11	Sequence 11, Appl
94	28	96.6	666	49	US-60-556-841-8103	Sequence 8103, Ap	167	27	93.1	6	37	US-10-728-028-10	Sequence 10, Appl
95	28	96.6	666	49	US-60-592-978-7496	Sequence 7496, Ap	168	27	93.1	6	37	US-10-728-028-27	Sequence 27, Appl
96	28	96.6	854	37	US-10-760-320A-3865	Sequence 3865, Ap	169	27	93.1	6	38	US-10-728-028-28	Sequence 28, Appl
97	28	96.6	854	37	US-10-760-320A-3865	Sequence 3865, Ap	170	27	93.1	6	38	US-10-825-958-7	Sequence 7, Appli
98	28	96.6	922	1	PCT-US03-28227-3501	Sequence 3501, Ap	171	27	93.1	7	1	US-10-825-958-18	Sequence 18, Appl
99	28	96.6	925	1	PCT-US03-10870-2031	Sequence 2031, Ap	172	27	93.1	7	1	PCT-US02-08803-3	Sequence 3, Appli
100	28	96.6	925	31	US-10-170-205E-28729	Sequence 28729, A	173	27	93.1	7	11	PCT-US94-10083-13	Sequence 13, Appl
101	28	96.6	925	33	US-10-370-715B-8	Sequence 8, Appli	174	27	93.1	7	11	US-08-117-927A-13	Sequence 13, Appl
102	28	96.6	925	34	US-10-408-765-2031	Sequence 2031, Ap	175	27	93.1	7	15	US-08-117-927B-13	Sequence 13, Appl
103	28	96.6	925	34	US-10-408-765A-2031	Sequence 2031, Ap	176	27	93.1	7	15	US-08-548-998-6	Sequence 6, Appli
104	28	96.6	925	36	US-10-631-467-680	Sequence 680, App	177	27	93.1	7	16	US-08-548-998A-6	Sequence 6, Appli
105	28	96.6	925	36	US-10-631-467-747	Sequence 747, App	178	27	93.1	7	16	US-08-616-081-7	Sequence 7, Appli
106	28	96.6	925	37	US-10-755-889-234	Sequence 234, App	179	27	93.1	7	17	US-08-616-081A-7	Sequence 7, Appli
107	28	96.6	925	39	US-10-930-328-9394	Sequence 9394, Ap	180	27	93.1	7	17	US-08-797-782-13	Sequence 13, Appl
108	28	96.6	925	39	US-10-930-328A-9394	Sequence 9394, Ap	181	27	93.1	7	17	US-08-797-782-13	Sequence 13, Appl
109	28	96.6	925	47	US-60-389-987-2031	Sequence 2031, Ap	182	27	93.1	7	27	US-09-724-842-10	Sequence 10, Appl
110	28	96.6	925	48	US-60-412-418-2031	Sequence 2031, Ap	183	27	93.1	7	27	US-09-724-842-25	Sequence 25, Appl
111	28	96.6	925	48	US-60-440-068-234	Sequence 234, App	184	27	93.1	7	27	US-09-724-842A-10	Sequence 10, Appl
112	28	96.6	925	48	US-60-452-680-17249	Sequence 17249, A	185	27	93.1	7	27	US-09-724-842A-25	Sequence 25, Appl
113	28	96.6	925	48	US-60-469-757-234	Sequence 234, App	186	27	93.1	7	27	US-09-724-842A-26	Sequence 26, Appl
114	28	96.6	925	48	US-60-470-166-915	Sequence 915, App	187	27	93.1	7	28	US-09-867-847-12	Sequence 12, Appl
115	28	96.6	1143	27	US-09-791-537-141966	Sequence 141966,	188	27	93.1	7	28	US-09-867-847-27	Sequence 27, Appl
116	28	96.6	1144	8	US-07-841-641A-5	Sequence 5, Appli	189	27	93.1	7	28	US-09-867-847-28	Sequence 28, Appl
117	28	96.6	1144	9	US-07-921-798A-1	Sequence 1, Appli	190	27	93.1	7	28	US-09-867-847A-12	Sequence 12, Appl
118	28	96.6	1144	9	US-07-921-798A-2	Sequence 2, Appli	191	27	93.1	7	28	US-09-867-847A-27	Sequence 27, Appl
119	28	96.6	1144	13	US-08-361-063-12	Sequence 12, Appl	192	27	93.1	7	28	US-09-867-847A-28	Sequence 28, Appl
120	28	96.6	1144	15	US-08-553-503-2	Sequence 2, Appli	193	27	93.1	7	29	US-09-915-092-2	Sequence 2, Appli
121	28	96.6	1144	27	US-09-751-708A-124	Sequence 124, App	194	27	93.1	7	29	US-09-915-092-17	Sequence 17, Appl
122	28	96.6	1144	27	US-09-791-537-141967	Sequence 141967,	195	27	93.1	7	29	US-09-915-092-18	Sequence 18, Appl
123	28	96.6	1144	27	US-09-791-537-141969	Sequence 141969,	196	27	93.1	7	29	US-09-972-475-7	Sequence 7, Appli
124	28	96.6	1144	27	US-09-791-537-141970	Sequence 141970,	197	27	93.1	7	29	US-09-972-475A-7	Sequence 7, Appli
125	28	96.6	1144	27	US-09-791-537-141971	Sequence 141971,	198	27	93.1	7	30	US-10-009-122-2	Sequence 2, Appli
126	28	96.6	1144	27	US-09-791-537-141973	Sequence 141973,	199	27	93.1	7	30	US-10-009-122-18	Sequence 18, Appl
127	28	96.6	1144	28	US-09-870-759-124	Sequence 124, App	200	27	93.1	7	30	US-10-009-122-19	Sequence 19, Appl
128	28	96.6	1144	34	US-10-428-817A-120	Sequence 120, App	201	27	93.1	7	30	US-10-030-137-3	Sequence 3, Appli

202	27	93.1	7	30	US-10-030-137A-3	Sequence 3, Appli	275	27	93.1	10	27	US-09-723-544-23	Sequence 23, Appl
203	27	93.1	7	30	US-10-030-137A-5	Sequence 5, Appli	276	27	93.1	10	27	US-09-723-544-24	Sequence 24, Appl
204	27	93.1	7	30	US-10-030-138A-4	Sequence 4, Appli	277	27	93.1	10	27	US-09-723-544-25	Sequence 25, Appl
205	27	93.1	7	30	US-10-030-138A-5	Sequence 5, Appli	278	27	93.1	10	27	US-09-723-544-26	Sequence 26, Appl
206	27	93.1	7	34	US-10-463-729-7	Sequence 7, Appli	279	27	93.1	10	27	US-09-723-544-27	Sequence 27, Appl
207	27	93.1	7	35	US-10-505-313-269	Sequence 269, App	280	27	93.1	10	27	US-09-723-544-28	Sequence 28, Appl
208	27	93.1	7	37	US-10-705-028-2	Sequence 2, Appli	281	27	93.1	10	27	US-09-723-544-29	Sequence 29, Appl
209	27	93.1	7	37	US-10-705-028-18	Sequence 18, Appli	282	27	93.1	10	27	US-09-724-288-20	Sequence 20, Appl
210	27	93.1	7	37	US-10-705-028-19	Sequence 19, Appli	283	27	93.1	10	27	US-09-724-288-21	Sequence 21, Appl
211	27	93.1	7	37	US-10-728-028-2	Sequence 2, Appli	284	27	93.1	10	27	US-09-724-288-22	Sequence 22, Appl
212	27	93.1	7	37	US-10-728-028-17	Sequence 17, Appli	285	27	93.1	10	27	US-09-724-288-23	Sequence 23, Appl
213	27	93.1	7	37	US-10-728-028-18	Sequence 18, Appli	286	27	93.1	10	27	US-09-724-288-24	Sequence 24, Appl
214	27	93.1	7	38	US-10-810-881A-128	Sequence 128, App	287	27	93.1	10	27	US-09-724-288-25	Sequence 25, Appl
215	27	93.1	7	38	US-10-825-958-10	Sequence 10, Appli	288	27	93.1	10	27	US-09-724-288-26	Sequence 26, Appl
216	27	93.1	7	38	US-10-825-958-25	Sequence 25, Appli	289	27	93.1	10	27	US-09-724-288-27	Sequence 27, Appl
217	27	93.1	7	38	US-10-825-958-26	Sequence 26, Appli	290	27	93.1	10	27	US-09-724-288-28	Sequence 28, Appl
218	27	93.1	8	1	PCT-US04-42701-51	Sequence 51, Appli	291	27	93.1	10	28	US-09-867-847A-29	Sequence 29, Appl
219	27	93.1	8	1	PCT-US04-42701-54	Sequence 54, Appli	292	27	93.1	10	29	US-09-867-847A-30	Sequence 30, Appl
220	27	93.1	8	1	PCT-US04-44093-51	Sequence 51, Appli	293	27	93.1	10	29	US-09-979-701-20	Sequence 20, Appl
221	27	93.1	8	1	PCT-US04-44093-54	Sequence 54, Appli	294	27	93.1	10	29	US-09-979-701-21	Sequence 21, Appl
222	27	93.1	8	14	US-08-478-326A-1	Sequence 1, Appli	295	27	93.1	10	29	US-09-979-701-22	Sequence 22, Appl
223	27	93.1	8	15	US-08-548-998A-4	Sequence 4, Appli	296	27	93.1	10	29	US-09-979-701-23	Sequence 23, Appl
224	27	93.1	8	15	US-08-548-998A-4	Sequence 4, Appli	297	27	93.1	10	29	US-09-979-701-24	Sequence 24, Appl
225	27	93.1	8	16	US-08-612-785-5	Sequence 5, Appli	298	27	93.1	10	37	US-10-728-028-19	Sequence 19, Appl
226	27	93.1	8	16	US-08-616-081-5	Sequence 5, Appli	299	27	93.1	10	37	US-10-728-028-20	Sequence 20, Appl
227	27	93.1	8	16	US-08-616-081A-5	Sequence 5, Appli	300	27	93.1	10	37	US-10-728-028-21	Sequence 21, Appl
228	27	93.1	8	28	US-09-850-061A-44	Sequence 44, Appli						US-10-728-028-22	Sequence 22, Appl
229	27	93.1	8	29	US-09-972-475-5	Sequence 5, Appli							
230	27	93.1	8	29	US-09-972-475-5	Sequence 5, Appli							
231	27	93.1	8	32	US-10-235-483-1	Sequence 1, Appli							
232	27	93.1	8	32	US-10-281-092-42	Sequence 42, Appli							
233	27	93.1	8	34	US-10-463-729-5	Sequence 5, Appli							
234	27	93.1	8	37	US-10-721-774-44	Sequence 44, Appli							
235	27	93.1	8	38	US-10-810-881A-125	Sequence 125, App							
236	27	93.1	8	38	US-10-817-979-73	Sequence 73, Appli							
237	27	93.1	9	1	PCT-US04-42701-45	Sequence 45, Appli							
238	27	93.1	9	1	PCT-US04-42701-48	Sequence 48, Appli							
239	27	93.1	9	1	PCT-US04-44093-45	Sequence 45, Appli							
240	27	93.1	9	1	PCT-US04-44093-48	Sequence 48, Appli							
241	27	93.1	9	8	US-07-877-675A-23	Sequence 23, Appli							
242	27	93.1	9	8	US-07-877-675A-25	Sequence 25, Appli							
243	27	93.1	9	28	US-09-867-847-9	Sequence 9, Appli							
244	27	93.1	9	28	US-09-867-847A-9	Sequence 9, Appli							
245	27	93.1	9	28	US-09-899-815-2	Sequence 2, Appli							
246	27	93.1	9	30	US-10-009-122-20	Sequence 20, Appli							
247	27	93.1	9	32	US-10-235-483-64	Sequence 64, Appli							
248	27	93.1	9	36	US-10-619-454-3	Sequence 3, Appli							
249	27	93.1	9	36	US-10-619-454-25	Sequence 25, Appli							
250	27	93.1	9	36	US-10-619-454-28	Sequence 28, Appli							
251	27	93.1	9	36	US-10-619-454-57	Sequence 57, Appli							
252	27	93.1	9	36	US-10-619-454-157	Sequence 157, App							
253	27	93.1	9	37	US-10-705-028-20	Sequence 20, Appli							
254	27	93.1	10	1	PCT-US05-29497-1	Sequence 1, Appli							
255	27	93.1	10	1	PCT-US05-38125-194	Sequence 194, App							
256	27	93.1	10	1	PCT-US05-38125-195	Sequence 195, App							
257	27	93.1	10	1	PCT-US05-38125-196	Sequence 196, App							
258	27	93.1	10	1	PCT-US05-38125-197	Sequence 197, App							
259	27	93.1	10	1	PCT-US05-38125-198	Sequence 198, App							
260	27	93.1	10	23	US-09-395-234-3	Sequence 3, Appli							
261	27	93.1	10	25	US-09-580-015-20	Sequence 20, Appli							
262	27	93.1	10	25	US-09-580-015-21	Sequence 21, Appli							
263	27	93.1	10	25	US-09-580-015-22	Sequence 22, Appli							
264	27	93.1	10	25	US-09-580-015-23	Sequence 23, Appli							
265	27	93.1	10	25	US-09-580-015-24	Sequence 24, Appli							
266	27	93.1	10	25	US-09-580-015-25	Sequence 25, Appli							
267	27	93.1	10	25	US-09-580-019-20	Sequence 20, Appli							
268	27	93.1	10	25	US-09-580-019-21	Sequence 21, Appli							
269	27	93.1	10	25	US-09-580-019-22	Sequence 22, Appli							
270	27	93.1	10	25	US-09-580-019-23	Sequence 23, Appli							
271	27	93.1	10	26	US-09-652-559B-3	Sequence 3, Appli							
272	27	93.1	10	27	US-09-723-544-20	Sequence 20, Appli							
273	27	93.1	10	27	US-09-723-544-21	Sequence 21, Appli							
274	27	93.1	10	27	US-09-723-544-22	Sequence 22, Appli							

ALIGNMENTS

RESULT 1

US-09-724-842-9

; Sequence 9, Application US/09724842

; GENERAL INFORMATION:

; APPLICANT: Chalifour, Robert

; APPLICANT: Hebert, Lise

; APPLICANT: Kong, Xiang

; APPLICANT: Gervais, Francine

; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S

; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES

; FILE REFERENCE: 14445-501

; CURRENT APPLICATION NUMBER: US/09/724,842

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: 60/168,594

; PRIOR FILING DATE: 1999-11-29

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 6

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: All D peptides

; OTHER INFORMATION: or peptidomimetics

US-09-724-842-9

Query Match 100.0%; Score 29; DB 27; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.2e+06;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 1 KIVFFA 6

RESULT 2

US-09-724-842-17

; Sequence 17, Application US/09724842

; GENERAL INFORMATION:

; APPLICANT: Chalifour, Robert

; APPLICANT: Hebert, Lise

; APPLICANT: Kong, Xiang

; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-724-842-17

Query Match 100.0%; Score 29; DB 27; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 3
US-09-724-842A-9
; Sequence 9, Application US/09724842A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-724-842A-9

Query Match 100.0%; Score 29; DB 27; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 4
US-09-724-842A-17
; Sequence 17, Application US/09724842A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi

; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842A
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-724-842A-17

Query Match 100.0%; Score 29; DB 27; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 5
US-09-867-847-11
; Sequence 11, Application US/09867847
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-11

Query Match 100.0%; Score 29; DB 28; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 6
US-09-867-847-19
; Sequence 19, Application US/09867847
; GENERAL INFORMATION:

APPLICANT: Chalfour, Robert
APPLICANT: Hebert, Lise
APPLICANT: Kong, Xianqi
APPLICANT: Gervais, Francine
TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
FILE REFERENCE: 14445-501 CIP
CURRENT APPLICATION NUMBER: US/09/867,847
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 60/168,594
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/724,842
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 19
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: All D peptides
OTHER INFORMATION: or peptidomimetics
NAME/KEY: MOD_RES
LOCATION: (6)
OTHER INFORMATION: AMIDATION
US-09-867-847-19

Query Match 100.0%; Score 29; DB 28; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
DB 1 KIVFFA 6

RESULT 7

US-09-867-847A-11
Sequence 11, Application US/09867847A
GENERAL INFORMATION:
APPLICANT: Chalfour, Robert
APPLICANT: Hebert, Lise
APPLICANT: Kong, Xianqi
APPLICANT: Gervais, Francine
TITLE OF INVENTION: Vaccine for the Prevention and Treatment
TITLE OF INVENTION: of Alzheimer's and Amyloid Related Diseases
FILE REFERENCE: 50291/005001
CURRENT APPLICATION NUMBER: US/09/867,847A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 09/724,842
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/168,594
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic, All D peptides or peptidomimetics
US-09-867-847A-11

Query Match 100.0%; Score 29; DB 28; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
DB 1 KIVFFA 6

RESULT 8

US-09-867-847A-19
Sequence 19, Application US/09867847A
GENERAL INFORMATION:
APPLICANT: Chalfour, Robert
APPLICANT: Hebert, Lise
APPLICANT: Kong, Xianqi
APPLICANT: Gervais, Francine
TITLE OF INVENTION: Vaccine for the Prevention and Treatment
TITLE OF INVENTION: of Alzheimer's and Amyloid Related Diseases
FILE REFERENCE: 50291/005001
CURRENT APPLICATION NUMBER: US/09/867,847A
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: 09/724,842
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/168,594
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic, All D peptides or peptidomimetics
NAME/KEY: MOD_RES
LOCATION: 6
OTHER INFORMATION: Amidation
US-09-867-847A-19

Query Match 100.0%; Score 29; DB 28; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
DB 1 KIVFFA 6

RESULT 9

US-09-915-092-1
Sequence 1, Application US/09915092
GENERAL INFORMATION:
APPLICANT: Gervais, Francine
APPLICANT: Kong, Xianqi
APPLICANT: Chalfour, Robert
APPLICANT: Migneault, David
TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: NBI-139
CURRENT APPLICATION NUMBER: US/09/915,092
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: 60/220,808
PRIOR FILING DATE: 2000-07-25
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 6
TYPE: PRT
ORGANISM: Homo sapiens
US-09-915-092-1

Query Match 100.0%; Score 29; DB 29; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
DB 1 KIVFFA 6

RESULT 10
US-09-915-092-9

```

; Sequence 9, Application US/09915092
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NEI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-9

Query Match      100.0%; Score 29; DB 29; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 11
US-10-009-122-1
; Sequence 1, Application US/10009122
; GENERAL INFORMATION:
; APPLICANT: NEUROCHEM INC.
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: GERVAIS, Francine
; APPLICANT: GUPTA, Ajay
; TITLE OF INVENTION: STEREOSELECTIVE ANTIFIBRILLOGENIC
; FILE REFERENCE: 14228-1PCT
; CURRENT APPLICATION NUMBER: US/10/009,122
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/132,592
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide having antifibrillogenic activity and/or
; OTHER INFORMATION: neuroprotection
US-10-009-122-1

Query Match      100.0%; Score 29; DB 30; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 12
US-10-009-122-10
; Sequence 10, Application US/10009122
; GENERAL INFORMATION:
; APPLICANT: NEUROCHEM INC.
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: GERVAIS, Francine
; APPLICANT: GUPTA, Ajay
; TITLE OF INVENTION: STEREOSELECTIVE ANTIFIBRILLOGENIC
; FILE REFERENCE: 14228-1PCT
; CURRENT APPLICATION NUMBER: US/10/009,122
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/132,592
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide having antifibrillogenic activity and/or
; OTHER INFORMATION: neuroprotection
US-10-009-122-10

Query Match      100.0%; Score 29; DB 30; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 13
US-10-705-028-1
; Sequence 1, Application US/10705028
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NEI-088CN
; CURRENT APPLICATION NUMBER: US/10/705,028
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: 09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-028-1

Query Match      100.0%; Score 29; DB 37; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KIVFFA 6

RESULT 14
US-10-705-028-10
; Sequence 10, Application US/10705028
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NEI-088CN
; CURRENT APPLICATION NUMBER: US/10/705,028
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: 09/747,408

```

; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-028-10

Query Match 100.0%; Score 29; DB 37; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
Db 1 KIVFFA 6

RESULT 15

US-10-728-028-1
; Sequence 1, Application US/10728028
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-1

Query Match 100.0%; Score 29; DB 37; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
Db 1 KIVFFA 6

RESULT 16

US-10-728-028-9
; Sequence 9, Application US/10728028
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29

; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-9

Query Match 100.0%; Score 29; DB 37; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
Db 1 KIVFFA 6

RESULT 17

US-10-825-958-9
; Sequence 9, Application US/10825958
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-9

Query Match 100.0%; Score 29; DB 38; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|||
Db 1 KIVFFA 6

RESULT 18

US-10-825-958-17
; Sequence 17, Application US/10825958
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16

; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)-
; OTHER INFORMATION: AMIDATION
US-10-825-958-17

Query Match 100.0%; Score 29; DB 38; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 1 KIVFFA 6

RESULT 19
US-10-425-115-280164
; Sequence 280164, Application US/10425115
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 280164
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_187087C.1.pep
US-10-425-115-280164

Query Match 100.0%; Score 29; DB 34; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 28 KIVFFA 33

RESULT 20
US-10-424-599-165325
; Sequence 165325, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 165325
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_120303C.1.pep
US-10-424-599-165325

Query Match 100.0%; Score 29; DB 34; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 21 KIVFFA 26

RESULT 21
US-10-424-599-240310
; Sequence 240310, Application US/10424599
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 240310
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59027C.1.pep
US-10-424-599-240310

Query Match 100.0%; Score 29; DB 34; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
| | | | |
Db 34 KIVFFA 39

RESULT 22
PCT-US01-08631-56957
; Sequence 56957, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORE2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354Z, p-value=2.452e-13, raw score
; OTHER INFORMATION: 9.06

```
; NAME/KEY: misc_feature
; LOCATION: (1)...(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
PCT-US01-08631-56957

Query Match      100.0%; Score 29; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      63 KIVFFA 68

RESULT 23
US-10-450-763-56957
; Sequence 56957, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 56957
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (13)..(62)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354Z, p-value=2.452e-13, raw score
; OTHER INFORMATION: 9.06
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(99)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-56957

Query Match      100.0%; Score 29; DB 34; Length 99;
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      63 KIVFFA 68

RESULT 24
US-60-581-351-2850
; Sequence 2850, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2850
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Tropheryma whipplei TW08/27

US-60-581-351-2850
Query Match      100.0%; Score 29; DB 49; Length 690;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      526 KIVFFA 531

RESULT 25
US-60-581-351-2835
; Sequence 2835, Application US/60581351
; GENERAL INFORMATION:
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
; FILE REFERENCE: 38-21(53372)B
; CURRENT APPLICATION NUMBER: US/60/581,351
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: US 60/479,962
; PRIOR FILING DATE: 2003-06-19
; NUMBER OF SEQ ID NOS: 13980
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2835
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Tropheryma whipplei str. Twist
US-60-581-351-2835

Query Match      100.0%; Score 29; DB 49; Length 698;
Best Local Similarity 100.0%; Pred. No. 2e+03; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      534 KIVFFA 539

RESULT 26
US-09-724-842-16
; Sequence 16, Application US/09724842
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiang
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-724-842-16

Query Match      96.6%; Score 28; DB 27; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      1 KIVFFA 6
```

RESULT 27
US-09-724-842-24
; Sequence 24, Application US/09724842
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-724-842-24

Query Match 96.6%; Score 28; DB 27; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 28
US-09-724-842A-16
; Sequence 16, Application US/09724842A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-724-842A-16

Query Match 96.6%; Score 28; DB 27; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 29
US-09-724-842A-24
; Sequence 24, Application US/09724842A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501
; CURRENT APPLICATION NUMBER: US/09/724,842A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-724-842A-24

Query Match 96.6%; Score 28; DB 27; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6

RESULT 30
US-09-867-847-18
; Sequence 18, Application US/09867847
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-18

Query Match 96.6%; Score 28; DB 28; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6


```
Db          |:|||||
            1 KVVFFA 6

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

RESULT 31
US-09-867-847-26
; Sequence 26, Application US/09867847
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-26

Query Match      96.6%;  Score 28;  DB 28;  Length 6;
Best Local Similarity 83.3%;  Pred. No. 7.2e+06;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 KIVFFA 6
            |:|||||
            1 KVVFFA 6

Db          1 KVVFFA 6

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

RESULT 32
US-09-867-847A-18
; Sequence 18, Application US/09867847A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Vaccine for the Prevention and Treatment
; TITLE OF INVENTION: of Alzheimer's and Amyloid Related Diseases
; FILE REFERENCE: 50291/005001
; CURRENT APPLICATION NUMBER: US/09/867,847A
; CURRENT FILING DATE: 2001-05-29
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic, All D peptides or peptidomimetics
US-09-867-847A-18

Query Match      96.6%;  Score 28;  DB 28;  Length 6;
Best Local Similarity 83.3%;  Pred. No. 7.2e+06;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 KIVFFA 6
            |:|||||
            1 KVVFFA 6

Db          1 KVVFFA 6

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

RESULT 33
US-09-867-847A-26
; Sequence 26, Application US/09867847A
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Vaccine for the Prevention and Treatment
; TITLE OF INVENTION: of Alzheimer's and Amyloid Related Diseases
; FILE REFERENCE: 50291/005001
; CURRENT APPLICATION NUMBER: US/09/867,847A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic, All D peptides or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: 6
; OTHER INFORMATION: Amidation
US-09-867-847A-26

Query Match      96.6%;  Score 28;  DB 28;  Length 6;
Best Local Similarity 83.3%;  Pred. No. 7.2e+06;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

QY          1 KIVFFA 6
            |:|||||
            1 KVVFFA 6

Db          1 KVVFFA 6

Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;

RESULT 34
US-09-915-092-8
; Sequence 8, Application US/09915092
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-8

Query Match      96.6%;  Score 28;  DB 29;  Length 6;
Best Local Similarity 83.3%;  Pred. No. 7.2e+06;
Matches      5;  Conservative      1;  Mismatches      0;  Indels      0;  Gaps      0;
```

```
Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 35
US-09-915-092-16
; Sequence 16, Application US/09915092
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-16

Query Match 96.6%; Score 28; DB 29; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 36
US-10-009-122-9
; Sequence 9, Application US/10009122
; GENERAL INFORMATION:
; APPLICANT: NEUROCHEM INC.
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: GERVAIS, Francine
; APPLICANT: GUPTA, Ajay
; TITLE OF INVENTION: STEREOSELECTIVE ANTIFIBRILLOGENIC
; FILE REFERENCE: 14228-1PCT
; CURRENT APPLICATION NUMBER: US/10/009,122
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/132,592
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: peptide having antifibrillogenetic activity and/or
; OTHER INFORMATION: neuroprotection
US-10-009-122-9

Query Match 96.6%; Score 28; DB 30; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 37
US-10-009-122-17
; Sequence 17, Application US/10009122
; GENERAL INFORMATION:
; APPLICANT: NEUROCHEM INC.
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: GERVAIS, Francine
; APPLICANT: GUPTA, Ajay
; TITLE OF INVENTION: STEREOSELECTIVE ANTIFIBRILLOGENIC
; FILE REFERENCE: 14228-1PCT
; CURRENT APPLICATION NUMBER: US/10/009,122
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/132,592
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: peptide having antifibrillogenetic activity and/or
; NAME/KEY: AMIDATION
; LOCATION: (6)...(6)
US-10-009-122-17

Query Match 96.6%; Score 28; DB 30; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 38
US-10-705-028-9
; Sequence 9, Application US/10705028
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: NBI-088CN
; CURRENT APPLICATION NUMBER: US/10/705,028
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: 09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-028-9

Query Match 96.6%; Score 28; DB 37; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1 KVVFFA 6

RESULT 39
US-10-705-028-17
; Sequence 17, Application US/10705028
; GENERAL INFORMATION:
```

```
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE REFERENCE: Cerebral Amyloid Angiopathy
; CURRENT APPLICATION NUMBER: US/10/705,028
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: 09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-705-028-17
```

```
Query Match 96.6%; Score 28; DB 37; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6
```

```
RESULT 40
US-10-728-028-8
; SEQUENCE 8, Application US/10728028
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xiangqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: US/10/728,028
; CURRENT APPLICATION NUMBER: 60/443291
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-8
```

```
Query Match 96.6%; Score 28; DB 37; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6
```

```
RESULT 41
US-10-728-028-16
; SEQUENCE 16, Application US/10728028
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: KONG, Xiangqi
; APPLICANT: CHALIFOUR, Robert
```

```
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE REFERENCE: US/10/728,028
; CURRENT APPLICATION NUMBER: 60/443291
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-16
```

```
Query Match 96.6%; Score 28; DB 37; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6
```

```
RESULT 42
US-10-825-958-16
; SEQUENCE 16, Application US/10825958
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-16
```

```
Query Match 96.6%; Score 28; DB 38; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KIVFFA 6
|:||||
Db 1 KVVFFA 6
```

```
RESULT 43
US-10-825-958-24
; SEQUENCE 24, Application US/10825958
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
```

```
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-24

Query Match          96.6%; Score 28; DB 38; Length 6;
Best Local Similarity 83.3%; Pred. No. 7.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      1 KVVFFA 6

RESULT 44
PCT-US03-25626-7
; Sequence 7, Application PC/TUS0325626
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyi, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; TITLE OF INVENTION: eNOS
; FILE REFERENCE: 52339AWOM1
; CURRENT APPLICATION NUMBER: PCT/US03/25626
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US03-25626-7

Query Match          96.6%; Score 28; DB 1; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      18 KVVFFA 23

RESULT 45
US-09-807-877-16
; Sequence 16, Application US/09807877
; GENERAL INFORMATION:
; APPLICANT: STAPLETON, DAVID IAN
```

```
; APPLICANT: CHEN, ZHIPING
; APPLICANT: MICHELL, BELINDA JOYCE
; APPLICANT: KEMP, BRUCE ERNEST
; APPLICANT: MITCHELL, KENNETH IAN
; TITLE OF INVENTION: REGULATION OF NITRIC OXIDE SYNTHASE ACTIVITY
; FILE REFERENCE: 4050.000900
; CURRENT APPLICATION NUMBER: US/09/807,877
; CURRENT FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: PCT/AU99/00968
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: P66976
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 37
; TYPE: PRT
; ORGANISM: mus musculus
US-09-807-877-16

Query Match          96.6%; Score 28; DB 28; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      18 KVVFFA 23

RESULT 46
US-10-641-924-7
; Sequence 7, Application US/10641924
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kauser, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: eNOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 5303SAUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-641-924-7

Query Match          96.6%; Score 28; DB 36; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      18 KVVFFA 23

RESULT 47
US-10-642-255-7
; Sequence 7, Application US/10642255
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kauser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubanyi, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; TITLE OF INVENTION: eNOS
; FILE REFERENCE: 52339AUSM1
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
```

; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-255-7

Query Match 96.6%; Score 28; DB 36; Length 37;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 18 KVVFFA 23

RESULT 48
US-10-437-963-173619
; Sequence 173619, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 173619
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71639C.1.pap
US-10-437-963-173619

Query Match 96.6%; Score 28; DB 34; Length 60;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 4 KVVFFA 9

RESULT 49
US-10-793-479-6921
; Sequence 6921, Application US/10793479
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/10/793,479
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US/05/513,999
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6921
; LENGTH: 77
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-793-479-6921

Query Match 96.6%; Score 28; DB 37; Length 77;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 38 KVVFFA 43

RESULT 50
US-10-437-963-133986
; Sequence 133986, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 133986
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35803C.1.pap
US-10-437-963-133986

Query Match 96.6%; Score 28; DB 34; Length 87;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 6 KVVFFA 11

RESULT 51
US-09-708-427-14352
; Sequence 14352, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14352
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..85
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc feature
; LOCATION: 1..88
; OTHER INFORMATION: Ceres Seq. ID 1827650
US-09-708-427-14352

Query Match 96.6%; Score 28; DB 27; Length 88;

```
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 35 KLIFFA 40

RESULT 52
US-09-708-427-14351
; Sequence 14351, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
; NUMBER OF SEQ ID NOS: 85364
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14351
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..91
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc_feature
; LOCATION: 1..91
; OTHER INFORMATION: Ceres Seq. ID 1827649
US-09-708-427-14351

Query Match 96.6%; Score 28; DB 27; Length 91;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 38 KLIFFA 43

RESULT 53
US-10-437-963-105773
; Sequence 105773, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105773
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102988C.1.pep
US-10-437-963-105773

Query Match 96.6%; Score 28; DB 34; Length 109;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
```

```
Db 4 KIVFFA 9

RESULT 54
US-09-733-089-9030
; Sequence 9030, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: Mcininch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 9030
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(112)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-733-089-9030

Query Match 96.6%; Score 28; DB 27; Length 112;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 21 KIVFFA 26

RESULT 55
US-09-816-660-9030
; Sequence 9030, Application US/09816660
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: Mcininch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: )
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 9030
; LENGTH: 112
```

; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(112)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-816-660-9030

Query Match 96.6%; Score 28; DB 28; Length 112;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 21 KVVFFA 26

RESULT 56
US-10-437-963-141578
; Sequence 141578, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141578
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42668C.1.pap
US-10-437-963-141578

Query Match 96.6%; Score 28; DB 34; Length 135;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 4 KVVFFA 9

RESULT 57
US-09-733-089-23062
; Sequence 23062, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: Mcininch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19

; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23062
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-733-089-23062

Query Match 96.6%; Score 28; DB 27; Length 140;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 96 KVVFFA 101

RESULT 58
US-09-816-660-23062
; Sequence 23062, Application US/09816660
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: Mcininch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER:) US 09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23062
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-816-660-23062

Query Match 96.6%; Score 28; DB 28; Length 140;
Best Local Similarity 83.3%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
DB 96 KVVFFA 101

RESULT 59
US-09-417-507-41853
; Sequence 41853, Application US/09417507
; GENERAL INFORMATION:
; APPLICANT: KEITH G. WEINSTOCK ET AL.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
; TITLE OF INVENTION: FUNIGATUS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH99-10
; CURRENT APPLICATION NUMBER: US/09/417,507
; CURRENT FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 44312
; SEQ ID NO 41853
; LENGTH: 156
; TYPE: PRT
; ORGANISM: A. fumigatus
US-09-417-507-41853

```
Query Match      96.6%; Score 28; DB 24; Length 156;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      93 KLIFFA 98

RESULT 60
US-09-733-089-23064
; Sequence 23064, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: Mcininch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US 09/620,392
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23064
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-733-089-23064

Query Match      96.6%; Score 28; DB 27; Length 158;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      114 KIVFFA 119

RESULT 61
US-09-816-660-23064
; Sequence 23064, Application US/09816660
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: Mcininch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: )
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
```

```
; SEQ ID NO 23064
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-816-660-23064

Query Match      96.6%; Score 28; DB 28; Length 158;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      114 KIVFFA 119

RESULT 62
US-09-733-089-23060
; Sequence 23060, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: Mcininch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23060
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(165)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-733-089-23060

Query Match      96.6%; Score 28; DB 27; Length 165;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KIVFFA 6
Db      121 KIVFFA 126

RESULT 63
US-09-816-660-23060
; Sequence 23060, Application US/09816660
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: Mcininch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
```


; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER:) US 09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23060
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(165)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-816-660-23060

Query Match 96.6%; Score 28; DB 28; Length 165;
Best Local Similarity 83.3%; Pred. No. 7.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 121 KVVFFA 126

RESULT 64
US-10-220-366A-25111
; Sequence 25111, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 25111
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(175)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-25111

Query Match 96.6%; Score 28; DB 32; Length 175;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 128 KVVFFA 133

RESULT 65
US-10-437-963-122124
; Sequence 122124, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 122124
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(175)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_25081C.1.pep
US-10-437-963-122124

Query Match 96.6%; Score 28; DB 34; Length 175;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 66
US-09-733-089-23063
; Sequence 23063, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyva, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23063
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(181)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-733-089-23063

Query Match 96.6%; Score 28; DB 27; Length 181;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 137 KVVFFA 142

RESULT 67
US-09-816-660-23063
; Sequence 23063, Application US/09816660
; GENERAL INFORMATION:

```
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE OF INVENTION: Transcription In Plants
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US 09/816,660
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/733,089
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: ) US 09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23063
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(181)
; OTHER INFORMATION: unsure at all Xaa locations
US-09-816-660-23063

Query Match 96.6%; Score 28; DB 28; Length 181;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 137 KVVFFA 142

RESULT 68
US-10-481-032A-214
; Sequence 214, Application US/10481032A
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wengqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 228
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-214

Query Match 96.6%; Score 28; DB 34; Length 186;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 70
US-10-437-963-172476
; Sequence 172476, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
```

```
; ORGANISM: Oryza sativa
US-10-481-032A-214

Query Match 96.6%; Score 28; DB 34; Length 186;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 69
US-10-481-032A-228
; Sequence 228, Application US/10481032A
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Cheng, Wengqiong
; APPLICANT: Briggs, Steven
; APPLICANT: Cooper, Bret
; APPLICANT: Goff, Stephen A.
; APPLICANT: Moughamer, Todd
; APPLICANT: Glazebrook, Jane
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicolas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
; FILE REFERENCE: 60148USPCT
; CURRENT APPLICATION NUMBER: US/10/481,032A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/300,112
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/342,327
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: PCT/IB02/02450
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 1201
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 228
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-481-032A-228

Query Match 96.6%; Score 28; DB 34; Length 186;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 4 KVVFFA 9

RESULT 70
US-10-437-963-172476
; Sequence 172476, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
```

```
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172476
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(188)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70608C.1.pap
US-10-437-963-172476

Query Match          96.6%; Score 28; DB 34; Length 188;
Best Local Similarity 83.3%; Pred. No. 8.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      4 KVVFFA 9

RESULT 71
PCT-US01-01354-11385
; Sequence 11385, Application PC/TUS0101354
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC004PCT
; CURRENT APPLICATION NUMBER: PCT/US01/01354
; CURRENT FILING DATE: 2001-03-17
; NUMBER OF SEQ ID NOS: 42506
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11385
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (174)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (175)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-01354-11385

Query Match          96.6%; Score 28; DB 1; Length 190;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KIVFFA 6
Db      14 KVVFFA 19

RESULT 72
US-09-764-905-11385
; Sequence 11385, Application US/09764905
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC004
; CURRENT APPLICATION NUMBER: US/09/764,905
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
```

; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,245
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297

; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,398

Query Match 96.6%; Score 28; DB 27; Length 190;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6

Db 14 KVVFFA 19

RESULT 73

US-10-092-399-11385
; Sequence 11385, Application US/10092399

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PC004C1

; CURRENT APPLICATION NUMBER: US/10/092,399

; CURRENT FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 42506

; Prior Application removed - See File Wrapper or Palm

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11385

; LENGTH: 190

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (174)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: misc feature

; LOCATION: (175)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-10-092-399-11385

Query Match 96.6%; Score 28; DB 30; Length 190;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 14 KVVFFA 19

RESULT 74
US-10-437-963-172452
; Sequence 172452, Application US/10437963
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172452
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(198)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_70587C.1.pep
US-10-437-963-172452

Query Match 96.6%; Score 28; DB 34; Length 198;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 4 KVVFFA 9

RESULT 75
US-09-733-089-23065
; Sequence 23065, Application US/09733089
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lutfiyeva, Linda L.
; APPLICANT: McIninch, James
; APPLICANT: Wu, Wei
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Transcription In Plants
; FILE REFERENCE: 38-21(15300)D
; CURRENT APPLICATION NUMBER: US/09/733,089
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/474,435
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/620,392
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 24143
; SEQ ID NO 23065
; LENGTH: 199
; TYPE: PRT

; ORGANISM: Oryza sativa
US-09-733-089-23065

Query Match 96.6%; Score 28; DB 27; Length 199;
Best Local Similarity 83.3%; Pred. No. 8.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:||||
Db 155 KVVFFA 160

Search completed: December 29, 2005, 18:37:16
Job time : 263.871 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-10
Perfect score: 29
Sequence: 1 KIVPFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : A_Geneseq_21.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	4 AAB48483	Aab48483 Antifibri
2	29	100.0	6	4 AAB48474	Aab48474 Antifibri
3	29	100.0	6	4 AAB82623	Aab82623 All-D pep
4	29	100.0	6	4 AAB82631	Aab82631 All-D pep
5	29	100.0	6	5 AAU96819	Aau96819 Amyloid t
6	29	100.0	6	5 AAU96811	Aau96811 Amyloid t
7	29	100.0	6	5 AAU11657	Aau11657 Peptide #
8	29	100.0	6	5 AAU11648	Aau11648 Peptide #
9	29	100.0	6	6 AAE35446	Aae35446 Abeta pep
10	29	100.0	6	6 AAE35438	Aae35438 Abeta pep
11	29	100.0	6	8 ADQ37322	Adq37322 Antifibri
12	29	100.0	6	8 ADQ37270	Adq37270 Vaccine a
13	29	100.0	6	8 ADQ37313	Adq37313 Antifibri
14	29	100.0	6	8 ADQ37262	Adq37262 Vaccine a
15	29	100.0	6	9 ADY37921	Ady37921 Amyloid-t
16	29	100.0	6	9 ADY37929	Ady37929 Amyloid-t
17	29	100.0	99	4 ABG26598	Abg26598 Novel hum
18	28	96.6	6	4 AAB48482	Aab48482 Antifibri
19	28	96.6	6	4 AAB48490	Aab48490 Antifibri
20	28	96.6	6	4 AAB82630	Aab82630 All-D pep
21	28	96.6	6	4 AAB82638	Aab82638 All-D pep
22	28	96.6	6	5 AAU96818	Aau96818 Amyloid t
23	28	96.6	6	5 AAU96826	Aau96826 Amyloid t
24	28	96.6	6	5 AAU11664	Aau11664 Peptide #

25	28	96.6	6	5 AAU11656	Aau11656 Peptide #
26	28	96.6	6	6 AAE35452	Aae35452 Abeta pep
27	28	96.6	6	8 ADQ37277	Adq37277 Vaccine a
28	28	96.6	6	8 ADQ37321	Adq37321 Antifibri
29	28	96.6	6	8 ADQ37329	Adq37329 Antifibri
30	28	96.6	6	9 ADY37928	Ady37928 Amyloid-t
31	28	96.6	6	9 ADY37936	Ady37936 Amyloid-t
32	28	96.6	22	8 ADQ09761	Adq09761 Rice 26kd
33	28	96.6	23	8 ADY37938	Ady37938 Rice 26 k
34	28	96.6	37	3 AAB05910	Aab05910 Mouse ind
35	28	96.6	37	8 ADK34080	Adk34080 Human nno
36	28	96.6	37	8 ADL70727	Adl70727 Mouse ino
37	28	96.6	77	3 AAG02840	Aag02840 Human sec
38	28	96.6	175	4 AAO11219	Aao11219 Human pol
39	28	96.6	186	7 ADC07962	Adc07962 Rice prot
40	28	96.6	186	7 ADC07948	Adc07948 Rice prot
41	28	96.6	190	4 AAM83792	Aam83792 Human imm
42	28	96.6	564	4 ABB61977	Abb61977 Drosophila
43	28	96.6	854	8 ADM66704	Adm66704 Novel hum
44	28	96.6	922	8 ABM83252	Abm83252 Human dia
45	28	96.6	925	7 ADF76335	Adf76335 Novel hum
46	28	96.6	925	7 ADJ70225	Adj70225 Human hea
47	28	96.6	925	8 ADJ75428	Adj75428 Marker ge
48	28	96.6	925	8 ADJ75495	Adj75495 Marker ge
49	28	96.6	925	8 ADN04860	Adn04860 Antipsori
50	28	96.6	925	8 ADRI4233	Adri4233 Human NF-
51	28	96.6	925	8 ADF25011	Adf25011 PRO polyp
52	28	96.6	925	8 ADP97294	Adp97294 Human RIG
53	28	96.6	925	9 AEA23525	Aea23525 Human PRO
54	28	96.6	925	9 AEA23525	Aea23525 Human PRO
55	28	96.6	1144	2 AAR77360	Aar77360 Inducible
56	28	96.6	1144	2 AAW51246	Aaw51246 Inducible
57	28	96.6	1144	4 AAG64500	Aag64500 Mouse ind
58	28	96.6	1144	6 ADF43404	Adf43404 iNOS poly
59	28	96.6	1144	7 ADJ77432	Adj77432 Mouse ind
60	28	96.6	1144	8 ADJ76212	Adj76212 Marker ge
61	28	96.6	1144	8 ADJ76136	Adj76136 Marker ge
62	28	96.6	1144	8 ABA03075	Aba03075 VEGF amin
63	28	96.6	1144	9 ABB68472	Abb68472 Drosophila
64	28	96.6	1443	4 AAW02314	Aaw02314 Beta-amyl
65	27	93.1	6	2 AAW89378	Aaw89378 Beta-amyl
66	27	93.1	6	4 AAB48484	Aab48484 Antifibri
67	27	93.1	6	4 AAB48476	Aab48476 Antifibri
68	27	93.1	6	4 AAB82632	Aab82632 All-D pep
69	27	93.1	6	5 ABG71009	Abg71009 Long form
70	27	93.1	6	5 AAU96820	Aau96820 Amyloid t
71	27	93.1	6	5 ABB83305	Abb83305 Amyloid-b
72	27	93.1	6	5 AAU11658	Aau11658 Peptide #
73	27	93.1	6	5 AAU11650	Aau11650 Peptide #
74	27	93.1	6	6 AAE35445	Aae35445 Abeta pep
75	27	93.1	6	6 AAE35434	Aae35434 Abeta pep
76	27	93.1	6	6 ADJ64060	Adj64060 Human bet
77	27	93.1	6	8 ADQ37271	Adq37271 Vaccine a
78	27	93.1	6	8 ADQ37315	Adq37315 Antifibri
79	27	93.1	6	8 ADQ37368	Adq37368 Beta-amyl
80	27	93.1	6	8 ADQ37269	Adq37269 Vaccine a
81	27	93.1	6	8 ADQ37292	Adq37292 Vaccine a
82	27	93.1	6	8 ADQ37258	Adq37258 Vaccine a
83	27	93.1	6	8 ADQ37353	Adq37353 Beta-amyl
84	27	93.1	6	8 ADQ37323	Adq37323 Antifibri
85	27	93.1	6	8 ADY37930	Ady37930 Amyloid-t
86	27	93.1	6	9 ADY37948	Ady37948 Amyloid-t
87	27	93.1	6	9 ADY37947	Ady37947 Amyloid-t
88	27	93.1	6	9 AEA23039	Aea23039 Human bet
89	27	93.1	6	9 AAB88300	Aab88300 Non-amnes
90	27	93.1	7	2 AAR87921	Aar87921 Test pept
91	27	93.1	7	2 AAW02312	Aaw02312 Beta-amyl
92	27	93.1	7	2 AAW89376	Aaw89376 Residues
93	27	93.1	7	2 AAB67281	Aab67281 Residues
94	27	93.1	7	4 AAB48475	Aab48475 Antifibri
95	27	93.1	7	4 AAB48492	Aab48492 Antifibri
96	27	93.1	7	4 AAB48492	Aab48492 Antifibri
97	27	93.1	7	4 AAB48492	Aab48492 Antifibri

98	27	93.1	7	4	AB48491	Aab48491 Antifibri	171	27	93.1	10	4	AAB46226	Aab46226 Human APP
99	27	93.1	7	4	AB82624	Aab82624 All-D pep	172	27	93.1	10	4	AAB46225	Aab46225 Human APP
100	27	93.1	7	4	AB2640	Aab2640 All-D pep	173	27	93.1	10	4	AAB46224	Aab46224 Human APP
101	27	93.1	7	4	AB82639	Aab82639 All-D pep	174	27	93.1	10	4	AAB46224	Aab46224 Human APP
102	27	93.1	7	5	AB71007	Abg71007 Long form	175	27	93.1	10	4	AB46227	Ab46227 Human APP
103	27	93.1	7	5	AB05155	Ab05155 Beta amyl	176	27	93.1	10	4	AB46227	Ab46227 Human APP
104	27	93.1	7	5	AAU96827	Aau96827 Amyloid t	177	27	93.1	10	5	AAU96829	Aau96829 Amyloid t
105	27	93.1	7	5	AAU96812	Aau96812 Amyloid t	178	27	93.1	10	6	ABP57511	Abp57511 Different
106	27	93.1	7	5	AAU96828	Aau96828 Amyloid t	179	27	93.1	10	6	AAE35455	Aae35455 Beta pep
107	27	93.1	7	5	AB04920	Abb04920 Human amy	180	27	93.1	10	8	ADQ37280	Adq37280 Vaccine a
108	27	93.1	7	5	AAU11665	Aau11665 Peptide #	181	27	93.1	10	8	ADQ37371	Adq37371 Amyloid-b
109	27	93.1	7	5	AAU11649	Aau11649 Peptide #	182	27	93.1	10	8	ADQ37374	Adq37374 Amyloid-b
110	27	93.1	7	5	AB82630	Abb82630 Peptide #	183	27	93.1	10	9	ADY37939	Ady37939 Amyloid-t
111	27	93.1	7	6	AB82630	Abb82630 Beta fib	184	27	93.1	11	2	AAW32560	Aaw32560 Anti-amyl
112	27	93.1	7	6	AB82630	Abb82630 Beta fib	185	27	93.1	11	4	AAW52586	Aaw52586 Peptide #
113	27	93.1	7	6	AB82630	Abb82630 Beta fib	186	27	93.1	11	5	AAU99431	Aau99431 Human amy
114	27	93.1	7	6	AB82630	Abb82630 Beta fib	187	27	93.1	11	5	AAE29504	Aae29504 Amyloid b
115	27	93.1	7	6	AB82630	Abb82630 Beta fib	188	27	93.1	11	6	ABU79013	Abu79013 Amyloidog
116	27	93.1	7	6	AB82630	Abb82630 Beta fib	189	27	93.1	11	7	ABR84683	AbR84683 Aggreca
117	27	93.1	7	7	ADD20746	Add20746 Human bet	190	27	93.1	11	7	ABW00147	Abw00147 Amyloid-b
118	27	93.1	7	7	ADF50855	Adf50855 Human cal	191	27	93.1	12	6	AAE35464	Aae35464 Beta pep
119	27	93.1	7	8	ADP64058	Adp64058 Human bet	192	27	93.1	12	6	AAE35435	Aae35435 Beta pep
120	27	93.1	7	8	ADP64922	Adp64922 Beta-amyl	193	27	93.1	12	6	AAE35466	Aae35466 Beta pep
121	27	93.1	7	8	ADQ37278	Adq37278 Vaccine a	194	27	93.1	12	7	ADD20745	Add20745 Human bet
122	27	93.1	7	8	ADQ37314	Adq37314 Antifibri	195	27	93.1	12	7	ADD20744	Add20744 Human bet
123	27	93.1	7	8	ADQ37263	Adq37263 Vaccine a	196	27	93.1	12	8	ADJ71476	Adj71476 N-termina
124	27	93.1	7	8	ADQ37279	Adq37279 Vaccine a	197	27	93.1	12	8	ADQ37407	Adq37407 Amyloid-b
125	27	93.1	7	8	ADQ37330	Adq37330 Antifibri	198	27	93.1	12	8	ADQ37289	Adq37289 Vaccine a
126	27	93.1	7	8	ADQ37331	Adq37331 Antifibri	199	27	93.1	12	8	ADQ37259	Adq37259 Vaccine a
127	27	93.1	7	8	ADQ37351	Adq37351 Beta-amyl	200	27	93.1	12	9	ADZ08890	Adz08890 Human bet
128	27	93.1	7	9	ADY37922	Ady37922 Amyloid-t	201	27	93.1	12	9	ADZ08892	Adz08892 Human bet
129	27	93.1	7	9	ADY37938	Ady37938 Amyloid-t	202	27	93.1	13	6	AAE35465	Aae35465 Beta pep
130	27	93.1	7	9	ADY37937	Ady37937 Amyloid-t	203	27	93.1	13	6	AAE35467	Aae35467 Beta pep
131	27	93.1	7	9	ADZ08903	Adz08903 Human bet	204	27	93.1	13	6	ADA37467	Ada37467 Human amy
132	27	93.1	8	2	AAW02310	Aaw02310 Beta-amyl	205	27	93.1	13	8	ADJ71477	Adj71477 N-termina
133	27	93.1	8	2	AAW45967	Aaw45967 Peptide d	206	27	93.1	13	8	ADJ71464	Adj71464 N-termina
134	27	93.1	8	2	AAW32551	Aaw32551 Amyloidog	207	27	93.1	13	8	ADQ37408	Adq37408 Amyloid-b
135	27	93.1	8	2	AAW89374	Aaw89374 Beta-amyl	208	27	93.1	13	8	ADQ37290	Adq37290 Vaccine a
136	27	93.1	8	4	AAE10663	Aae10663 Human amy	209	27	93.1	14	6	ADA89887	Ada89887 Beta-A4 s
137	27	93.1	8	4	AAE02615	Aae02615 Human amy	210	27	93.1	14	6	ADJ71452	Adj71452 N-termina
138	27	93.1	8	5	ABG71005	Abg71005 Long form	211	27	93.1	14	8	ADJ71465	Adj71465 N-termina
139	27	93.1	8	5	ABG78624	Abg78624 Human alp	212	27	93.1	14	8	ADJ71478	Adj71478 N-termina
140	27	93.1	8	5	ABW05153	Abw05153 Beta amyl	213	27	93.1	14	9	ADZ08889	Adz08889 Human bet
141	27	93.1	8	6	ABU09765	Abu09765 Amyloidog	214	27	93.1	15	2	AAW02334	Aaw02334 Beta-amyl
142	27	93.1	8	6	ABR61959	AbR61959 Human amy	215	27	93.1	15	2	AAW89358	Aaw89358 Beta-amyl
143	27	93.1	8	7	ABW00134	Abw00134 Beta-amyl	216	27	93.1	15	2	AAW89354	Aaw89354 Beta-amyl
144	27	93.1	8	8	ADJ64056	Adj64056 Human bet	217	27	93.1	15	5	ABG71014	Abg71014 Long form
145	27	93.1	8	8	ADQ37385	Adq37385 Antifibri	218	27	93.1	15	5	ABB05162	Abb05162 Beta amyl
146	27	93.1	8	8	ADQ37349	Adq37349 Human bet	219	27	93.1	15	5	AAE26271	Aae26271 Human bet
147	27	93.1	8	8	ADZ08900	Adz08900 Human bet	220	27	93.1	15	6	ABU79057	Abu79057 Aggregati
148	27	93.1	8	9	AEA51423	Aea51423 C-Abeta 1	221	27	93.1	15	6	ABU79064	Abu79064 Aggregati
149	27	93.1	8	9	AEA51420	Aea51420 A 16-22-C	222	27	93.1	15	6	ABU79059	Abu79059 Aggregati
150	27	93.1	8	9	AEA62831	Aea62831 Immunocon	223	27	93.1	15	6	ABU79060	Abu79060 Aggregati
151	27	93.1	8	9	AEA62834	Aea62834 Immunocon	224	27	93.1	15	6	ABU79055	Abu79055 Aggregati
152	27	93.1	9	2	AAW45239	Aaw45239 Mutant am	225	27	93.1	15	6	ABU79056	Abu79056 Aggregati
153	27	93.1	9	4	AAE48493	Aae48493 Antifibri	226	27	93.1	15	6	ABU79062	Abu79062 Aggregati
154	27	93.1	9	5	AAU11667	Aau11667 Peptide #	227	27	93.1	15	7	ABW00190	Abw00190 Peptide #
155	27	93.1	9	6	ABP57517	Abp57517 Different	228	27	93.1	15	7	ABW00191	Abw00191 Peptide #
156	27	93.1	9	6	ABU79063	Abu79063 Aggregati	229	27	93.1	15	7	ABW00196	Abw00196 Peptide #
157	27	93.1	9	6	AAE35436	Aae35436 Beta pep	230	27	93.1	15	7	ABW00189	Abw00189 Peptide #
158	27	93.1	9	7	ABW00197	Abw00197 Peptide #	231	27	93.1	15	7	ABW00193	Abw00193 Peptide #
159	27	93.1	9	8	ADI36003	Adi36003 Amyloid b	232	27	93.1	15	7	ABW00191	Abw00191 Peptide #
160	27	93.1	9	8	ADI35849	Adi35849 Amyloid b	233	27	93.1	15	7	ABW00194	Abw00194 Peptide #
161	27	93.1	9	8	ADI35874	Adi35874 Amyloid b	234	27	93.1	15	7	ADK82695	Adk82695 Beta-amyl
162	27	93.1	9	8	ADI35871	Adi35871 Amyloid b	235	27	93.1	15	7	ADK82697	Adk82697 Beta-amyl
163	27	93.1	9	8	ADI35903	Adi35903 Amyloid b	236	27	93.1	15	7	ADK82700	Adk82700 Beta-amyl
164	27	93.1	9	8	ADQ37260	Adq37260 Vaccine a	237	27	93.1	15	7	ADK82698	Adk82698 Beta-amyl
165	27	93.1	9	8	ADQ37332	Adq37332 Antifibri	238	27	93.1	15	7	ADK82699	Adk82699 Beta-amyl
166	27	93.1	9	9	AEA51414	Aea51414 A 16-23-C	239	27	93.1	15	8	ADJ71466	Adj71466 N-termina
167	27	93.1	9	9	AEA51417	Aea51417 C-A 16-23	240	27	93.1	15	8	ADJ71453	Adj71453 N-termina
168	27	93.1	9	9	AEA62825	Aea62825 Immunocon	241	27	93.1	15	8	ADJ71479	Adj71479 N-termina
169	27	93.1	9	9	AEA62828	Aea62828 Immunocon	242	27	93.1	15	8	ADJ71440	Adj71440 N-termina
170	27	93.1	10	3	AA79938	Aay79938 Beta-amyl	243	27	93.1	15	8	ADJ64065	Adj64065 Human bet

XX Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 1 KIVFFA 6
 RESULT 3
 ID AAB82623
 AC AAB82623;
 XX 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 DE Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1..6
 FT /note= "all D-form residues"
 FT Modified-site 6
 FT /note= "C-terminal amide"
 XX WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX Disclosure; Page 10; 31pp; English.
 XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 1 KIVFFA 6
 RESULT 4
 ID AAB82631
 AC AAB82631;
 XX 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 DE Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Misc-difference 1..6
 FT /note= "all D-form residues"
 FT Modified-site 6
 FT /note= "C-terminal amide"
 XX WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 XX Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), Familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |||||
 Db 1 KIVFFPA 6

RESULT 5

ID AAU96819
 AC AAU96819 standard; peptide; 6 AA.

XX AAU96819;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #9.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

PH Key Difference 1..6

FT Misc-difference 6 /note= "Preferably D-form residue"

FT Modified-site 6 /note= "Ala is amidated"

XX WO200207781-A2.

XX 31-JAN-2002.

XX

PF 25-JUL-2001; 2001WO-CA001071.

XX 25-JUL-2000; 2000US-0220808P.

PR 24-JUL-2001; 2001US-00915092.

XX (NEUR-) NEUROCHEM INC.

XX Gervais F, Kong X, Chalifour R, Migneault D;

XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A-t-(A₁n₁k)-z-A₁l₁a₁b₁ (I) where z = 0 - 1;
 CC A₁t = an amyloid targeting moiety; A₁n₁k = a linker moiety; and A₁l₁a₁b₁
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), Kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |||||

Db 1 KIVFFPA 6

RESULT 6

AAU96811
 ID AAU96811 standard; peptide; 6 AA.

XX AAU96811;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #1.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

```

FH Key                               Location/Qualifiers
FT Misc-difference 1..6
XX                                     /note= "Preferably D-form residue"
XX WO200207781-A2.
XX 31-JAN-2002.
XX
XX 25-JUL-2001; 2001WO-CA001071.
XX
XX 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX WPI; 2002-371447/40.
XX
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX plaques and/or for the treatment of amyloidosis disorders.
XX
XX Claim 49; Page 21; 57pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent comprising an
XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX agent is of general formula A_t-(A_l)_n_k)-z-A_l_a_b (I) where z = 0 - 1;
XX A_t = an amyloid targeting moiety; A_l_n_k = a linker moiety; and A_l_a_b
XX = a labelling moiety. Also included are imaging amyloid deposition or
XX diagnosing an amyloid-related condition in a patient involving
XX administering (I) to the patient, and ultrasound imaging (I) in the
XX patient to determine the presence of amyloid or amyloid-related condition
XX ; and a kit for preparing a radiopharmaceutical preparation comprising
XX (I), a reducing agent, a buffering agent, a transchelating agent, and
XX instructions for the preparation and use of the radiopharmaceutical in
XX the imaging of amyloid or an amyloid-related condition. The agents are
XX used for imaging amyloid deposition and for diagnosing an amyloid related
XX condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX cerebral amyloidosis (transmissible virus dementias), familial CJD,
XX scrapie, transmissible mink encephalopathy, bovine spongiform
XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX primary amyloidosis, feline spongiform encephalopathy, non-transmissible
XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX amyloid angiopathy. The agents are capable of crossing the blood-brain
XX barrier and are capable of binding specifically to amyloid plaques. The
XX present sequence is a peptide forming the amyloid targeting moiety of the
XX agent of the invention
XX
XX Sequence 6 AA;
XX
XX Query Match          100.0%; Score 29; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy      1 KIVFFFA 6
XX        |||||
XX Db      1 KIVFFFA 6
XX
XX RESULT 8
XX AAU11648
XX ID AAU11648 standard; peptide; 6 AA.
XX
XX AC AAU11648;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Peptide #1, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; nootropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX OS Synthetic.
XX
XX PN WO200185093-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 22-DEC-2000; 2000WO-IB002078.
XX
XX PR 23-DEC-1999; 99US-0171877P.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Green AM, Gervais F;
XX WPI; 2002-075222/10.
XX
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX inhibitor.
XX
XX Disclosure; Page 10; 68pp; English.
XX
XX The present invention relates to a new method of inhibiting cerebral
XX amyloid angiopathy. The new method of the invention involves contacting a
XX blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX can be used for treating disease states characterised by cerebral amyloid
XX angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX The present sequence represents one of a group of peptides (AAU11648-
XX AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX was used in the invention to treat a disease state characterised by
XX cerebral amyloid angiopathy (CAA)
XX
XX Sequence 6 AA;
XX
XX Query Match          100.0%; Score 29; DB 5; Length 6;
XX Best Local Similarity 100.0%; Pred. No. 2e+06;
XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy      1 KIVFFFA 6
XX        |||||
XX Db      1 KIVFFFA 6
XX
XX RESULT 8
XX AAU11648
XX ID AAU11648 standard; peptide; 6 AA.
XX
XX AC AAU11648;
XX
XX DT 09-APR-2002 (first entry)
XX
XX DE Peptide #1, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; nootropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX OS Synthetic.
XX
XX PN WO200185093-A2.
XX
XX PD 15-NOV-2001.
XX
XX PF 22-DEC-2000; 2000WO-IB002078.
XX
XX PR 23-DEC-1999; 99US-0171877P.

```

XX (NEUR-) NEUROCHEM INC.
 XX Green AM, Gervais F;
 XX WPI; 2002-075222/10.
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.
 XX Disclosure; Page 10; 68pp; English.
 XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 1 KIVFFA 6
 RESULT 9
 AAE35446
 ID AAE35446 standard; peptide; 6 AA.
 AC AAE35446;
 XX 17-JUN-2003 (first entry)
 DT
 DE Abeta peptide #17.
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 1..6 /note= "D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX WO200296937-A2.
 XX
 XX 05-DEC-2002.
 XX
 XX 29-MAY-2002; 2002WO-CA000763.
 XX
 XX 29-MAY-2001; 2001US-00867847.
 XX
 XX (NEUR-) NEUROCHEM INC.
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;
 PI

XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX Claim 1; Page 59; 44pp; English.
 XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX Sequence 6 AA;
 SQ
 Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 1 KIVFFA 6
 RESULT 10
 AAE35438
 ID AAE35438 standard; peptide; 6 AA.
 XX AAE35438;
 AC AAE35438;
 XX 17-JUN-2003 (first entry)
 DT
 DE Abeta peptide #9.
 XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FH Misc-difference 1..6 /note= "D-form residues"
 FT
 XX WO200296937-A2.
 XX
 XX 05-DEC-2002.
 XX
 XX 29-MAY-2002; 2002WO-CA000763.
 XX
 XX 29-MAY-2001; 2001US-00867847.
 XX
 XX (NEUR-) NEUROCHEM INC.
 XX Gervais F, Hebert L, Chalifour RJ, Kong X;
 PI

PI	Gervais F, Hebert L, Challifour RJ, Kong X;
XX	WPI; 2003-201269/19.
XX	Prevention and/or treatment of an amyloid-related disease e.g.
XX	Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
PT	Claim 1; Page 58; 44pp; English.
XX	The invention relates to a method for prevention and/or treatment of an
XX	amyloid-related disease which comprises administration of an all-D -
CC	amyloid-beta peptide. The method is used for preventing and/or treating
CC	Alzheimer's and other amyloid related disease e.g. cerebral amyloid
CC	angiopathy; for altering serum levels of amyloid-beta in a mammal and
CC	favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
CC	the mammal; and reducing or inhibiting the formation of plaques. It is
CC	also used for treating AA (reactive) amyloid diseases including
CC	inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
CC	arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
CC	Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
CC	disease. AA deposits are also produced as a result of chronic microbial
CC	infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
CC	ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
CC	Certain malignant neoplasms can also result in AA fibril amyloid deposits
CC	including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
CC	and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
CC	present sequence is an Abeta peptide used to illustrate the method of the
CC	invention
XX	Sequence 6 AA;
SQ	Query Match 100.0%; Score 29; DB 6; Length 6; Best Local Similarity 100.0%; Pred. No. 2e+06; Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 KIVFFA 6
Db	1 KIVFFA 6
RESULT 11	
ID	ADQ37322
AC	ADQ37322 standard; peptide; 6 AA.
AC	ADQ37322;
DT	07-OCT-2004 (first entry)
DE	Antifibrillogenic amyloidosis inhibiting peptide.
XX	amyloid-beta; amyloid-beta related disease;
KW	amyloid-beta fibril formation; immune response; neurotropic;
KW	neuroprotective; cerebroprotective; haemostatic; ophthalmological;
KW	antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
KW	anticongulant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
KW	cardiant; antidepressant; endocrine; hypnotic;
KW	amyloid-beta fibril formation modulator; immune system modulator;
KW	Alzheimer's disease; mild cognitive impairment;
KW	mild-to-moderate cognitive impairment; vascular dementia;
KW	cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
KW	senile dementia; Down's syndrome; inclusion body myositis;
KW	age-related macular degeneration; hypothyroidism;
KW	cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
KW	behavioural dysfunction; neurological condition; psychological condition;
KW	vaccine antigen.
OS	Synthetic.
FH	Key Location/Qualifiers
FT	Modified-site 6
FT	/note= "amidated"
PB	WO2004/058239-A1.

XX ADQ37270;
 XX 07-OCT-2004 (first entry)
 XX Vaccine antigen amyloid-beta related amino acid sequence.
 XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "D-form residues"
 FT Modified-site 6 /note= "amidated"
 FT
 XX
 XX WO2004058239-A1.
 XX
 XX 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX
 XX (NEUR-) NEUROCHEM INT LTD.
 XX
 XX Gervais F, Bellini F;
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 67; 143pp; English.
 PS
 PS The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic, tranquilliser,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, muscular,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,

CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |||||
 DB 1 KIVFFA 6

RESULT 13
 ADQ37313
 ID ADQ37313 standard; peptide; 6 AA.
 XX AC ADQ37313;
 XX DT 07-OCT-2004 (first entry)
 XX DE Antifibrillogenic amyloidosis inhibiting peptide.
 XX

KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.

Synthetic.

WO2004058239-A1.

15-JUL-2004.

24-DEC-2003; 2003WO-CA002021.

24-DEC-2002; 2002US-0436379P.

23-JUN-2003; 2003US-0482214P.

(NEUR-) NEUROCHEM INT LTD.

Gervais F, Bellini F;

WPI; 2004-543342/52.

Composition for treating e.g. Alzheimer's disease comprises first agent

PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS
 XX
 XX Disclosure; Page 69; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a behavioural condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6

Db 1 KIVFFA 6

RESULT 14

ADQ37262

ID ADQ37262 standard; peptide; 6 AA.

XX ADQ37262;

DT 07-OCT-2004 (first entry)

XX Vaccine antigen amyloid-beta related amino acid sequence.

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquiliser; uteropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6 /note= "D-form residues"

PN WO2004058239-A1.

XX 15-JUN-2004.

XX 24-DEC-2003; 2003WO-CA002021.

XX 24-DEC-2002; 2002US-0436379P.

XX 23-JUN-2003; 2003US-0482214P.

XX (NEUR-) NEUROCHEM INT LTD.

XX Gervais F, Bellini F;

XX WPI; 2004-543342/52..

XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.

PS Disclosure; Page 67; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 CC uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a behavioural condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-12

Perfect score: 31

Sequence: 1 KVFPPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	6	2	US-09-747-408-4
2	31	100.0	6	2	US-09-747-408-12
3	30	96.8	1283	2	US-09-248-796A-18091
4	28	90.3	490	2	US-08-830-230A-438
5	28	90.3	506	2	US-08-888-998-2
6	28	90.3	506	2	US-09-362-633-2
7	28	90.3	506	2	US-09-877-476-2
8	28	90.3	506	2	US-09-877-476-28
9	28	90.3	506	2	US-09-877-476-30
10	28	90.3	506	2	US-09-877-476-36
11	28	90.3	508	2	US-09-830-230A-437
12	27	87.1	67	2	US-09-248-796A-26311
13	27	87.1	82	2	US-09-513-999C-4859
14	27	87.1	98	2	US-09-270-767-40694
15	27	87.1	98	2	US-09-270-767-55910
16	27	87.1	104	2	US-09-823-153-4
17	27	87.1	116	2	US-09-270-767-57813
18	27	87.1	238	2	US-09-902-540-10859
19	27	87.1	240	2	US-09-134-001C-5445
20	27	87.1	266	2	US-09-270-767-42516
21	27	87.1	320	2	US-09-248-796A-19539
22	27	87.1	340	2	US-09-270-767-40453
23	27	87.1	340	2	US-09-270-767-55669
24	27	87.1	475	2	US-09-270-767-45548
25	27	87.1	475	2	US-09-270-767-34763
26	27	87.1	525	2	US-09-270-767-49980
27	27	87.1	579	2	US-08-704-711A-1

28	87.1	579	2	US-09-521-220-1	Sequence 1, Appli
29	87.1	582	2	US-08-704-711A-2	Sequence 2, Appli
30	87.1	582	2	US-08-448-483-1	Sequence 1, Appli
31	87.1	582	2	US-09-211-704A-9	Sequence 9, Appli
32	87.1	582	2	US-09-521-220-2	Sequence 2, Appli
33	87.1	582	2	US-09-391-104-28	Sequence 28, Appli
34	87.1	582	2	US-09-919-497-84	Sequence 84, Appli
35	87.1	582	2	US-09-689-730-1	Sequence 1, Appli
36	87.1	1024	2	US-10-449-315-2	Sequence 2, Appli
37	87.1	1204	2	US-10-449-315-5	Sequence 5, Appli
38	83.9	45	2	US-09-270-767-37091	Sequence 37091, A
39	83.9	45	2	US-09-270-767-52308	Sequence 52308, A
40	83.9	46	2	US-09-798-635A-41	Sequence 41, Appli
41	83.9	60	2	US-10-125-258-44	Sequence 44, Appli
42	83.9	61	2	US-09-583-110-4885	Sequence 4885, Ap
43	83.9	65	2	US-10-125-258-43	Sequence 43, Appli
44	83.9	84	2	US-09-270-767-60733	Sequence 60733, A
45	83.9	104	2	US-09-621-976-6739	Sequence 6739, Ap
46	83.9	111	2	US-09-205-258-303	Sequence 303, App
47	83.9	111	2	US-10-004-860-303	Sequence 303, App
48	83.9	118	2	US-09-627-376-17	Sequence 17, Appli
49	83.9	118	2	US-10-047-676B-17	Sequence 17, Appli
50	83.9	156	2	US-09-270-767-45241	Sequence 45241, A
51	83.9	177	2	US-09-270-767-35390	Sequence 35390, A
52	83.9	177	2	US-09-270-767-50607	Sequence 50607, A
53	83.9	186	2	US-09-251-645-4	Sequence 4, Appli
54	83.9	201	2	US-09-270-767-33463	Sequence 33463, A
55	83.9	201	2	US-09-270-767-48680	Sequence 48680, A
56	83.9	249	2	US-09-270-767-38186	Sequence 38186, A
57	83.9	249	2	US-09-270-767-53403	Sequence 53403, A
58	83.9	249	2	US-09-248-796A-27128	Sequence 27128, A
59	83.9	310	2	US-09-830-910-2	Sequence 2, Appli
60	83.9	328	2	US-09-248-796A-15301	Sequence 15301, A
61	83.9	394	2	US-09-270-767-41366	Sequence 41366, A
62	83.9	394	2	US-09-270-767-56582	Sequence 56582, A
63	83.9	402	2	US-09-252-991A-25289	Sequence 25289, A
64	83.9	414	2	US-09-902-540-11308	Sequence 11308, A
65	83.9	426	2	US-09-602-787A-424	Sequence 424, App
66	83.9	437	2	US-09-489-039A-8958	Sequence 8958, Ap
67	83.9	446	2	US-09-252-991A-17185	Sequence 17185, A
68	83.9	453	2	US-09-489-039A-8303	Sequence 8303, Ap
69	83.9	493	2	US-09-252-991A-28992	Sequence 28992, A
70	83.9	557	2	US-09-540-236-2206	Sequence 2206, Ap
71	83.9	573	2	US-09-489-039A-11884	Sequence 11884, A
72	83.9	597	2	US-09-252-991A-22560	Sequence 22560, A
73	83.9	745	2	US-09-902-540-10275	Sequence 10275, A
74	83.9	892	2	US-09-540-236-2074	Sequence 2074, Ap
75	80.6	6	1	US-08-612-785B-9	Sequence 9, Appli
76	80.6	6	2	US-08-703-675C-32	Sequence 32, Appli
77	80.6	6	2	US-08-617-267C-9	Sequence 9, Appli
78	80.6	6	2	US-09-747-408-1	Sequence 1, Appli
79	80.6	6	2	US-09-747-408-3	Sequence 3, Appli
80	80.6	6	2	US-09-747-408-10	Sequence 10, Appli
81	80.6	6	2	US-09-747-408-11	Sequence 11, Appli
82	80.6	7	1	US-08-127-904-14	Sequence 14, Appli
83	80.6	7	1	US-08-612-785B-7	Sequence 7, Appli
84	80.6	7	2	US-08-703-675C-30	Sequence 30, Appli
85	80.6	7	2	US-08-617-267C-7	Sequence 7, Appli
86	80.6	7	2	US-09-264-709A-13	Sequence 13, Appli
87	80.6	7	2	US-09-747-408-2	Sequence 2, Appli
88	80.6	7	2	US-09-747-408-18	Sequence 18, Appli
89	80.6	7	2	US-09-747-408-19	Sequence 19, Appli
90	80.6	7	4	PCT-US94-10475-14	Sequence 14, Appli
91	80.6	8	1	US-08-612-785B-5	Sequence 5, Appli
92	80.6	8	1	US-08-630-645-1	Sequence 1, Appli
93	80.6	8	2	US-08-703-675C-28	Sequence 28, Appli
94	80.6	8	2	US-08-617-267C-5	Sequence 5, Appli
95	80.6	8	2	US-09-095-106A-44	Sequence 44, Appli
96	80.6	8	2	US-08-766-596A-1	Sequence 1, Appli
97	80.6	8	4	US-09-668-314C-73	Sequence 73, Appli
98	80.6	8	4	PCT-US96-10220-1	Sequence 1, Appli
99	80.6	9	2	US-08-766-596A-64	Sequence 64, Appli
100	80.6	9	2	US-09-747-408-20	Sequence 20, Appli

101	25	80.6	10	2	US-08-970-833-3	Sequence 3, Appli	174	25	80.6	28	1	US-08-293-284A-4	Sequence 4, Appli
102	25	80.6	10	2	US-09-724-961-20	Sequence 20, Appli	175	25	80.6	28	1	US-08-461-216-2	Sequence 2, Appli
103	25	80.6	10	2	US-09-724-961-21	Sequence 21, Appli	176	25	80.6	28	2	US-09-388-890-2	Sequence 2, Appli
104	25	80.6	10	2	US-09-724-961-22	Sequence 22, Appli	177	25	80.6	28	2	US-09-388-890-3	Sequence 3, Appli
105	25	80.6	10	2	US-09-724-961-23	Sequence 23, Appli	178	25	80.6	28	2	US-09-388-890-4	Sequence 4, Appli
106	25	80.6	10	2	US-09-724-961-24	Sequence 24, Appli	179	25	80.6	28	2	US-09-388-890-5	Sequence 5, Appli
107	25	80.6	10	2	US-09-580-018-20	Sequence 20, Appli	180	25	80.6	28	2	US-09-388-890-6	Sequence 6, Appli
108	25	80.6	10	2	US-09-580-018-21	Sequence 21, Appli	181	25	80.6	28	2	US-09-388-890-7	Sequence 7, Appli
109	25	80.6	10	2	US-09-580-018-22	Sequence 22, Appli	182	25	80.6	28	2	US-09-388-890-8	Sequence 8, Appli
110	25	80.6	10	2	US-09-580-018-23	Sequence 23, Appli	183	25	80.6	28	2	US-09-388-890-9	Sequence 9, Appli
111	25	80.6	10	2	US-09-580-018-24	Sequence 24, Appli	184	25	80.6	28	2	US-09-388-890-10	Sequence 10, Appli
112	25	80.6	10	2	US-09-724-551-20	Sequence 20, Appli	185	25	80.6	28	2	US-09-388-890-12	Sequence 12, Appli
113	25	80.6	10	2	US-09-724-551-21	Sequence 21, Appli	186	25	80.6	28	2	US-09-388-890-13	Sequence 13, Appli
114	25	80.6	10	2	US-09-724-551-22	Sequence 22, Appli	187	25	80.6	28	2	US-09-388-890-14	Sequence 14, Appli
115	25	80.6	10	2	US-09-724-551-23	Sequence 23, Appli	188	25	80.6	28	2	US-09-264-709A-1	Sequence 1, Appli
116	25	80.6	10	2	US-09-724-551-24	Sequence 24, Appli	189	25	80.6	28	2	US-08-723-661B-2	Sequence 2, Appli
117	25	80.6	10	2	US-09-724-940-20	Sequence 20, Appli	190	25	80.6	28	2	US-09-660-954-2	Sequence 2, Appli
118	25	80.6	10	2	US-09-724-940-21	Sequence 21, Appli	191	25	80.6	28	2	US-09-660-954-3	Sequence 3, Appli
119	25	80.6	10	2	US-09-724-940-22	Sequence 22, Appli	192	25	80.6	28	2	US-09-660-954-4	Sequence 4, Appli
120	25	80.6	10	2	US-09-724-940-23	Sequence 23, Appli	193	25	80.6	28	2	US-09-660-954-5	Sequence 5, Appli
121	25	80.6	10	2	US-09-724-940-24	Sequence 24, Appli	194	25	80.6	28	2	US-09-660-954-6	Sequence 6, Appli
122	25	80.6	11	1	US-08-630-645-14	Sequence 14, Appli	195	25	80.6	28	2	US-09-660-954-7	Sequence 7, Appli
123	25	80.6	11	2	US-08-766-596A-14	Sequence 14, Appli	196	25	80.6	28	2	US-09-660-954-8	Sequence 8, Appli
124	25	80.6	11	2	US-09-988-842-9	Sequence 9, Appli	197	25	80.6	28	2	US-09-660-954-9	Sequence 9, Appli
125	25	80.6	11	2	US-09-988-842-25	Sequence 25, Appli	198	25	80.6	28	2	US-09-660-954-10	Sequence 10, Appli
126	25	80.6	11	4	PCR-US96-10220-14	Sequence 14, Appli	199	25	80.6	28	2	US-09-660-954-12	Sequence 12, Appli
127	25	80.6	14	2	US-09-594-366-5	Sequence 5, Appli	200	25	80.6	28	2	US-09-660-954-13	Sequence 13, Appli
128	25	80.6	14	2	US-09-993-800-5	Sequence 5, Appli	201	25	80.6	28	2	US-09-660-954-14	Sequence 14, Appli
129	25	80.6	15	1	US-08-612-785B-14	Sequence 14, Appli	202	25	80.6	28	2	US-08-898-300-4	Sequence 4, Appli
130	25	80.6	15	1	US-08-612-785B-37	Sequence 37, Appli	203	25	80.6	28	2	US-08-824-513-4	Sequence 4, Appli
131	25	80.6	15	2	US-08-617-267C-14	Sequence 14, Appli	204	25	80.6	28	2	US-09-623-548A-959	Sequence 959, App
132	25	80.6	15	2	US-08-766-596A-56	Sequence 56, Appli	205	25	80.6	28	2	US-09-623-548A-965	Sequence 965, App
133	25	80.6	15	2	US-08-766-596A-57	Sequence 57, Appli	206	25	80.6	28	2	US-09-623-548A-976	Sequence 976, App
134	25	80.6	15	2	US-08-766-596A-58	Sequence 58, Appli	207	25	80.6	28	2	US-09-623-548A-992	Sequence 992, App
135	25	80.6	15	2	US-08-766-596A-60	Sequence 60, Appli	208	25	80.6	28	2	US-09-623-548A-1003	Sequence 1003, Ap
136	25	80.6	15	2	US-08-766-596A-61	Sequence 61, Appli	209	25	80.6	28	2	US-09-657-276-959	Sequence 959, App
137	25	80.6	15	2	US-08-766-596A-63	Sequence 63, Appli	210	25	80.6	28	2	US-09-657-276-965	Sequence 965, App
138	25	80.6	15	2	US-08-766-596A-65	Sequence 65, Appli	211	25	80.6	28	2	US-09-657-276-976	Sequence 976, App
139	25	80.6	17	2	US-09-264-709A-2	Sequence 2, Appli	212	25	80.6	28	2	US-09-657-276-992	Sequence 992, App
140	25	80.6	17	2	US-09-594-366-3	Sequence 3, Appli	213	25	80.6	28	2	US-09-657-276-1003	Sequence 1003, Ap
141	25	80.6	17	2	US-09-623-548A-950	Sequence 950, App	214	25	80.6	28	2	US-09-865-294A-66	Sequence 66, Appli
142	25	80.6	17	2	US-09-623-548A-983	Sequence 983, App	215	25	80.6	30	1	US-08-609-090-3	Sequence 3, Appli
143	25	80.6	17	2	US-09-992-800-3	Sequence 3, Appli	216	25	80.6	30	2	US-09-861-847A-1	Sequence 1, Appli
144	25	80.6	17	2	US-09-657-276-950	Sequence 950, App	217	25	80.6	33	1	US-08-609-090-4	Sequence 4, Appli
145	25	80.6	17	2	US-09-657-276-983	Sequence 983, App	218	25	80.6	34	1	US-08-475-579A-4	Sequence 4, Appli
146	25	80.6	19	2	US-09-870-833-11	Sequence 11, Appli	219	25	80.6	35	1	US-08-304-585-6	Sequence 6, Appli
147	25	80.6	19	2	US-09-723-384-5	Sequence 5, Appli	220	25	80.6	35	1	US-08-612-785B-16	Sequence 16, Appli
148	25	80.6	19	2	US-09-724-961-75	Sequence 75, Appli	221	25	80.6	35	1	US-08-612-785B-36	Sequence 36, Appli
149	25	80.6	19	2	US-09-724-552-5	Sequence 5, Appli	222	25	80.6	35	1	US-08-612-785B-38	Sequence 38, Appli
150	25	80.6	19	2	US-09-580-018-75	Sequence 75, Appli	223	25	80.6	35	1	US-08-612-785B-40	Sequence 40, Appli
151	25	80.6	19	2	US-09-723-927-5	Sequence 5, Appli	224	25	80.6	35	2	US-08-617-267C-16	Sequence 16, Appli
152	25	80.6	19	2	US-09-724-489-5	Sequence 5, Appli	225	25	80.6	35	2	US-09-623-548A-979	Sequence 979, App
153	25	80.6	19	2	US-09-724-477-5	Sequence 5, Appli	226	25	80.6	35	2	US-09-623-548A-1006	Sequence 1006, Ap
154	25	80.6	19	2	US-09-723-762-5	Sequence 5, Appli	227	25	80.6	35	2	US-09-657-276-979	Sequence 979, App
155	25	80.6	19	2	US-09-201-430-5	Sequence 5, Appli	228	25	80.6	35	2	US-09-657-276-1006	Sequence 1006, Ap
156	25	80.6	19	2	US-09-724-551-75	Sequence 75, Appli	229	25	80.6	36	1	US-08-609-090-6	Sequence 6, Appli
157	25	80.6	19	2	US-10-815-353-5	Sequence 5, Appli	230	25	80.6	36	2	US-09-861-847A-6	Sequence 6, Appli
158	25	80.6	19	2	US-10-816-529-5	Sequence 5, Appli	231	25	80.6	36	2	US-09-861-847A-11	Sequence 11, Appli
159	25	80.6	19	2	US-10-815-391-5	Sequence 5, Appli	232	25	80.6	38	1	US-08-302-808-1	Sequence 1, Appli
160	25	80.6	19	2	US-10-816-022-5	Sequence 5, Appli	233	25	80.6	38	1	US-07-737-371E-68	Sequence 68, Appli
161	25	80.6	19	2	US-09-724-940-75	Sequence 75, Appli	234	25	80.6	38	1	US-08-986-948-1	Sequence 1, Appli
162	25	80.6	19	2	US-10-934-609-5	Sequence 5, Appli	235	25	80.6	38	2	US-09-623-548A-975	Sequence 975, App
163	25	80.6	19	2	US-10-884-892-5	Sequence 5, Appli	236	25	80.6	38	2	US-09-623-548A-1002	Sequence 1002, Ap
164	25	80.6	20	2	US-08-970-833-10	Sequence 10, Appli	237	25	80.6	38	2	US-09-657-276-975	Sequence 975, App
165	25	80.6	20	2	US-09-724-953-33	Sequence 33, Appli	238	25	80.6	38	2	US-09-657-276-1002	Sequence 1002, Ap
166	25	80.6	20	2	US-09-724-567-33	Sequence 33, Appli	239	25	80.6	39	1	US-08-304-585-5	Sequence 5, Appli
167	25	80.6	20	2	US-09-979-952-33	Sequence 33, Appli	240	25	80.6	39	1	US-08-302-808-2	Sequence 2, Appli
168	25	80.6	20	2	US-09-585-817-33	Sequence 33, Appli	241	25	80.6	39	1	US-08-609-090-7	Sequence 7, Appli
169	25	80.6	26	1	US-08-304-585-7	Sequence 7, Appli	242	25	80.6	39	1	US-08-682-245A-1	Sequence 1, Appli
170	25	80.6	28	1	US-08-346-849-4	Sequence 4, Appli	243	25	80.6	39	1	US-08-986-948-2	Sequence 2, Appli
171	25	80.6	28	1	US-08-302-808-7	Sequence 7, Appli	244	25	80.6	40	1	US-07-744-767A-1	Sequence 1, Appli
172	25	80.6	28	1	US-08-609-090-2	Sequence 2, Appli	245	25	80.6	40	1	US-08-235-400-2	Sequence 2, Appli
173	25	80.6	28	1	US-08-986-948-7	Sequence 7, Appli	246	25	80.6	40	1	US-08-476-464A-2	Sequence 2, Appli

```
247 25 80.6 40 1 US-08-304-585-1 Sequence 1, Appli
248 25 80.6 40 1 US-08-304-585-8 Sequence 8, Appli
249 25 80.6 40 1 US-08-302-808-3 Sequence 3, Appli
250 25 80.6 40 1 US-08-433-734-1 Sequence 1, Appli
251 25 80.6 40 1 US-08-609-090-8 Sequence 8, Appli
252 25 80.6 40 1 US-07-737-371B-69 Sequence 69, Appli
253 25 80.6 40 1 US-08-682-245A-2 Sequence 2, Appli
254 25 80.6 40 1 US-08-986-948-3 Sequence 3, Appli
255 25 80.6 40 1 US-08-461-216-1 Sequence 1, Appli
256 25 80.6 40 2 US-08-959-148-1 Sequence 1, Appli
257 25 80.6 40 2 US-09-242-724-22 Sequence 22, Appli
258 25 80.6 40 2 US-08-723-661B-1 Sequence 1, Appli
259 25 80.6 40 2 US-09-062-365-3 Sequence 3, Appli
260 25 80.6 40 2 US-09-133-866-1 Sequence 1, Appli
261 25 80.6 40 2 US-09-861-847A-7 Sequence 7, Appli
262 25 80.6 40 2 US-09-861-847A-8 Sequence 8, Appli
263 25 80.6 40 2 US-09-988-842-3 Sequence 3, Appli
264 25 80.6 40 2 US-10-455-218-1 Sequence 1, Appli
265 25 80.6 40 2 US-10-151-614-1 Sequence 1, Appli
266 25 80.6 40 2 US-09-623-548A-956 Sequence 956, App
267 25 80.6 40 2 US-09-623-548A-962 Sequence 962, App
268 25 80.6 40 2 US-09-623-548A-968 Sequence 968, App
269 25 80.6 40 2 US-09-623-548A-978 Sequence 978, App
270 25 80.6 40 2 US-09-623-548A-989 Sequence 989, App
271 25 80.6 40 2 US-09-623-548A-995 Sequence 995, App
272 25 80.6 40 2 US-09-623-548A-1005 Sequence 1005, Ap
273 25 80.6 40 2 US-09-657-276-956 Sequence 956, App
274 25 80.6 40 2 US-09-657-276-962 Sequence 962, App
275 25 80.6 40 2 US-09-657-276-968 Sequence 968, App
276 25 80.6 40 2 US-09-657-276-978 Sequence 978, App
277 25 80.6 40 2 US-09-657-276-989 Sequence 989, App
278 25 80.6 40 2 US-09-657-276-995 Sequence 995, App
279 25 80.6 40 2 US-09-657-276-1005 Sequence 1005, Ap
280 25 80.6 40 2 US-09-962-955D-36 Sequence 36, Appli
281 25 80.6 40 4 PCT-US92-06700-1 Sequence 1, Appli
282 25 80.6 41 1 US-07-819-361-1 Sequence 1, Appli
283 25 80.6 41 1 US-08-302-808-4 Sequence 4, Appli
284 25 80.6 41 1 US-08-682-245A-3 Sequence 3, Appli
285 25 80.6 41 1 US-08-986-948-4 Sequence 4, Appli
286 25 80.6 42 1 US-07-744-767A-2 Sequence 2, Appli
287 25 80.6 42 1 US-08-179-574-1 Sequence 1, Appli
288 25 80.6 42 1 US-08-271-162-5 Sequence 5, Appli
289 25 80.6 42 1 US-08-347-144-1 Sequence 1, Appli
290 25 80.6 42 1 US-08-462-859A-19 Sequence 19, Appli
291 25 80.6 42 1 US-08-123-659A-19 Sequence 19, Appli
292 25 80.6 42 1 US-08-464-247A-19 Sequence 19, Appli
293 25 80.6 42 1 US-08-464-248A-19 Sequence 19, Appli
294 25 80.6 42 1 US-08-476-464A-1 Sequence 1, Appli
295 25 80.6 42 1 US-08-304-585-2 Sequence 2, Appli
296 25 80.6 42 1 US-08-302-808-5 Sequence 5, Appli
297 25 80.6 42 1 US-08-268-348A-1 Sequence 1, Appli
298 25 80.6 42 1 US-08-268-348A-2 Sequence 2, Appli
299 25 80.6 42 1 US-08-268-348A-3 Sequence 3, Appli
300 25 80.6 42 1 US-08-268-348A-4 Sequence 4, Appli
```

ALIGNMENTS

```
RESULT 1
US-09-747-408-4
; Sequence 4, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
```

```
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-4

Query Match          100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6
|||||

RESULT 2
US-09-747-408-12
; Sequence 12, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; TITLE OF INVENTION: Compounds And Methods For Modulating
; Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-12

Query Match          100.0%; Score 31; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      1 KVFVFA 6
|||||

RESULT 3
US-09-248-796A-18091
; Sequence 18091, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18091
; LENGTH: 1283
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18091

Query Match          96.8%; Score 30; DB 2; Length 1283;
Best Local Similarity 83.3%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```


; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..506

; OTHER INFORMATION: /note= "Amino acid sequence of FAE1

; OTHER INFORMATION: protein."

US-09-362-633-2

Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 5.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFPPA 6

||:||||

356 KFLFFA 361

RESULT 7

US-09-877-476-2

; Sequence 2, Application US/09877476

; Patent No. 6713664

; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.

; APPLICANT: Blacklock, Brenda J.

; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

; FILE REFERENCE: 07148-108001

; CURRENT APPLICATION NUMBER: US/09/877,476

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,326

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 506

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-09-877-476-2

Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 5.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFPPA 6

||:||||

356 KFLFFA 361

RESULT 8

US-09-877-476-28

; Sequence 28, Application US/09877476

; Patent No. 6713664

; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.

; APPLICANT: Blacklock, Brenda J.

; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

; FILE REFERENCE: 07148-108001

; CURRENT APPLICATION NUMBER: US/09/877,476

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,326

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; LENGTH: 506

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 5' 176 amino acids from B. napus elongase KCS (SEQ

; OTHER INFORMATION: ID NO:4) and 3' 330 amino acids from A. thaliana

; OTHER INFORMATION: FAE1 (SEQ ID NO:2); designated Bn176

US-09-877-476-28

Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 5.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFPPA 6

||:||||

356 KFLFFA 361

RESULT 9

US-09-877-476-30

; Sequence 30, Application US/09877476

; Patent No. 6713664

; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.

; APPLICANT: Blacklock, Brenda J.

; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

; FILE REFERENCE: 07148-108001

; CURRENT APPLICATION NUMBER: US/09/877,476

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,326

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 506

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 5' 399 amino acids from A. thaliana FAE1 (SEQ ID

; OTHER INFORMATION: NO:2) and 3' 107 amino acids from B. napus

; OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399

; NAME/KEY: VARIANT

; LOCATION: (0)...(0)

; OTHER INFORMATION: Xaa = Pro or Gln

US-09-877-476-30

Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 5.1e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFPPA 6

||:||||

356 KFLFFA 361

RESULT 10

US-09-877-476-36

; Sequence 36, Application US/09877476

; Patent No. 6713664

; GENERAL INFORMATION:

; APPLICANT: Jaworski, Jan G.

; APPLICANT: Blacklock, Brenda J.

; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA

; FILE REFERENCE: 07148-108001

; CURRENT APPLICATION NUMBER: US/09/877,476

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,326

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 36

; LENGTH: 506

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: 506 amino acids from A. thaliana FAE1 (SEQ ID

; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated

; OTHER INFORMATION: At K92R; hypothetical

US-09-877-476-36

Query Match 90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
||:|:
Db 356 KFLPFA 361

RESULT 11
US-09-830-230A-437
; Sequence 437, Application US/09830230A
; Patent No. 6902893
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481US
; CURRENT APPLICATION NUMBER: US/09/830,230A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 437
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-830-230A-437

Query Match 90.3%; Score 28; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
:||||
Db 41 REVFFA 46

RESULT 12
US-09-248-796A-26311
; Sequence 26311, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26311
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26311

Query Match 87.1%; Score 27; DB 2; Length 67;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
||:|:
Db 16 KFIFFA 21

RESULT 13
US-09-513-999C-4859
; Sequence 4859, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4859
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-4859

Query Match 87.1%; Score 27; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
||||
Db 32 KFVFF 36

RESULT 14
US-09-270-767-40694
; Sequence 40694, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40694
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40694

Query Match 87.1%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
||||
Db 84 KFVFF 88

RESULT 15
US-09-270-767-55910
; Sequence 55910, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55910
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55910

Query Match 87.1%; Score 27; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 84 KVVFF 88

RESULT 16

US-09-823-153-4
; Sequence 4; Application US/09823153
; Patent No. 6713248
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Roberts, Susan
; APPLICANT: Pak, Roger
; APPLICANT: Lewis, Martin
; APPLICANT: Smith, David
; APPLICANT: Hendrick, Joseph
; APPLICANT: Vinitesky, Alexander
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004
; CURRENT APPLICATION NUMBER: US/09/823,153
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Human Beta App
US-09-823-153-4

Query Match 87.1%; Score 27; DB 2; Length 104;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
Db 21 EFVFFA 26

RESULT 17

US-09-270-767-57813
; Sequence 57813, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57813
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57813

Query Match 87.1%; Score 27; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
Db 62 KVVFF 66

RESULT 18

US-09-902-540-10859
; Sequence 10859, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10859
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10859

Query Match 87.1%; Score 27; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
Db 132 KVVFF 136

RESULT 19

US-09-134-001C-5445
; Sequence 5445, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5445
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5445

Query Match 87.1%; Score 27; DB 2; Length 240;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFFA 6
Db 168 QVVFFA 173

```
RESULT 20
US-09-270-767-42516
; Sequence 42516, Application US/09270767
; Patent No. 6703491
; ORGANISM: Drosophila melanogaster
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42516
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-42516
Query Match      87.1%; Score 27; DB 2; Length 266;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 62 KPVFF 66

RESULT 21
US-09-248-796A-19539
; Sequence 19539, Application US/09248796A
; Patent No. 6747137
; ORGANISM: Candida albicans
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19539
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19539
Query Match      87.1%; Score 27; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 23 KPVFF 27

RESULT 22
US-09-270-767-40453
; Sequence 40453, Application US/09270767
; Patent No. 6703491
; ORGANISM: Drosophila melanogaster
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40453
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40453
Query Match      87.1%; Score 27; DB 2; Length 340;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
Db 310 KYIFFA 315

RESULT 23
US-09-270-767-55669
; Sequence 55669, Application US/09270767
; Patent No. 6703491
; ORGANISM: Drosophila melanogaster
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55669
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55669
Query Match      87.1%; Score 27; DB 2; Length 340;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
Db 310 KYIFFA 315

RESULT 24
US-09-270-767-45548
; Sequence 45548, Application US/09270767
; Patent No. 6703491
; ORGANISM: Drosophila melanogaster
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45548
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45548
Query Match      87.1%; Score 27; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 7.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
Db 49 KPVFF 53
```



```

RESULT 25
US-09-270-767-34763
; Sequence 34763, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34763
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34763

Query Match      87.1%; Score 27; DB 2; Length 525;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 6
      |:|||
Db      446 KYIFFA 451

RESULT 26
US-09-270-767-49980
; Sequence 49980, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49980
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-49980

Query Match      87.1%; Score 27; DB 2; Length 525;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFF 6
      |:|||
Db      446 KYIFFA 451

RESULT 27
US-08-704-711A-1
; Sequence 1, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>

```

```

; CLTY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-1

Query Match      87.1%; Score 27; DB 2; Length 579;
Best Local Similarity 100.0%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
      |:|||
Db      375 KVFVF 379

RESULT 28
US-09-521-220-1
; Sequence 1, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>

```

```

; 21-OCT-1994
; 17-MAR-1994
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/704,711
;   FILING DATE: <Unknown>
;   APPLICATION NUMBER: DE 4438838.1
;   FILING DATE: 21-OCT-1994
;   APPLICATION NUMBER: DE 4409663.1
;   FILING DATE: 17-MAR-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: GRANADOS, Patricia D.
;     REGISTRATION NUMBER: 33,683
;     REFERENCE/DOCKET NUMBER: 26083/124
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (202) 672-5300
;       TELEFAX: (202) 672-5399
;       TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 579 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
;
; US-09-521-220-1
;
; Query Match      87.1%; Score 27; DB 2; Length 579;
; Best Local Similarity 100.0%; Pred. No. 9e+02;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy      1 KPVFF 5
;         |||||
; Db      375 KPVFF 379
;
;
; RESULT 29
; US-08-704-711A-2
; Sequence 2, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
;   APPLICANT: WILL, Horst
;   APPLICANT: HINZMANN, Bernd
;   TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
;   TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
;   NUMBER OF SEQUENCES: 22
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: 3000 K Street, N.W., Suite 500
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: USA
;     ZIP: 20007-5109
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/704,711A
;     FILING DATE: 20-NOV-1996
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: WO PCT/DE95/00357
;     FILING DATE: 17-MAR-1995
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: DE 4438838.1
;     FILING DATE: 21-OCT-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: DE 4409663.1
;     FILING DATE: 17-MAR-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: GRANADOS, Patricia D.
;     REGISTRATION NUMBER: 33,683

```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/211,704A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/005,263
; FILING DATE: 09-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SP0781K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-211-704A-9

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVFF 5
DB      378 KPVFF 382

RESULT 32
US-09-521-220-2
; Sequence 2, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 582 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-521-220-2

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVFF 5
DB      378 KPVFF 382

RESULT 33
US-09-391-104-28
; Sequence 28, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; FALDUTO, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE.
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-391-104-28

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVFF 5
DB      378 KPVFF 382

RESULT 34
US-09-919-497-84
; Sequence 84, Application US/09919497
; Patent No. 6773883
; GENERAL INFORMATION:
; APPLICANT: Muter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 582
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-09-519-497-84

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KPVFF 5
Db 378 KPVFF 382

RESULT 35
US-09-689-730-1
; Sequence 1, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-689-730-1

Query Match      87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 9.1e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KPVFF 5
Db 378 KPVFF 382

RESULT 36
US-10-449-315-2
; Sequence 2, Application US/10449315
; Patent No. 6942984
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1024
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-2

Query Match      87.1%; Score 27; DB 2; Length 1024;
Best Local Similarity 100.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KPVFF 5
Db 378 KPVFF 382
```

```
Db 198 KPVFF 202

RESULT 37
US-10-449-315-5
; Sequence 5, Application US/10449315
; Patent No. 6942984
; GENERAL INFORMATION:
; APPLICANT: Bertin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-329001
; CURRENT APPLICATION NUMBER: US/10/449,315
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US/09/841,739
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 09/697,089
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,822
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1204
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-315-5

Query Match      87.1%; Score 27; DB 2; Length 1204;
Best Local Similarity 100.0%; Pred. No. 1.7e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KPVFF 5
Db 355 KPVFF 359

RESULT 38
US-09-270-767-37091
; Sequence 37091, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37091
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-37091

Query Match      83.9%; Score 26; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 2 FVFFA 6
Db 16 FVFFA 20

RESULT 39
US-09-270-767-52308
; Sequence 52308, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
```

; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52308
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-52308

Query Match 83.9%; Score 26; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
|||
Db 16 FVFFA 20

RESULT 40
US-09-798-635A-41
; Sequence 41, Application US/09798635A
; Patent No. 6936432
; GENERAL INFORMATION:
; APPLICANT: Gopalan, Venkat
; APPLICANT: Jovanovic, Milan
; APPLICANT: Eder, Paul S.
; APPLICANT: Giordano, Tony
; APPLICANT: Powers, Gordon D.
; APPLICANT: Xavier, K. Asish
; TITLE OF INVENTION: Their Use in Identifying Antibacterial Compounds
; FILE REFERENCE: 50093/016002
; CURRENT APPLICATION NUMBER: US/09/798, 635A
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/516,061
; PRIOR FILING DATE: 2000-03-01
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-798-635A-41

Query Match 83.9%; Score 26; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
|||
Db 39 FVFFA 43

RESULT 41
US-10-125-258-44
; Sequence 44, Application US/10125258
; Patent No. 6891085
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnail, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 44
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis
US-10-125-258-44

Query Match 83.9%; Score 26; DB 2; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
|||
Db 8 FVFFA 12

RESULT 42
US-09-583-110-4885
; Sequence 4885, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4885
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4885

Query Match 83.9%; Score 26; DB 2; Length 61;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFF 5
||:|
Db 44 KTIFF 48

RESULT 43
US-10-125-258-43
; Sequence 43, Application US/10125258
; Patent No. 6891085
; GENERAL INFORMATION:
; APPLICANT: Altier, Daniel J.
; APPLICANT: Herrmann, Rafael
; APPLICANT: Lu, Albert L.
; APPLICANT: McCutchen, Billy F.
; APPLICANT: Presnail, James K.
; APPLICANT: Weaver, Janine L.
; APPLICANT: Wong, James F. H.
; TITLE OF INVENTION: Antimicrobial Polypeptides and Their
; FILE REFERENCE: 35718/246215
; CURRENT APPLICATION NUMBER: US/10/125,258
; CURRENT FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: 60/285,355
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Ostrinia nubilalis

US-10-125-258-43

Query Match 83.9%; Score 26; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
DB 8 FVFFA 12

RESULT 44

US-09-270-767-60733
; Sequence 60733, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60733
; LENGTH: 84
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-60733

Query Match 83.9%; Score 26; DB 2; Length 84;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
|||:
DB 48 KFIFF 52

RESULT 45

US-09-621-976-6739
; Sequence 6739, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6739
; LENGTH: 104
; TYPE: PRT
; ORGANISM: *Homo sapiens*
US-09-621-976-6739

Query Match 83.9%; Score 26; DB 2; Length 104;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|||||
DB 31 FVFFA 35

RESULT 46

US-09-205-258-303
; Sequence 303, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.

; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007E1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963

```
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 303
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-205-258-303

Query Match      83.9%; Score 26; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |||||
Db      79 FVFFA 83

RESULT 47
US-10-004-860-303
; Sequence 303, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 303
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-004-860-303

Query Match      83.9%; Score 26; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |||||
Db      79 FVFFA 83

RESULT 48
US-09-627-376-17
; Sequence 17, Application US/09627376
; Patent No. 6342385
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17402/22
; CURRENT APPLICATION NUMBER: US/09/627,376

Query Match      83.9%; Score 26; DB 2; Length 156;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVPFF 5
      |||||
```

```
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-09-627-376-17

Query Match      83.9%; Score 26; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |||||
Db      39 FVFFA 43

RESULT 49
US-10-047-676B-17
; Sequence 17, Application US/10047676B
; Patent No. 6699970
; GENERAL INFORMATION:
; APPLICANT: Qi, Fengxia
; APPLICANT: Caulfield, Page W.
; APPLICANT: Chen, Ping
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS
; FILE REFERENCE: UAB-17403/22
; CURRENT APPLICATION NUMBER: US/10/047,676B
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 09/627,376
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-047-676B-17

Query Match      83.9%; Score 26; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |||||
Db      39 FVFFA 43

RESULT 50
US-09-270-767-45241
; Sequence 45241, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45241
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45241

Query Match      83.9%; Score 26; DB 2; Length 156;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVPFF 5
      |||||
```

```
Db 120 KFIFF 124

; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: CCG1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-09-251-645-4

Query Match 83.9%; Score 26; DB 2; Length 186;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
Db 134 QFIFFA 139

RESULT 54
US-09-270-767-33463
; Sequence 33463, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33463
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33463

Query Match 83.9%; Score 26; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 80 FVFFA 84

RESULT 55
US-09-270-767-48680
; Sequence 48680, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48680
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48680

Query Match 83.9%; Score 26; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 80 FVFFA 84

; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; FILE REFERENCE: CCG1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-09-251-645-4

Query Match 83.9%; Score 26; DB 2; Length 186;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
Db 134 QFIFFA 139

RESULT 54
US-09-270-767-33463
; Sequence 33463, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33463
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33463

Query Match 83.9%; Score 26; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 122 FVFFA 126

RESULT 52
US-09-270-767-50607
; Sequence 50607, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50607
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50607

Query Match 83.9%; Score 26; DB 2; Length 177;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 122 FVFFA 126

RESULT 53
US-09-251-645-4
; Sequence 645-4, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.
```


Db 80 FVFFA 84

RESULT 56

US-09-270-767-38186
; Sequence 38186, Application US/09270767
; Patent No. 6703491

GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 38186

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-38186

Query Match 83.9%; Score 26; DB 2; Length 249;

Best Local Similarity 80.0%; Pred. No. 6.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5

||:|

Db 196 KFIFF 200

RESULT 57

US-09-270-767-53403

; Sequence 53403, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 53403

; LENGTH: 249

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-53403

Query Match 83.9%; Score 26; DB 2; Length 249;

Best Local Similarity 80.0%; Pred. No. 6.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5

||:|

Db 196 KFIFF 200

RESULT 58

US-09-248-796A-27128

; Sequence 27128, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; LOCATION: (4), (5)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-15301

Query Match 83.9%; Score 26; DB 2; Length 328;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 6 QVIFFA 11

RESULT 61

US-09-270-767-41366
; Sequence 41366, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 41366
; LENGTH: 394
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-41366

Query Match 83.9%; Score 26; DB 2; Length 394;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 267 KPVWFA 272

RESULT 62

US-09-270-767-56582
; Sequence 56582, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 56582
; LENGTH: 394
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-56582

Query Match 83.9%; Score 26; DB 2; Length 394;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 267 KPVWFA 272

RESULT 63

US-09-252-991A-25289

; Sequence 25289, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25289
; LENGTH: 402
; TYPE: PRT
; ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-25289

Query Match 83.9%; Score 26; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFFA 6
:|||||
Db 309 FVFFFA 313

RESULT 64

US-09-902-540-11308
; Sequence 11308, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11308
; LENGTH: 414
; TYPE: PRT
; ORGANISM: *Myxococcus xanthus*
US-09-902-540-11308

Query Match 83.9%; Score 26; DB 2; Length 414;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFFA 6
:|||||
Db 185 FVFFFA 189

RESULT 65

US-09-602-787A-424
; Sequence 424, Application US/09602787A
; Patent No. 6696561
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Mark
; APPLICANT: Krüger, Burkhard
; APPLICANT: Schöder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauser, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT

FILE REFERENCE: BGI-125CP
CURRENT APPLICATION NUMBER: US/09/602,787A
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: USSN 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 19931454.3
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931478.0
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19931563.9
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: DE 19932122.1
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932124.8
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932125.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932180.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932182.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932190.6
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932191.4
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932209.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932212.0
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932227.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932228.7
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932229.5
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932230.9
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932927.3
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19940764.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940765.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940766.5
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940830.0
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940831.9
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940832.7
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19940833.5
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: DE 19941378.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941395.9
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942077.7
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942078.5
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942079.3
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03

NUMBER OF SEQ ID NOS: 678
SEQ ID NO 424
LENGTH: 426
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-602-787A-424
Query Match 83.9%; Score 26; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FVFFA 6
Db 120 FVFFA 124
RESULT 66
US-09-489-039A-8958
Sequence 8958, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8958
LENGTH: 437
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8958
Query Match 83.9%; Score 26; DB 2; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FVFFA 6
Db 36 FVFFA 40
RESULT 67
US-09-252-991A-17185
Sequence 17185, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17185
LENGTH: 446
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17185
Query Match 83.9%; Score 26; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FVFFA 6
Db 11111

Db 48 FVFFA 52

RESULT 68

US-09-489-039A-8303
; Sequence 8303, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 8303

; LENGTH: 453

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (133)

; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-489-039A-8303

Query Match

Best Local Similarity 83.9%; Score 26; DB 2; Length 453;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6

|||||

Db 266 FVFFA 270

RESULT 69

US-09-252-991A-28992
; Sequence 28992, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 28992

; LENGTH: 493

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-28992

Query Match

Best Local Similarity 83.9%; Score 26; DB 2; Length 493;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5

|||||

Db 2 KPIFF 6

RESULT 70

US-09-540-236-2206
; Sequence 2206, Application US/09540236
; Patent No. 6673910

; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARR

; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236

; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840

; SEQ ID NO 2206

; LENGTH: 557

; TYPE: PRT

; ORGANISM: M.catarrhalis

US-09-540-236-2206

Query Match

Best Local Similarity 83.9%; Score 26; DB 2; Length 557;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6

|||||

Db 355 FVFFA 359

RESULT 71

US-09-489-039A-11884
; Sequence 11884, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 11884

; LENGTH: 573

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-11884

Query Match

Best Local Similarity 83.9%; Score 26; DB 2; Length 573;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6

|||||

Db 511 FVFFA 515

RESULT 72

US-09-252-991A-22560
; Sequence 22560, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 22560

; LENGTH: 597

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-22560

Query Match

83.9%; Score 26; DB 2; Length 597;

Best Local Similarity 100.0%; Pred. No. 1.4e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 2 FVFFA 6
|
|
|
|
Db 90 FVFFA 94

RESULT 73

US-09-540-540-10275
; Sequence 10275, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 39-10(11849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10275
; LENGTH: 745
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-540-540-10275

Query Match 83.9%; Score 26; DB 2; Length 745;

Best Local Similarity 100.0%; Pred. No. 1.8e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 2 FVFFA 6
|
|
|
|
Db 185 FVFFA 189

RESULT 74

US-09-540-236-2074
; Sequence 2074, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2074
; LENGTH: 892
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2074

Query Match 83.9%; Score 26; DB 2; Length 892;

Best Local Similarity 100.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 2 FVFFA 6
|
|
|
|
Db 658 FVFFA 662

RESULT 75

US-08-612-785B-9
; Sequence 9, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: Ab Peptides that Modulate b-Amyloid

; TITLE OF INVENTION: Aggregation
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/612,785B
; FILING DATE: Herewith
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/404,831
; FILING DATE: 14-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-612-785B-9

Query Match 80.6%; Score 25; DB 1; Length 6;

Best Local Similarity 83.3%; Pred. No. 4.6e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1;

Qy 1 KVFFFA 6
|
|
|
|
Db 1 KLVFFA 6

Search completed: December 29, 2005, 17:52:38
Job time : 21.1323 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-12
Perfect score: 31
Sequence: 1 KVFPPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

A_Geneseq_21.*

1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*
9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	6	4	AAB48477
2	31	100.0	6	4	AAB48485
3	31	100.0	6	4	AAB82625
4	31	100.0	6	4	AAB82633
5	31	100.0	6	5	AAB96813
6	31	100.0	6	5	AAB96821
7	31	100.0	6	5	AAB11659
8	31	100.0	6	5	AAB11651
9	31	100.0	6	6	AAB35447
10	31	100.0	6	6	AAB35440
11	31	100.0	6	8	ADQ37264
12	31	100.0	6	8	ADQ37316
13	31	100.0	6	8	ADQ37324
14	31	100.0	6	8	ADQ37272
15	31	100.0	6	9	ADY37931
16	31	100.0	6	9	ADY37923
17	31	100.0	336	6	ABM89186
18	30	96.8	202	5	ADK35620
19	28	90.3	75	4	ABBI17989
20	28	90.3	452	8	ADN23626
21	28	90.3	485	8	ADN46740
22	28	90.3	490	2	AAV19993
23	28	90.3	506	2	AAV95594
24	28	90.3	506	5	AAI17850

25	28	90.3	506	5	AAE17622	Aae17622 A. thalia
26	28	90.3	506	5	AAE17625	Aae17625 Arabidops
27	28	90.3	506	5	AAE17621	Aae17621 Brassica
28	28	90.3	506	5	AAE17608	Aae17608 Arabidops
29	28	90.3	506	9	AEA37517	Aea37517 Arabidops
30	28	90.3	508	2	AAV19992	Aav19992 B. burgdo
31	28	90.3	508	6	ABU19128	Abu19128 Protein e
32	28	90.3	508	6	ABU24005	Abu24005 Protein e
33	28	90.3	571	6	ADN19501	Adn19501 Bacterial
34	28	90.3	1089	8	ADN19501	Adn19501 Bacterial
35	27	87.1	52	3	AAE17622	Aae17622 A. thalia
36	27	87.1	52	3	AAE17625	Aae17625 Arabidops
37	27	87.1	52	3	AAE17608	Aae17608 Arabidops
38	27	87.1	52	3	AAE17621	Aae17621 Brassica
39	27	87.1	52	3	AAE17608	Aae17608 Arabidops
40	27	87.1	52	3	AAE17621	Aae17621 Brassica
41	27	87.1	52	3	AAE17608	Aae17608 Arabidops
42	27	87.1	52	3	AAE17621	Aae17621 Brassica
43	27	87.1	52	3	AAE17608	Aae17608 Arabidops
44	27	87.1	52	3	AAE17621	Aae17621 Brassica
45	27	87.1	52	3	AAE17608	Aae17608 Arabidops
46	27	87.1	52	3	AAE17621	Aae17621 Brassica
47	27	87.1	52	3	AAE17608	Aae17608 Arabidops
48	27	87.1	52	3	AAE17621	Aae17621 Brassica
49	27	87.1	52	3	AAE17608	Aae17608 Arabidops
50	27	87.1	52	3	AAE17621	Aae17621 Brassica
51	27	87.1	52	3	AAE17608	Aae17608 Arabidops
52	27	87.1	52	3	AAE17621	Aae17621 Brassica
53	27	87.1	52	3	AAE17608	Aae17608 Arabidops
54	27	87.1	52	3	AAE17621	Aae17621 Brassica
55	27	87.1	52	3	AAE17608	Aae17608 Arabidops
56	27	87.1	52	3	AAE17621	Aae17621 Brassica
57	27	87.1	52	3	AAE17608	Aae17608 Arabidops
58	27	87.1	52	3	AAE17621	Aae17621 Brassica
59	27	87.1	52	3	AAE17608	Aae17608 Arabidops
60	27	87.1	52	3	AAE17621	Aae17621 Brassica
61	27	87.1	52	3	AAE17608	Aae17608 Arabidops
62	27	87.1	52	3	AAE17621	Aae17621 Brassica
63	27	87.1	52	3	AAE17608	Aae17608 Arabidops
64	27	87.1	52	3	AAE17621	Aae17621 Brassica
65	27	87.1	52	3	AAE17608	Aae17608 Arabidops
66	27	87.1	52	3	AAE17621	Aae17621 Brassica
67	27	87.1	52	3	AAE17608	Aae17608 Arabidops
68	27	87.1	52	3	AAE17621	Aae17621 Brassica
69	27	87.1	52	3	AAE17608	Aae17608 Arabidops
70	27	87.1	52	3	AAE17621	Aae17621 Brassica
71	27	87.1	52	3	AAE17608	Aae17608 Arabidops
72	27	87.1	52	3	AAE17621	Aae17621 Brassica
73	27	87.1	52	3	AAE17608	Aae17608 Arabidops
74	27	87.1	52	3	AAE17621	Aae17621 Brassica
75	27	87.1	52	3	AAE17608	Aae17608 Arabidops
76	27	87.1	52	3	AAE17621	Aae17621 Brassica
77	27	87.1	52	3	AAE17608	Aae17608 Arabidops
78	27	87.1	52	3	AAE17621	Aae17621 Brassica
79	27	87.1	52	3	AAE17608	Aae17608 Arabidops
80	27	87.1	52	3	AAE17621	Aae17621 Brassica
81	27	87.1	52	3	AAE17608	Aae17608 Arabidops
82	27	87.1	52	3	AAE17621	Aae17621 Brassica
83	27	87.1	52	3	AAE17608	Aae17608 Arabidops
84	27	87.1	52	3	AAE17621	Aae17621 Brassica
85	27	87.1	52	3	AAE17608	Aae17608 Arabidops
86	27	87.1	52	3	AAE17621	Aae17621 Brassica
87	27	87.1	52	3	AAE17608	Aae17608 Arabidops
88	27	87.1	52	3	AAE17621	Aae17621 Brassica
89	27	87.1	52	3	AAE17608	Aae17608 Arabidops
90	27	87.1	52	3	AAE17621	Aae17621 Brassica
91	27	87.1	52	3	AAE17608	Aae17608 Arabidops
92	27	87.1	52	3	AAE17621	Aae17621 Brassica
93	27	87.1	52	3	AAE17608	Aae17608 Arabidops
94	27	87.1	52	3	AAE17621	Aae17621 Brassica
95	27	87.1	52	3	AAE17608	Aae17608 Arabidops
96	27	87.1	52	3	AAE17621	Aae17621 Brassica
97	27	87.1	52	3	AAE17608	Aae17608 Arabidops

98	27	87.1	582	2	AAR75648	Aar75648 Human pla	171	26	83.9	223	8	ADE75401	Ade75401 Goat alph
99	27	87.1	582	2	AAW52134	Aaw52134 Rabbit me	172	26	83.9	243	8	ADN24282	Adn24282 Bacterial
100	27	87.1	582	4	AAE10423	Aae10423 Human aci	173	26	83.9	289	3	AAU30371	Aau30371 Novel hum
101	27	87.1	582	4	AAE10423	Aae10423 Human mat	174	26	83.9	289	3	AAU30371	Aau30371 Novel hum
102	27	87.1	582	5	AAU84294	Aau84294 Human end	175	26	83.9	289	3	AAU30371	Aau30371 Novel hum
103	27	87.1	582	5	AAE21037	Aae21037 Human mem	176	26	83.9	291	4	AAU30371	Aau30371 Novel hum
104	27	87.1	582	5	AAU50865	Aau50865 Matrix me	177	26	83.9	291	5	AAU30371	Aau30371 Novel hum
105	27	87.1	582	7	ADC15498	Adc15498 Human bas	178	26	83.9	293	3	AAU30371	Aau30371 Novel hum
106	27	87.1	582	7	AD641179	Ad641179 Human pro	179	26	83.9	293	3	AAU30371	Aau30371 Novel hum
107	27	87.1	582	7	AD641177	Ad641177 Rat Prote	180	26	83.9	293	3	AAU30371	Aau30371 Novel hum
108	27	87.1	582	7	ADP13708	Adp13708 Tumor-Asa	181	26	83.9	293	3	AAU30371	Aau30371 Novel hum
109	27	87.1	582	7	ADN95889	Adn95889 Human BEC	182	26	83.9	293	3	AAU30371	Aau30371 Novel hum
110	27	87.1	582	8	ADN97703	Adn97703 Human mat	183	26	83.9	295	6	ABU37645	Abu37645 Protein e
111	27	87.1	582	8	ABN81541	Abn81541 Tumour-as	184	26	83.9	299	6	ABP77830	Abp77830 N. gonorr
112	27	87.1	582	8	ADP23426	Adp23426 PRO polyt	185	26	83.9	317	6	ABP78259	Abp78259 N. gonorr
113	27	87.1	582	9	AE94378	Aeb94378 Human MTP	186	26	83.9	321	7	ADG90764	Adg90764 Hepatic s
114	27	87.1	592	6	ABP79179	Abp79179 N. gonorr	187	26	83.9	321	8	ADP04189	Adp04189 Human col
115	27	87.1	592	6	ABU37131	Abu37131 Protein e	188	26	83.9	322	8	ADP04189	Adp04189 Human col
116	27	87.1	626	8	AUS22906	Ad22906 Bacterial	189	26	83.9	322	4	AAU30371	Aau30371 Novel hum
117	27	87.1	738	4	AAU67526	Aag67526 Amino aci	190	26	83.9	330	4	AAU30371	Aau30371 Novel hum
118	27	87.1	833	8	ADM98835	Adm98835 HMG-CoA r	191	26	83.9	330	6	ABM46194	Abm46194 Propionib
119	27	87.1	841	4	AAU23595	Aam23595 Murine ES	192	26	83.9	339	4	AAU23595	Aam23595 Murine OR
120	27	87.1	856	8	ADM98920	Adm98920 HMG-CoA r	193	26	83.9	344	7	ADG72670	Adg72670 Murine OR
121	27	87.1	856	8	ADM98784	Adm98784 HMG-CoA r	194	26	83.9	346	7	ADG72670	Adg72670 Murine OR
122	27	87.1	856	8	ADM98820	Adm98820 HMG-CoA r	195	26	83.9	369	7	ADG72670	Adg72670 Murine OR
123	27	87.1	1024	4	AAU02880	Aau02880 Human cas	196	26	83.9	371	3	AAU75248	Aau75248 Neisseria
124	27	87.1	1024	5	AAU080861	Aau080861 Human CIA	197	26	83.9	371	3	AAU75248	Aau75248 Neisseria
125	27	87.1	1024	5	ABU81720	Abu81720 Human cas	198	26	83.9	384	6	ADN12503	Adn12503 Alloicoc
126	27	87.1	1024	6	ABG72211	Abg72211 Human cas	199	26	83.9	390	8	ADN23888	Adn23888 Bacterial
127	27	87.1	1024	6	ABG72211	Abg72211 Human cas	200	26	83.9	393	8	ADN23888	Adn23888 Bacterial
128	27	87.1	1070	4	ABG67527	Abg67527 Amino aci	201	26	83.9	395	6	ABP77710	Abp77710 N. gonorr
129	27	87.1	1204	6	ABG72212	Abg72212 Protein e	202	26	83.9	397	5	ABB49314	Abb49314 Liateria
130	27	87.1	2697	6	ABG72212	Abg72212 Protein e	203	26	83.9	397	7	ADG74113	Adg74113 Human GPC
131	27	87.1	2697	6	ABG72212	Abg72212 Protein e	204	26	83.9	402	8	ADT58012	Adt58012 Plant pol
132	26	83.9	45	6	ABU02448	Abo02448 S. pneumo	205	26	83.9	402	7	ABO76543	Ab076543 Pseudomon
133	26	83.9	53	8	ADK80309	Adk80309 Plant ful	206	26	83.9	404	8	ADS26059	Ads26059 Bacterial
134	26	83.9	60	8	ABP55940	Abp55940 Ostrinia	207	26	83.9	405	6	ABM67471	Abm67471 Photornab
135	26	83.9	61	8	ADK48370	Adk48370 Streptoco	208	26	83.9	414	6	ABU20391	Abu20391 Protein e
136	26	83.9	62	1	AAU94262	Aau94262 Antibacte	209	26	83.9	414	8	ADS22533	Ads22533 Bacterial
137	26	83.9	63	1	AAU94262	Aau94262 Antibacte	210	26	83.9	414	9	ABM92109	Abm92109 M. xanthu
138	26	83.9	65	6	ABO13635	Ab013635 Human pol	211	26	83.9	416	3	AAU41542	Aau41542 Arabidops
139	26	83.9	65	6	ABP55939	Abp55939 Ostrinia	212	26	83.9	418	6	ABP79629	Abp79629 N. gonorr
140	26	83.9	69	9	ABE41581	Aeb41581 L. pneumo	213	26	83.9	426	4	ABP76721	Abp76721 Corynebac
141	26	83.9	72	4	ABG21901	Abg21901 Novel hum	214	26	83.9	426	4	AAU92282	Aau92282 C. glutami
142	26	83.9	72	5	ADK36142	Adk36142 Novel hum	215	26	83.9	426	7	ADL65521	Adl65521 C. glutam
143	26	83.9	72	9	AEA20997	Aea20997 Novel hum	216	26	83.9	431	7	ADD69592	Add69592 Human REM
144	26	83.9	74	3	AAU10736	Aau10736 Arabidops	217	26	83.9	437	6	ADN11164	Adn11164 Alloicoc
145	26	83.9	84	3	AAU61260	Aau61260 Arabidops	218	26	83.9	437	7	ABO62441	Ab062441 Klebsiell
146	26	83.9	84	3	AAU61260	Aau61260 Arabidops	219	26	83.9	438	6	ADA48730	Ada48730 Rice prot
147	26	83.9	87	3	ABE38299	Aeb38299 L. pneumo	220	26	83.9	444	8	ADN27113	Adn27113 Bacterial
148	26	83.9	90	4	AAU31916	Aau31916 Novel hum	221	26	83.9	446	7	ABO68439	Ab068439 Pseudomon
149	26	83.9	91	3	AAU31916	Aau31916 Novel hum	222	26	83.9	448	8	ADG25774	Adg25774 Mycobacte
150	26	83.9	93	4	AAU92337	Aau92337 Human dig	223	26	83.9	453	7	ABO61786	Ab061786 Klebsiell
151	26	83.9	96	3	AAU92337	Aau92337 Human dig	224	26	83.9	459	8	ADS29238	Ads29238 Bacterial
152	26	83.9	96	3	AAU92337	Aau92337 Human dig	225	26	83.9	479	3	AAU41541	Aau41541 Arabidops
153	26	83.9	101	8	ADK94447	Adk94447 Plant ful	226	26	83.9	483	8	ADN22834	Adn22834 Bacterial
154	26	83.9	111	4	ABE50355	Abb50355 Human sec	227	26	83.9	483	7	ADN22833	Adn22833 Pseudomon
155	26	83.9	111	6	ABO44612	Ab044612 Novel hum	228	26	83.9	493	7	ABO80246	Ab080246 Pseudomon
156	26	83.9	111	7	ABO26092	Ab026092 Human pro	229	26	83.9	504	4	ABB64964	Abb64964 Drosophil
157	26	83.9	115	8	ADP84584	Adp84584 Human bre	230	26	83.9	510	8	ADM67214	Adm67214 Murine ad
158	26	83.9	116	6	ABP71848	Abp71848 Human fur	231	26	83.9	511	6	ABM68291	Abm68291 Photornab
159	26	83.9	118	5	ABO9650	Abb09650 Amino aci	232	26	83.9	512	3	AAU41540	Aau41540 Arabidops
160	26	83.9	118	6	ABG72548	Abg72548 Streptoco	233	26	83.9	518	5	ABP74027	Abp74027 Candida a
161	26	83.9	118	8	ADU80825	Adu80825 OrfZ, SEQ	234	26	83.9	526	8	ADN12171	Adn12171 Bacterial
162	26	83.9	137	4	AAO05457	Aao05457 Human pol	235	26	83.9	540	7	ABM86731	Abm86731 Rice abio
163	26	83.9	138	4	AAO08691	Aao08691 Human pol	236	26	83.9	548	6	ABU35322	Abu35322 Protein e
164	26	83.9	186	2	AAU33725	Aau33725 Photornab	237	26	83.9	557	7	ADL04520	Adl04520 M. cattar
165	26	83.9	187	6	ABM69853	Abm69853 Photornab	238	26	83.9	573	8	ABO65367	Ab065367 Klebsiell
166	26	83.9	188	5	ABE54792	Abb54792 Lactococc	239	26	83.9	581	4	ABB63013	Abb63013 Drosophil
167	26	83.9	191	4	AAU92339	Aau92339 C. glutami	240	26	83.9	597	7	ABO73814	Ab073814 Pseudomon
168	26	83.9	218	5	ABE55107	Abb55107 Lactococc	241	26	83.9	618	4	ABG26117	Abg26117 Novel hum
169	26	83.9	220	6	ABP78312	Abp78312 N. gonorr	242	26	83.9	641	4	ABG25497	Abg25497 Novel hum
170	26	83.9	223	5	AAE17475	Aae17475 Alpha-S2	243	26	83.9	673	6	ABM65701	Abm65701 Propionib
										690	8	ADY05578	Ady05578 Plant ful

XX Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 PT its isomer or peptidomimetic.
 XX Claim 7; Page 25; 46pp; English.
 XX Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFVFFA 6
 Db 1 KFVFFA 6
 RESULT 3
 AAB82625
 ID AAB82625 standard; peptide; 6 AA.
 AC AAB82625;
 XX 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "all D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 XX 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 DR Preventing/treating amyloid-related disease, especially Alzheimer's
 XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX Disclosure; Page 11; 31pp; English.
 XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and

CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis,
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFVFFA 6
 Db 1 KFVFFA 6
 RESULT 4
 AAB82633
 ID AAB82633 standard; peptide; 6 AA.
 AC AAB82633;
 XX 02-OCT-2001 (first entry)
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "all D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX WO200139796-A2.
 XX 07-JUN-2001.
 XX 29-NOV-2000; 2000WO-CA001413.
 PR 29-NOV-1999; 99US-0168594P.
 PR 28-NOV-2000; 2000US-00724842.
 XX (NEUR-) NEUROCHEM INC.
 PA Chalifour R, Hebert L, Kong X, Gervais F;
 XX WPI; 2001-441458/47.
 DR Preventing/treating amyloid-related disease, especially Alzheimer's
 XX disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,

PT which elicits production of antibodies to prevent fibrillogenesis and
 FT associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use in
 XX preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesized from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC CAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
 |||||
 DB 1 KVFVFFA 6

RESULT 5
 AAU96813
 ID AAU96813 standard; peptide; 6 AA.

XX AAU96813;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #3.

DE Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1..6 /note= "Preferably D-form residue"

XX WO200207781-A2.

XX 31-JAN-2002.

XX 25-JUL-2001; 2001WO-CA001071.

XX

PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 XX (NEUR-) NEUROCHEM INC.
 XX Gervais F, Kong X, Chalifour R, Migneault D;
 XX WPI; 2002-371447/40.
 XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 PT plaques and/or for the treatment of amyloidosis disorders.
 XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A_t-(A_l)_n_k-z-A_l_a_b (1) where z = 0 - 1;
 CC A_t = an amyloid targeting moiety; A_l)_n_k = a linker moiety; and A_l_a_b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (1) to the patient, and ultrasound imaging (1) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (1), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
 |||||
 DB 1 KVFVFFA 6

RESULT 6
 AAU96821
 ID AAU96821 standard; peptide; 6 AA.

XX AAU96821;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #11.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1..6

```

FT Modified-site 6 /note= "Preferably D-form residue"
FT FT /note= "Ala is amidated"
XX PN WO200207781-A2.
XX PD 31-JAN-2002.
XX PF 25-JUL-2001; 2001WO-CA001071.
XX PR 25-JUL-2000; 2000US-0220808P.
XX PR 24-JUL-2001; 2001US-00915092.
XX PA (NEUR-) NEUROCHEM INC.
XX PI Gervais F, Kong X, Chalifour R, Migneault D;
XX DR WPI; 2002-371447/40.
XX FT New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX FT plaques and/or for the treatment of amyloidosis disorders.
XX PS Claim 49; Page 21; 57pp; English.
XX CC The invention relates to an amyloid-targeting imaging agent comprising an
XX CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX CC agent is of general formula A t-(A 1 n k) z-A 1 a b (t) where z = 0 - 1;
XX CC A t = an amyloid targeting moiety; A 1 n k = a linker moiety; and A 1 a b
XX CC = a labelling moiety. Also included are imaging amyloid deposition or
XX CC diagnosing an amyloid-related condition in a patient involving
XX CC administering (i) to the patient, and ultrasound imaging (i) in the
XX CC patient to determine the presence of amyloid or amyloid-related condition
XX CC ; and a kit for preparing a radiopharmaceutical preparation comprising
XX CC (i), a reducing agent, a buffering agent, a transchelating agent, and
XX CC instructions for the preparation and use of the radiopharmaceutical in
XX CC the imaging of amyloid or an amyloid-related condition. The agents are
XX CC used for imaging amyloid deposition and for diagnosing an amyloid related
XX CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX CC cerebral amyloidoses (transmissible virus dementias), familial CJD,
XX CC scrapie, transmissible mink encephalopathy, bovine spongiform
XX CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
XX CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX CC amyloid angiopathy. The agents are capable of crossing the blood-brain
XX CC barrier and are capable of binding specifically to amyloid plaques. The
XX CC present sequence is a peptide forming the amyloid targeting moiety of the
XX CC agent of the invention
XX SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db |||||
1 KVFVFA 6

RESULT 7
AAU11659
ID AAU11659 standard; peptide; 6 AA.
XX AC AAU11659;
XX DT 09-APR-2002 (first entry)
XX DE Peptide #12, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db |||||
1 KVFVFA 6

RESULT 8
AAU11651
ID AAU11651 standard; peptide; 6 AA.
XX AC AAU11651;
XX DT 09-APR-2002 (first entry)
XX DE Peptide #4, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX OS Synthetic.
XX PN WO200185093-A2.
XX PD 15-NOV-2001.
XX PF 22-DEC-2000; 2000WO-IB002078.
XX PR 23-DEC-1999; 99US-0171877P.
XX PA (NEUR-) NEUROCHEM INC.
XX PI Green AM, Gervais F;
XX DR WPI; 2002-075222/10.
XX FT Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX FT disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX FT inhibitor.
XX PS Disclosure; Page 10; 68pp; English.
XX CC The present invention relates to a new method of inhibiting cerebral
XX CC amyloid angiopathy. The new method of the invention involves contacting a
XX CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX CC can be used for treating disease states characterised by cerebral amyloid
XX CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX CC The present sequence represents one of a group of peptides (AAU11648-
XX CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX CC was used in the invention to treat a disease state characterised by
XX CC cerebral amyloid angiopathy (CAA)
XX SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db |||||
1 KVFVFA 6

RESULT 8
AAU11651
ID AAU11651 standard; peptide; 6 AA.
XX AC AAU11651;
XX DT 09-APR-2002 (first entry)
XX DE Peptide #4, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX KW Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX KW CAA; neurotropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX KW cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX OS Synthetic.
XX PN WO200185093-A2.
XX PD 15-NOV-2001.
XX PF 22-DEC-2000; 2000WO-IB002078.
XX PR 23-DEC-1999; 99US-0171877P.

```

XX (NEUR-) NEUROCHEM INC.
 XX Green AM, Gervais F;
 XX WPI; 2002-075222/10.
 XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 XX disease comprises contacting blood vessel wall cell with amyloid-beta 40
 XX inhibitor.
 XX Disclosure; Page 10; 68pp; English.
 XX The present invention relates to a new method of inhibiting cerebral
 XX amyloid angiopathy. The new method of the invention involves contacting a
 XX blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 XX can be used for treating disease states characterised by cerebral amyloid
 XX angiopathy, particularly Alzheimer's disease, hereditary cerebral
 XX haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 XX The present sequence represents one of a group of peptides (AAU11648-
 XX AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 XX carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 XX was used in the invention to treat a disease state characterised by
 XX cerebral amyloid angiopathy (CAA)
 XX Sequence 6 AA;

Query Match 100.0%; Score 31; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
 |||||
 Db 1 KVFVFFA 6

RESULT 9
 AAE35447
 ID AAE35447 standard; peptide; 6 AA.
 XX
 AC AAE35447;

DT 17-JUN-2003 (first entry)

XX Abeta peptide #18.

XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; renal carcinoma; carcinomas of gut, lung
 KW ulcer; antiinflammatory; cytotatic; uropathic; therapy.

XX Unidentified.

XX Key Location/Qualifiers
 FH Misc-difference 1. .6 /note= "D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT

XX WO200296937-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

XX (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX Claim 1; Page 59; 44pp; English.
 XX The invention relates to a method for prevention and/or treatment of an
 XX amyloid-related disease which comprises administration of an all-D -
 XX amyloid-beta peptide. The method is used for preventing and/or treating
 XX Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 XX angiopathy; for altering serum levels of amyloid-beta in a mammal and
 XX favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 XX the mammal; and reducing or inhibiting the formation of plaques. It is
 XX also used for treating AA (reactive) amyloid diseases including
 XX inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 XX arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 XX Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 XX disease. AA deposits are also produced as a result of chronic microbial
 XX infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 XX ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 XX Certain malignant neoplasms can also result in AA fibril amyloid deposits
 XX including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 XX and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 XX present sequence is an Abeta peptide used to illustrate the method of the
 XX invention

SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
 |||||
 Db 1 KVFVFFA 6

RESULT 10
 AAE35440
 ID AAE35440 standard; peptide; 6 AA.
 XX
 AC AAE35440;

DT 17-JUN-2003 (first entry)

XX Abeta peptide #11.

XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; renal carcinoma; carcinomas of gut, lung
 KW ulcer; antiinflammatory; cytotatic; uropathic; therapy.

XX Unidentified.

XX Key Location/Qualifiers
 FH Misc-difference 1. .6 /note= "D-form residues"
 FT Modified-site 6 /note= "D-form residues"
 FT

XX WO200296937-A2.

XX 05-DEC-2002.

XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.

XX (NEUR-) NEUROCHEM INC.

PI Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 XX Claim 1; Page 59; 44pp; English.
 XX
 XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX
 XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 31; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
 |||||
 Db 1 KVFVFFA 6

RESULT 11
 ADQ37264
 ID ADQ37264 standard; peptide; 6 AA.
 XX
 AC ADQ37264;
 XX
 XX 07-OCT-2004 (first entry)
 XX
 XX Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquiliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..6
 FT /note= "D-form residues"
 FT
 XX
 FN WO2004058239-A1.

XX 15-JUL-2004.
 PD
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 PF
 XX
 XX 24-DEC-2002; 2002US-0436379P.
 PR
 XX 23-JUN-2003; 2003US-0482214P.
 PR
 XX (NEUR-) NEUROCHEM INT LTD.
 PA
 XX Gervais F, Bellini F;
 PI
 XX WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 XX Disclosure; Page 67; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquiliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX
 XX Sequence 6 AA;
 SQ

Query Match 100.0%; Score 31; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFFA 6
 |||||
 Db 1 KVFVFFA 6

RESULT 12
 ADQ37316
 ID ADQ37316 standard; peptide; 6 AA.

XX ADQ37316;
 AC
 DT 07-OCT-2004 (first entry)
 DE
 DE Antifibrillogenic amyloidosis inhibiting peptide.
 DE
 DE amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment; vascular dementia;
 KW mild-to-moderate cognitive impairment; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 XX WO2004058239-A1.
 PN
 XX 15-JUL-2004.
 PD
 XX 24-DEC-2003; 2003WO-CA002021.
 PP
 XX 24-DEC-2002; 2002US-0436379P.
 PR 23-JUN-2003; 2003US-0482214P.
 PR
 XX (NEUR-) NEUROCHEM INT LTD.
 PA
 XX Gervais F, Bellini F;
 PI WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 PT
 PS Disclosure; Page 69; 143pp; English.
 XX
 XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC neurotropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,

CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 31; DB 8; Length 6;
 Best Local Similarity 100.0%; Fred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 Db 1 KVFVFA 6
 RESULT 13
 ADQ37324
 ID ADQ37324 standard; peptide; 6 AA.
 AC
 XX ADQ37324;
 DT 07-OCT-2004 (first entry)
 DE Antifibrillogenic amyloidosis inhibiting peptide.
 DE
 DE amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 6
 FT /note= "amidated"
 FT
 XX WO2004058239-A1.
 PN
 XX 15-JUL-2004.
 PD
 XX 24-DEC-2003; 2003WO-CA002021.
 PP
 XX 24-DEC-2002; 2002US-0436379P.
 PR 23-JUN-2003; 2003US-0482214P.
 PR
 XX (NEUR-) NEUROCHEM INT LTD.
 PA
 XX Gervais F, Bellini F;
 PI WPI; 2004-543342/52.
 XX
 XX Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 PT

XX PS Disclosure; Page 70; 143pp; English.

XX CC The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

XX CC nontropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; having amyloid-beta deposits. The present sequence represents a peptide that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.

XX CC Sequence 6 AA;

XX SQ Query Match 100.0%; Score 31; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
|||||

Db 1 KPVFFA 6

RESULT 14

ADQ37272

ID ADQ37272 standard; peptide; 6 AA.

XX AC ADQ37272;

XX DT 07-OCT-2004 (first entry)

XX DE Vaccine antigen amyloid-beta related amino acid sequence.

XX KW amyloid-beta; amyloid-beta related disease;

KW ADQ37272

KW neuroprotective; cerebroprotective; haemostatic; ophthalmological; antithyroid; vasotropic; cardiovascular; tranquilliser; uteropathic; anticonvulsant; anti-HIV; antiparkinsonian; muscular; cardiant; antidepressant; endocrine; hypnotic;

KW amyloid-beta fibril formation modulator; immune system modulator;

KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;

KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;

senile dementia; Down's syndrome; inclusion body myositis; age-related macular degeneration; hypothyroidism; cerebrovascular disease; cardiovascular disease; memory loss; anxiety; behavioural dysfunction; neurological condition; psychological condition; vaccine antigen.

Synthetic.

Key Location/Qualifiers

Misc-difference 1..6 /note= "D-form residues"

Modified-site 6 /note= "amidated"

WO2004058239-A1.

15-JUN-2004.

24-DEC-2003; 2003WO-CA002021.

24-DEC-2002; 2002US-0436379P.

23-JUN-2003; 2003US-0482214P.

(NEUR-) NEUROCHEM INT LTD.

Gervais F, Bellini F;

WPI; 2004-543342/52.

Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.

Disclosure; Page 67; 143pp; English.

The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have

XX CC nontropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser, uteropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular, neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy, aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or posthypoxic illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt)) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene; having amyloid-beta deposits. The present sequence represents a peptide that can be used as an antifibrillogenic amyloidosis inhibiting peptide in the exemplification of the present invention.

XX Sequence 6 AA;
SQ
Query Match 100.0%; Score 31; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFFA 6
Db 1 KPVFFA 6
RESULT 15
ADY37931
ID ADY37931 standard; peptide; 6 AA.
XX
AC ADY37931;
XX
DT 19-MAY-2005 (first entry)
XX
DE Amyloid-targeting peptide, SEQ ID NO:11, for use in imaging agent.
XX
DE Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimers disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 6 /note= "C-terminal amide"
FT
XX US2005048000-A1.
XX
XX 03-MAR-2005.
XX
XX 03-DEC-2003; 2003US-00728028.
XX
XX 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
PR 29-JAN-2003; 2003US-0443291P.
XX
XX (NEUR-) NEUROCHEM INT LTD.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX
XX WPI; 2005-212201/22.
XX
XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform encephalopathy, primary amyloidosis or Alzheimer's disease.
XX
XX Disclosure; SEQ ID NO 11; 34pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent. The imaging agent comprises an amyloid targeting moiety (such as a peptide) joined to a labeling moiety via a linking moiety, and is preferably able to cross the blood-brain barrier. The invention also relates to a kit for preparing a radiopharmaceutical preparation from the imaging agent of the invention, a method for imaging amyloid deposition in a patient and a method for diagnosing an amyloid-related condition in a patient. The amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-related conditions such as Creutzfeld-Jakob disease (CJD), Kuru, transmissible cerebral amyloidosis (also known as transmissible virus dementias), familial CJD, scrapie, transmissible mink encephalopathy, bovine spongiform encephalopathy (BSE), inflammation-associated amyloid, type II diabetes, primary amyloidosis, feline spongiform encephalopathy, non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a patient. The agent does not exhibit excessive toxicity or irritation, does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence prevention of the undesirable effects of such disorders. Sequences ADY37921-ADY37947 and ADY37949 represent peptides which may be used as the amyloid-targeting moiety in an imaging agent of the invention.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 31; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFFA 6
Db 1 KPVFFA 6
RESULT 16
ADY37923
ID ADY37923 standard; peptide; 6 AA.
XX
AC ADY37923;
XX
DT 19-MAY-2005 (first entry)
XX
DE Amyloid-targeting peptide, SEQ ID NO:3, for use in imaging agent.
XX
DE Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimers disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.
XX
OS Synthetic.
XX
XX US2005048000-A1.
XX
XX 03-MAR-2005.
XX
XX 03-DEC-2003; 2003US-00728028.
XX
XX 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
PR 29-JAN-2003; 2003US-0443291P.
XX
XX (NEUR-) NEUROCHEM INT LTD.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX
XX WPI; 2005-212201/22.
XX
XX New amyloid-targeting imaging agent, useful for diagnosing an amyloid-related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform encephalopathy, primary amyloidosis or Alzheimer's disease.
XX
XX Disclosure; SEQ ID NO 3; 34pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent. The imaging agent comprises an amyloid targeting moiety (such as a peptide) joined to a labeling moiety via a linking moiety, and is preferably able to cross the blood-brain barrier. The invention also relates to a kit for preparing a radiopharmaceutical preparation from the imaging agent of the invention, a method for imaging amyloid deposition in a patient and a method for diagnosing an amyloid-related condition in a patient. The amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-related conditions such as Creutzfeld-Jakob disease (CJD), Kuru, transmissible cerebral amyloidosis (also known as transmissible virus dementias), familial CJD, scrapie, transmissible mink encephalopathy, bovine spongiform encephalopathy (BSE), inflammation-associated amyloid, type II diabetes, primary amyloidosis, feline spongiform encephalopathy, non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-mediated diseases, dialysis-related amyloidosis, light chain-related amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a patient. The agent does not exhibit excessive toxicity or irritation, does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 31; DB 9; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||||
Db 1 KVFVFA 6

RESULT 17
ABM89186
ID ABM89186 standard; protein; 336 AA.

XX
AC ABM89186;

XX
DT 02-JUN-2005 (first entry)

XX
DE Rice abiotic stress responsive polypeptide SEQ ID NO:7432.

XX
KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.

XX
OS Oryza sativa.

XX
PN WO2003008540-A2.

XX
PD 30-JAN-2003.

XX
PF 21-JUN-2002; 2002WO-US019668.

XX
PR 22-JUN-2001; 2001US-0300112P.

XX
PR 24-AUG-2001; 2001US-0314662P.

XX
PR 26-SEP-2001; 2001US-0325277P.

XX
PR 21-NOV-2001; 2001US-0332132P.

XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX
PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;

XX
WPI; 2003-248011/24.

XX
DR New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.

XX
PS Claim 1; SEQ ID NO 7432; 89pp; English.

XX
CC The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX

SQ Sequence 336 AA;

Query Match 100.0%; Score 31; DB 7; Length 336;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFA 6
|||||
Db 80 KVFVFA 85

RESULT 18
ADK35620
ID ADK35620 standard; protein; 202 AA.

XX
AC ADK35620;

XX
DT 06-MAY-2004 (first entry)

XX
DE Novel human polypeptide SeqID7702.

XX
KW antiarthritic; antiparkinsonian; neuroprotective; neurotropic;
KW immunosuppressive; cytostatic; antipsoriatic; antiinflammatory;
KW antibacterial; antiviral; antifungal; antiparasitic; gene therapy;
KW arthritis; Parkinson's; Alzheimer's; autoimmune disease; cancer;
KW psoriasis; inflammatory bowel disease; infection; bacteria; virus;
KW fungus; parasite; human.

XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers

XX
FT Misc-difference 1..202

XX
FT /label= OTHER

XX
FT amino acids or the site of a stop codon within the DNA

XX
FT sequence"

XX
PN WO200216439-A2.

XX
PD 28-FEB-2002.

XX
PF 05-MAR-2001; 2001WO-US004941.

XX
PR 07-MAR-2000; 2000US-00519705.

XX
PR 19-MAY-2000; 2000US-00574454.

XX
PA (HYSE-) HYSEQ INC.

XX
PI Tang YT, Liu C, Drmanac RT;

XX
WPI; 2002-280918/32.

XX
PT Isolated polynucleotide encoding bone marrow derived polypeptides useful
PT for treating, e.g., Parkinson's, Alzheimer's, cancer, arthritis, Crohn's
PT disease, and inflammatory bowel disease.

XX
PS Claim 20; SEQ ID NO 7702; 504pp; English.

XX
CC This invention relates to a novel isolated polynucleotide comprising a
CC nucleotide sequence selected from one of 1680 sequences, a mature protein
CC coding portion of them, an active domain of them and their complementary
CC sequences. The invention may be useful for the production of compounds
CC with an antarthritic, antiparkinsonian, neuroprotective, neurotropic,
CC immunosuppressive, cytostatic, antipsoriatic, antiinflammatory,
CC antibacterial, antiviral, antifungal or antiparasitic activity. In
CC addition, the disclosed sequences may be useful for gene therapy. The
CC polypeptides or their antibodies are useful for treating many diseases
CC such as arthritis, Parkinson's, Alzheimer's, autoimmune diseases, cancer,
CC psoriasis, inflammatory bowel disease and infections caused by bacteria,
CC viruses, fungi or parasites. The present sequence is that of a human
CC polypeptide of the invention.
XX

SQ Sequence 202 AA;

Query Match 96.8%; Score 30; DB 5; Length 202;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db ||:||||
35 KVFVFA 40

RESULT 19
ABBI7989
ID ABB17989 standard; protein; 75 AA.
XX
AC ABB17989;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polypeptide SEQ ID NO 6646.
XX
KW Human; neurotropic; neuroprotective; cytostatic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
KW antiparkinsonian; antisickling; antianaemic; antiarthritis; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN WO200159063-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001334.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184654P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226686P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0234000P.
PR 14-SEP-2000; 2000US-023401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 20-OCT-2000; 2000US-0242221P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.

PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249297P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0256719P.
 PR 06-DEC-2000; 2000US-0251479P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 FI
 XX
 XX WPI; 2001-541565/60.
 DR N-PSDB; ABA14315.
 XX
 XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system cancers
 PT and metastases.
 PT
 XX
 XX Claim 11; SEQ ID NO 6646; 1701pp + Sequence Listing; English.
 PS
 XX
 XX The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (AB14678-AB18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
 CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 75 AA;
 SQ
 Query Match 90.3%; Score 28; DB 4; Length 75;
 Best Local Similarity 83.3%; Pred. No. 1.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 ||:||||
 Db 5 KFLVFA 10
 RESULT 20
 ADN23626
 ID ADN23626 standard; protein; 452 AA.
 XX
 AC ADN23626;
 XX
 DT 02-DEC-2004 (first entry)
 XX

DE Bacterial polypeptide #6279.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 XX US2003233675-A1.
 XX
 XX 18-DEC-2003.
 PD
 PD 20-FEB-2003; 2003US-00369493.
 PP
 PP 21-FEB-2002; 2002US-0360039P.
 PR
 XX (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 FI WPI; 2004-061375/06.
 DR
 XX
 XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.
 PT
 XX
 XX Claim 1; SEQ ID NO 6279; 122pp; English.
 PS
 XX
 XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. Improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 XX Sequence 452 AA;
 SQ
 Query Match 90.3%; Score 28; DB 8; Length 452;
 Best Local Similarity 83.3%; Pred. No. 9.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 :|||||
 Db 291 RLVVFA 296
 RESULT 21

ADN46740
 ID ADN46740 standard; protein; 485 AA.
 AC
 ADN46740;
 DT 01-JUL-2004 (first entry)
 XX Thermococcus kodakaraensis KOD1 protein sequence SeqID618.
 DE
 XX Gene disruption; gene targeting; marker gene; transformation;
 KW homologous recombination; hyperthermostable archaeobacterium; KOD1;
 KW gene structure; gene function; enzyme activity; medicine;
 KW forensic science; food; drug inspection; molecular biology; immunology.
 XX
 OS Thermococcus kodakaraensis.
 XX
 XX WO2004022736-A1.
 PN
 XX 18-MAR-2004.
 PD
 XX 29-AUG-2003; 2003WO-IB003597.
 PF
 XX 30-AUG-2002; 2002JP-00319011.
 PR
 XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 PA
 XX Imanaka T, Atomi H;
 PI
 XX WPI; 2004-257583/24.
 DR
 XX Method for disrupting targeted gene in genome of organism particularly
 PT thermostable bacterium and with genome chips for analysis, applicable in
 PT studying gene structure and functions.
 PT
 XX Claim 9; SEQ ID NO 618; 598pp; Japanese.
 PS
 XX This invention relates to a novel method for targeting disruption of an
 CC arbitrary gene in a genome of an organism which comprises providing the
 CC whole sequential data of the genome of such organism, selecting at least
 CC 1 arbitrary region in the sequence, providing a vector that contains a
 CC sequence homologous with the selected region and a marker gene,
 CC transformation, and homologous recombination. The genome is preferably
 CC the genome of a hyperthermostable archaeobacterium, particularly
 CC Thermococcus kodakaraensis KOD1. The method is for targeting the
 CC disruption of a gene in the genome of an organism, which is applicable in
 CC studying gene structure and functions as well as enzyme activities of
 CC encoded proteins and useful in medicine, forensic science, food or drug
 CC inspection, molecular biology and immunology. With this method, the
 CC disruption of a gene at an arbitrary position in a genome can be achieved
 CC efficiently and reliably. The present sequence is that of a protein
 CC encoded by the genome of Thermococcus kodakaraensis which was derived
 CC using the method of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 485 AA;
 Query Match 90.3%; Score 28; DB 8; Length 485;
 Best Local Similarity 83.3%; Pred. No. 9.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFVFFA 6
 Db :|||||
 339 RFVFFA 344
 RESULT 22
 AAY19993
 ID AAY19993 standard; protein; 490 AA.
 XX
 AC AAY19993;
 XX

DT 19-JUL-1999 (first entry)
 XX B. burgdorferi antigenic protein, t752.aa.
 DE
 XX Antigenic protein; vaccine; Lyme disease; infection; detection.
 KW
 XX Borrelia burgdorferi.
 OS
 XX WO9859071-A1.
 PN
 XX 30-DEC-1998.
 PD
 XX 18-JUN-1998; 98WO-US012718.
 PF
 XX 20-JUN-1997; 97US-0050359P.
 PR 22-JUL-1997; 97US-0053344P.
 PR 22-JUL-1997; 97US-0053377P.
 PR 03-SEP-1997; 97US-0057483P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA (MEDI-) MEDIMMUNE INC.
 XX
 XX Choi GH, Erwin AL, Hanson MS, Lathigra R;
 PI
 XX WPI; 1999-189980/16.
 DR N-PSDB; AAX61690.
 DR
 XX New isolated Borrelia burgdorferi nucleic acids - used to develop
 PT products for the diagnosis, prevention and treatment of diseases caused
 PT by Borrelia, particularly Lyme disease.
 PT
 XX Claim 12; Page 153; 275pp; English.
 PS
 XX This sequence represents a Borrelia burgdorferi (Bb) protein of the
 CC invention, which is suitable for use in a vaccine. The Bb polypeptides
 CC can be used in vaccines for eliciting protective antibodies to members of
 CC the Borrelia genus, particularly for the use against Lyme disease in
 CC humans and animals. They can be used for preventing or attenuating an
 CC infection caused by a member of the Borrelia genus. The products can also
 CC be used for detection of members of the Borrelia genus
 XX
 SQ Sequence 490 AA;
 Query Match 90.3%; Score 28; DB 2; Length 490;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFVFFA 6
 Db :|||||
 23 RFVFFA 28
 RESULT 23
 AAR95594
 ID AAR95594 standard; protein; 506 AA.
 XX
 AC AAR95594;
 XX
 XX 16-OCT-2003 (revised)
 DT 14-OCT-1996 (first entry)
 XX
 XX Arabidopsis fatty acid elongation FAE1 enzyme.
 DE
 XX Fatty acid elongation gene; FAE1; transgenic plant; seed oil;
 KW vegetable oil; Brassica napus; canola; oilseed rape; eicosenoic acid;
 KW erucic acid.
 KW
 XX Arabidopsis thaliana; ecotype Ws.
 OS
 XX WO9613582-A1.
 PN
 XX 09-MAY-1996.
 PD
 XX

XX	(UYMI-) UNIV MIAMI.
XX	Jaworeki JG, Blacklock BJ;
PI	WPI; 2002-154572/20.
XX	N-PSDB; AAD28537.
DR	New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic acids encoding the polypeptide, useful for producing very long chain fatty acids.
PT	
XX	
XX	Example 1; Page 114-115; 139pp; English.
PS	The invention relates to fatty acid elongase 3-ketoacyl CoA synthase (KCS) polypeptides with altered substrate specificity and/or catalytic activity and nucleic acid molecules encoding such polypeptides.
CC	Polypeptides of the invention are useful for catalyzing the condensation of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of C20 fatty acyl CoA. They are especially useful for producing very long chain fatty acids (VLCFA) and may be used in the development of reagents for various purposes, e.g., immunological reagents to monitor expression of elongase KCS polypeptides or nucleic acid probes or primers to monitor inheritance of an elongase KCS gene in plant breeding programs. The present sequence is an alternative version of Arabidopsis thaliana FAEL-Brassica napus elongase KCS chimeric protein designated as At399.
CC	(Updated on 29-AUG-2003 to standardise OS field)
CC	
XX	Sequence 506 AA;
SQ	
	Query Match 90.3%; Score 28; DB 5; Length 506;
	Best Local Similarity 83.3%; Pred. No. 1e+03;
	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KTVFFPA 6 :
Dd	356 KFLFFA 361
RESULT 25	
AAE17622	ID AAE17622 standard; protein; 506 AA.
XX	AAE17622;
AC	
XX	
DT	29-AUG-2003 (revised)
DT	22-APR-2002 (first entry)
XX	
DE	A. thaliana FAEL-Brassica napus elongase KCS chimeric protein, At399.
XX	
KW	Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme; very long chain fatty acid; VLCFA; FAEL protein; chimeric.
KW	
XX	Arabidopsis thaliana.
OS	Brassica napus.
OS	Chimeric.
XX	
FH	Key Location/Qualifiers
FT	Region 1..399
FT	/note= "Arabidopsis thaliana elongase KCS protein"
FT	Region 400..506
FT	/note= Brassica napus elongase KCS protein
XX	
PN	WO200194565-A2.
XX	
PD	13-DEC-2001.
XX	
Pf	08-JUN-2001; 2001WO-US018737.
XX	
PR	08-JUN-2000; 2000US-0210326P.
XX	
XX	(UYMI-) UNIV MIAMI.
XX	

PI Jaworski JG, Blacklock BJ;
 XX WPI; 2002-154572/20.
 DR N-PSDB; AAD28514.
 XX
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.
 XX
 PS Example 1; Fig 1-5; 139pp; English.
 XX
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is Arabidopsis thaliana FAE1- Brassica napus elongase
 CC KCS chimeric protein designated as At399. (Updated on 29-AUG-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 506 AA;
 Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFVFPA 6
 DB 356 KFLFPA 361
 ||:||||
 356 KFLFPA 361
 RESULT 26
 AAE17625
 ID AAE17625 standard; protein; 506 AA.
 XX
 AC AAE17625;
 DT 22-APR-2002 (first entry)
 XX
 DE Arabidopsis thaliana FAE1 protein mutant, At K92R.
 XX
 KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAE1 gene; mutant; mutain.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 92 /note= "Wild-type Lys substituted with Arg"
 FT
 PN WO200194565-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 08-JUN-2001; 2001WO-US018737.
 XX
 PR 08-JUN-2000; 2000US-0210326P.
 XX
 PA (UYMI-) UNIV MIAMI.
 XX
 PI Jaworski JG, Blacklock BJ;
 XX WPI; 2002-154572/20.
 DR N-PSDB; AAD28517.
 XX
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.

XX Claim 7; Fig 1-6; 139pp; English.
 PS
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is a mutant of Arabidopsis thaliana elongase KCS
 CC protein/FAE1 protein designated as At K92R
 XX
 SQ Sequence 506 AA;
 Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFVFPA 6
 DB 356 KFLFPA 361
 ||:||||
 356 KFLFPA 361
 RESULT 27
 AAE17621
 ID AAE17621 standard; protein; 506 AA.
 XX
 AC AAE17621;
 DT 29-AUG-2003 (revised)
 DT 22-APR-2002 (first entry)
 XX
 DE Brassica napus elongase KCS-A. thaliana FAE1 chimeric protein, Bn176.
 XX
 KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAE1 gene; chimeric.
 XX
 OS Brassica napus.
 OS Arabidopsis thaliana.
 OS Chimeric.
 FH Key Location/Qualifiers
 FT Region 1..176
 FT /note= "Brassica napus elongase KCS protein"
 FT Region 177..506
 FT /note= "Arabidopsis thaliana FAE1 protein"
 XX
 PN WO200194565-A2.
 XX
 PD 13-DEC-2001.
 XX
 PF 08-JUN-2001; 2001WO-US018737.
 XX
 PR 08-JUN-2000; 2000US-0210326P.
 XX
 PA (UYMI-) UNIV MIAMI.
 XX
 PI Jaworski JG, Blacklock BJ;
 XX WPI; 2002-154572/20.
 DR N-PSDB; AAD28513.
 XX
 PT New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.
 XX
 PS Example 1; Fig 1-5; 139pp; English.
 XX
 CC The invention relates to fatty acid elongase 3-ketoacyl CoA synthase

CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is *Brassica napus* elongase KCS- Arabidopsis thaliana
 CC FAEI chimeric protein designated as Bn176. (Updated on 25-AUG-2003 to
 CC standardise OS field)
 XX

SQ Sequence 506 AA;
 Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFPA 6
 ||:||||
 Db 356 KFLFPA 361

RESULT 28
 AAEL17608
 ID AAEL17608 standard; protein; 506 AA.
 AC AAEL17608;

DT 22-APR-2002 (first entry)

DE Arabidopsis thaliana elongase KCS protein.

KW Fatty acid elongase 3-ketoacyl CoA synthase; elongase KCS; enzyme;
 KW very long chain fatty acid; VLCFA; FAEI protein.

OS Arabidopsis thaliana.

PN WO200194565-A2.

PD 13-DEC-2001.

PF 08-JUN-2001; 2001WO-US018737.

PR 08-JUN-2000; 2000US-0210326P.

PS (UYMI-) UNIV MIAMI.

PI Jaworski JG, Blacklock BJ;

DR WPI; 2002-154572/20.

DR N-PSDB; AAD28500.

XX New fatty acid elongase 3-ketoacyl CoA synthase polypeptide and nucleic
 PT acids encoding the polypeptide, useful for producing very long chain
 PT fatty acids.

PS Example 3; Fig 1-1; 139pp; English.

XX The invention relates to fatty acid elongase 3-ketoacyl CoA synthase
 CC (KCS) polypeptides with altered substrate specificity and/or catalytic
 CC activity and nucleic acid molecules encoding such polypeptides.
 CC Polypeptides of the invention are useful for catalysing the condensation
 CC of C18 fatty acyl substrate and malonyl CoA, leading to the synthesis of
 CC C20 fatty acyl CoA. They are especially useful for producing very long
 CC chain fatty acids (VLCFA) and may be used in the development of reagents
 CC for various purposes, e.g., immunological reagents to monitor expression
 CC of elongase KCS polypeptides or nucleic acid probes or primers to monitor
 CC inheritance of an elongase KCS gene in plant breeding programs. The
 CC present sequence is Arabidopsis thaliana elongase KCS protein encoded by
 CC FAEI gene
 CC

SQ Sequence 506 AA;

Query Match 90.3%; Score 28; DB 5; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1e+03; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFPA 6
 ||:||||
 Db 356 KFLFPA 361

RESULT 29
 AEA37517
 ID AEA37517 standard; protein; 506 AA.
 AC AEA37517;

DT 11-AUG-2005 (first entry)

DE Arabidopsis sp. fatty acid elongase 1 (FAEI) protein.

KW vector; transformation; plant; fatty acid elongase 1;
 KW 3-ketoacyl-CoA synthase; promoter; gene expression; seed; oil; enzyme.

OS Arabidopsis sp.

PN WO2005052162-A1.

PD 09-JUN-2005.

PF 24-NOV-2004; 2004WO-CA002021.

PR 25-NOV-2003; 2003US-0524645P.

PS (CANA) NAT RES COUNCIL CANADA.

PI Mietkiewska E, Taylor DC, Katavic V;

DR WPI; 2005-418004/42.

DR N-PSDB; AEA37518.

XX New expression vector for transforming a cell comprising a gene coding
 PT for a plant fatty acid elongase, useful for altering erucic acid content
 PT or the very long chain fatty acid content (C20 or greater) in a plant.

PS Disclosure; SEQ ID NO 26; 72pp; English.

XX The invention relates to an expression vector for transforming a cell.
 CC The expression vector comprises a gene coding for a plant fatty acid
 CC elongase (FAE), also designated 3-ketoacyl-CoA synthase (KCS)) in reading
 CC frame alignment with a promoter capable of increasing the expression of
 CC the gene, when the transformed cell is in a seed, sufficient to increase
 CC the proportion of very long chain monounsaturated fatty acid when
 CC compared with a control cell. Also described are: (1) a cell comprising a
 CC heterologous gene coding for a heterologous plant fatty acid elongase or
 CC its allelic variant, the cell being capable of producing an increase in
 CC proportion of a very long chain monounsaturated fatty acid when compared
 CC a control cell lacking the heterologous gene; (2) a seed comprising the
 CC plant cells above; (3) a plant comprising the plant cells; and (4) a
 CC method of altering erucic acid content of a plant-derived oil. The gene
 CC coding for a plant fatty acid elongase is a Nasturtium, Crambe, or
 CC Arabidopsis fatty acid elongase gene. The cell is a fungal cell,
 CC preferably yeast cell, or a plant cell, specifically a plant seed cell.
 CC The plant cell additionally comprises a further heterologous gene coding
 CC for an additional heterologous plant fatty acid elongase or its allelic
 CC variant or a heterologous plant desaturase gene or its allelic variant.
 CC It is capable of producing oil with an increased content of erucic acid.
 CC or other very long chain fatty acid (C20 or greater). The heterologous
 CC gene codes for a 3-ketoacyl-CoA synthase. The very long chain
 CC monounsaturated fatty acid comprises erucic acid. The heterologous plant
 CC fatty acid elongase gene is useful for altering erucic acid content in a
 CC plant or the very long chain fatty acid content (C20 or greater) in a
 CC plant. The vector is useful for altering erucic acid content in a plant.

CC This sequence represents a *Arabidopsis* sp. PAE1.

XX Sequence 506 AA;

Query Match 90.3%; Score 28; DB 9; Length 506;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFFA 6

Db 356 KPLFFA 361

RESULT 30

AAV19992

ID RAY19992 standard; protein; 508 AA.

XX AC AAV19992;

XX DT 19-JUL-1999 (first entry)

XX DE B. burgdorferi antigenic protein, f752.aa.

XX KW Antigenic protein; vaccine; Lyme disease; infection; detection.

XX OS Borrelia burgdorferi.

XX PN WO9859071-A1.

XX PD 30-DEC-1998.

XX PF 18-JUN-1998; 98WO-US012718.

XX PR 20-JUN-1997; 97US-0050359P.

XX PR 23-JUL-1997; 97US-0053344P.

XX PR 22-JUL-1997; 97US-0053377P.

XX PR 03-SEP-1997; 97US-0057483P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (MEDI-) MEDIMUNE INC.

PI Choi GH, Erwin AL, Hanson MS, Lathigra R;

XX WPI; 1999-189980/16.

DR N-PSDB; AAX61689.

XX New isolated Borrelia burgdorferi nucleic acids - used to develop

PT products for the diagnosis, prevention and treatment of diseases caused

PT by Borrelia, particularly Lyme disease.

XX Claim 12; Page 153; 275pp; English.

PS This sequence represents a Borrelia burgdorferi (Bb) protein of the

CC invention, which is suitable for use in a vaccine. The Bb polypeptides

CC can be used in vaccines for eliciting protective antibodies to members of

CC the Borrelia genus, particularly for the use against Lyme disease in

CC humans and animals. They can be used for preventing or attenuating an

CC infection caused by a member of the Borrelia genus. The products can also

CC be used for detection of members of the Borrelia genus

XX Sequence 508 AA;

Qy 1 KPVFFA 6

Db 41 RLVFFA 46

RESULT 31

ABU19128

ID ABU19128 standard; protein; 508 AA.

XX AC ABU19128;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #4655.

XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS Borrelia burgdorferi.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR N-PSDB; ACA22998.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 47052; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for

CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

CC the target prokaryotic essential genes. Note: The sequence data for this

CC patent did not form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 508 AA;

Query Match

90.3%; Score 28; DB 6; Length 508;

Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
DB 41 RVVFFA 46

RESULT 32
ABU24005
ID ABU24005 standard; protein; 571 AA.
XX
AC ABU24005;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #9532.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Clostridium acetobutylicum.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0349232P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haseibeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
WPI; 2003-029926/02.
DR N-PSDB; ACA27875.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 51929; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 571 AA;

Query Match 90.3%; Score 28; DB 6; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
DB 314 KVFVFA 319

RESULT 33
ADN19501
ID ADN19501 standard; protein; 1089 AA.
XX
AC ADN19501;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #2154.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
XX (GOLD) GOLDMAN B S.
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 2154; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 SQ Sequence 1089 AA;

Query Match 90.3%; Score 28; DB 8; Length 1089;

Best Local Similarity 83.3%; Pred. No. 2.2e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFFA 6

Db 13 KPVFFS 18

RESULT 34

AAG61668

ID AAG61668 standard; protein; 52 AA.

XX

AC AAG61668;

XX

DT 18-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 80017.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

XX

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-00301439.

XX

PR 25-FEB-1999; 99US-0121825P.

PR

PR 05-MAR-1999; 99US-0123380P.

PR

PR 09-MAR-1999; 99US-01233548P.

PR

PR 23-MAR-1999; 99US-0125788P.

PR

PR 25-MAR-1999; 99US-0126264P.

PR

PR 29-MAR-1999; 99US-0126785P.

PR

PR 01-APR-1999; 99US-0127462P.

PR

PR 06-APR-1999; 99US-0128234P.

PR

PR 08-APR-1999; 99US-0128714P.

PR

PR 16-APR-1999; 99US-0129845P.

PR

PR 19-APR-1999; 99US-0130077P.

PR

PR 21-APR-1999; 99US-0130449P.

PR

PR 23-APR-1999; 99US-0130510P.

PR

PR 28-APR-1999; 99US-0130891P.

PR

PR 28-APR-1999; 99US-0131449P.

PR

PR 30-APR-1999; 99US-0132048P.

PR

PR 30-APR-1999; 99US-0132407P.

PR

PR 04-MAY-1999; 99US-0132484P.

PR

PR 05-MAY-1999; 99US-0132485P.

PR

PR 06-MAY-1999; 99US-0132486P.

PR

PR 06-MAY-1999; 99US-0132487P.

PR

PR 07-MAY-1999; 99US-0132863P.

PR

PR 11-MAY-1999; 99US-0134256P.

PR

PR 14-MAY-1999; 99US-0134218P.

PR

PR 14-MAY-1999; 99US-0134219P.

PR

PR 14-MAY-1999; 99US-0134221P.

PR

PR 14-MAY-1999; 99US-0134222P.

PR

PR 14-MAY-1999; 99US-0134370P.
 PR 18-MAY-1999; 99US-0134768P.
 PR 19-MAY-1999; 99US-0134941P.
 PR 20-MAY-1999; 99US-0135124P.
 PR 21-MAY-1999; 99US-0135353P.
 PR 24-MAY-1999; 99US-0135629P.
 PR 25-MAY-1999; 99US-0136021P.
 PR 27-MAY-1999; 99US-0136392P.
 PR 28-MAY-1999; 99US-0136782P.
 PR 01-JUN-1999; 99US-0137222P.
 PR 03-JUN-1999; 99US-0137528P.
 PR 04-JUN-1999; 99US-0137502P.
 PR 07-JUN-1999; 99US-0137724P.
 PR 08-JUN-1999; 99US-0138094P.
 PR 10-JUN-1999; 99US-0138540P.
 PR 10-JUN-1999; 99US-0138847P.
 PR 14-JUN-1999; 99US-0139119P.
 PR 16-JUN-1999; 99US-0139452P.
 PR 16-JUN-1999; 99US-0139453P.
 PR 17-JUN-1999; 99US-0139492P.
 PR 18-JUN-1999; 99US-0139454P.
 PR 18-JUN-1999; 99US-0139455P.
 PR 18-JUN-1999; 99US-0139456P.
 PR 18-JUN-1999; 99US-0139457P.
 PR 18-JUN-1999; 99US-0139458P.
 PR 18-JUN-1999; 99US-0139459P.
 PR 18-JUN-1999; 99US-0139460P.
 PR 18-JUN-1999; 99US-0139461P.
 PR 18-JUN-1999; 99US-0139462P.
 PR 18-JUN-1999; 99US-0139463P.
 PR 18-JUN-1999; 99US-0139750P.
 PR 18-JUN-1999; 99US-0139763P.
 PR 21-JUN-1999; 99US-0139817P.
 PR 22-JUN-1999; 99US-0139899P.
 PR 23-JUN-1999; 99US-0140353P.
 PR 24-JUN-1999; 99US-0140354P.
 PR 24-JUN-1999; 99US-0140695P.
 PR 28-JUN-1999; 99US-0140823P.
 PR 29-JUN-1999; 99US-0140991P.
 PR 30-JUN-1999; 99US-0141287P.
 PR 01-JUL-1999; 99US-0141842P.
 PR 01-JUL-1999; 99US-0142154P.
 PR 02-JUL-1999; 99US-0142055P.
 PR 06-JUL-1999; 99US-0142390P.
 PR 08-JUL-1999; 99US-0142803P.
 PR 09-JUL-1999; 99US-0142920P.
 PR 12-JUL-1999; 99US-0142977P.
 PR 13-JUL-1999; 99US-0143542P.
 PR 14-JUL-1999; 99US-0143624P.
 PR 15-JUL-1999; 99US-0144005P.
 PR 16-JUL-1999; 99US-0144085P.
 PR 16-JUL-1999; 99US-0144086P.
 PR 19-JUL-1999; 99US-0144325P.
 PR 19-JUL-1999; 99US-0144331P.
 PR 19-JUL-1999; 99US-0144332P.
 PR 19-JUL-1999; 99US-0144333P.
 PR 19-JUL-1999; 99US-0144334P.
 PR 19-JUL-1999; 99US-0144335P.
 PR 20-JUL-1999; 99US-0144352P.
 PR 20-JUL-1999; 99US-0144632P.
 PR 20-JUL-1999; 99US-0144884P.
 PR 21-JUL-1999; 99US-0144814P.
 PR 21-JUL-1999; 99US-0145086P.
 PR 21-JUL-1999; 99US-0145088P.
 PR 22-JUL-1999; 99US-0145085P.
 PR 22-JUL-1999; 99US-0145087P.
 PR 22-JUL-1999; 99US-0145089P.
 PR 22-JUL-1999; 99US-0145192P.
 PR 23-JUL-1999; 99US-0145145P.
 PR 23-JUL-1999; 99US-0145218P.
 PR 23-JUL-1999; 99US-0145224P.
 PR 26-JUL-1999; 99US-0145276P.
 PR 27-JUL-1999; 99US-0145513P.

```
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149360P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160981P.
PR 25-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.

PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match      87.1%; Score 27; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFP 5
Db 31 KFVFP 35
|||||
RESULT 35
ADX67964
ID ADX67964 standard; protein; 57 AA.
XX
AC ADX67964;
XX
DT 21-APR-2005 (first entry)
XX
Plant full length insert polypeptide seqid 38807.
XX
plant protectant; plant growth regulant; gene therapy; plant;
recombinant DNA construct; physical array; plant breeding marker;
cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
extreme osmotic condition; pathogen tolerance; pest tolerance;
growth rate; cell cycle pathway; disease resistance;
galactomannan production; lignin production; plant growth regulator;
yield; plant growth; plant development; seed oil; protein yield;
protein content.
XX
Unidentified.
XX
OS US2004034888-A1.
XX
PN 19-FEB-2004.
XX
PD 28-APR-2003; 2003US-00425114.
XX
PF 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
WPT; 2004-180133/17.
XX
New recombinant DNA construct, useful for improving plant tolerance to
cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
pests, for conferring increased resistance to plant disease, or for
improving yield.
XX
Claim 1; SEQ ID NO 38807; 15pp; English.
PS
The invention describes a recombinant DNA construct comprising a
polynucleotide consisting of a sequence encoding an amino acid sequence
available in electronic form from the US patent office at
ftp.seqdata.uspto.gov/sequence.html?docID:2004034888. The polynucleotide
of the invention are also useful in physical arrays of molecules and as
plant breeding markers. The recombinant DNA construct is useful for
improving plant tolerance to cold, heat, drought, herbicides, extreme
```

CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This is the amino acid sequence of a plant full length insert
 CC polypeptide that can be used in the recombinant DNA construct of the
 CC invention.

XX Sequence 57 AA;

Query Match 87.1%; Score 27; DB 8; Length 57;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 DB 29 KPVFF 33

RESULT 36

ABB03189

ID ABB03189 standard; protein; 62 AA.

XX AC ABB03189;

XX DT 08-JAN-2002 (first entry)

XX DE Human musculoskeletal system related polypeptide SEQ ID NO 1136.

XX KW Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
 KW anti-allergic; hepatocytic; antidiabetic; anti-inflammatory; antiulcer;
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
 KW neurological disease; infection; human; secreted protein;
 KW musculoskeletal system.

XX OS Homo sapiens.

XX PN WO200155367-A1.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US001338.

XX PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 30-JUN-2000; 2000US-0214886P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225213P.
 PR 14-AUG-2000; 2000US-0225214P.
 PR 14-AUG-2000; 2000US-0225266P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 14-AUG-2000; 2000US-0225759P.
 PR 18-AUG-2000; 2000US-0226279P.
 PR 22-AUG-2000; 2000US-0226681P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 22-AUG-2000; 2000US-0227182P.
 PR 23-AUG-2000; 2000US-0227009P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 01-SEP-2000; 2000US-0229345P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 06-SEP-2000; 2000US-0230437P.
 PR 06-SEP-2000; 2000US-0230438P.
 PR 08-SEP-2000; 2000US-0231242P.
 PR 08-SEP-2000; 2000US-0231243P.
 PR 08-SEP-2000; 2000US-0231244P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 08-SEP-2000; 2000US-0231414P.
 PR 08-SEP-2000; 2000US-0232080P.
 PR 08-SEP-2000; 2000US-0232081P.
 PR 12-SEP-2000; 2000US-0231968P.
 PR 14-SEP-2000; 2000US-0232397P.
 PR 14-SEP-2000; 2000US-0232398P.
 PR 14-SEP-2000; 2000US-0232399P.
 PR 14-SEP-2000; 2000US-0232400P.
 PR 14-SEP-2000; 2000US-0232401P.
 PR 14-SEP-2000; 2000US-0233063P.
 PR 14-SEP-2000; 2000US-0233064P.
 PR 14-SEP-2000; 2000US-0233065P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 25-SEP-2000; 2000US-0234998P.
 PR 26-SEP-2000; 2000US-0235484P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 27-SEP-2000; 2000US-0235836P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 02-OCT-2000; 2000US-0237040P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 13-OCT-2000; 2000US-0239937P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241221P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241786P.
 PR 20-OCT-2000; 2000US-0241787P.
 PR 20-OCT-2000; 2000US-0241808P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 20-OCT-2000; 2000US-0241826P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0254719P.
PR 06-DEC-2000; 2000US-0254719P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-451937/48.
DR N-PSDB; AAL34771.
XX
PT Isolated polypeptide for treating, preventing and/ or prognosing
PT disorders related to the musculoskeletal system including musculoskeletal
PT cancers and also for testing and detection e.g. diagnosis.
XX
PS Claim 11; SEQ ID NO 1136; 781pp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABB03087-ABB04109) associated with the musculoskeletal system useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. The genes are isolated from a range of human tissues
CC disclosed in the specification. The nucleic acids, proteins, antibodies
CC and (ant)agonists are useful in the diagnosis, treatment and prevention
CC of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the
CC adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver,
CC lung, or urogenital; (b) immune disorders e.g. Addison's disease,
CC allergies, autoimmune hemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; (c) cardiovascular disorders such as
CC myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g.
CC cerebral anoxia and epilepsy; and (f) infectious diseases such as viral,
CC bacterial, fungal and parasitic infections. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 62 AA;

Query Match 97.1%; Score 27; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFPP 5
Db 31 KVFPP 35
RESULT 37
ABU12483
ID ABU12483 standard; protein; 62 AA.
XX AC ABU12483;
XX DT 26-FEB-2003 (first entry)
XX DE Novel human musculoskeletal system antigen #103.
XX Musculoskeletal system antigen; cancer; metastasis; re-vascularisation;
KW thrombosis; arteriosclerosis; mineral content; cardiovascular condition;
KW wound; injury; burn; angiogenesis; ulcer; post-operative tissue repair;
KW limb regeneration; neuronal growth; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; AIDS-related complex;
KW chondrocyte growth; bone regeneration; periodontal regeneration;
KW tissue transport; bone graft; skin aging; keratinocyte growth; hair loss;
KW melanocyte growth; cell proliferation; cell growth; organ transplant;
KW cell differentiation; body height; weight; hair colour; eye colour; skin;
KW percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism;
KW biorhythm; cardiac rhythm; depression; tendency for violence; pain;
KW reproductive capability; hormone level; endocrine level; appetite;
KW libido; memory; stress; storage capability; fat content; lipid content;
KW protein content; carbohydrate content; vitamin content; cofactor content;
KW nutritional component.
XX Homo sapiens.
OS
XX US2002147140-A1.
XX 10-OCT-2002.
XX
XX 17-JAN-2001; 2001US-00764877.
XX
XX 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 28-JUN-2000; 2000US-0214886P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 22-AUG-2000; 2000US-0225758P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 08-SEP-2000; 2000US-0231413P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.

PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0237040P.
 PR 20-OCT-2000; 2000US-0240360P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 XX

(ROSE/) ROSEN C A.
 (RUBE/) RUBEN S M.
 (BARA/) BARASH S C.

Rosen CA, Ruben SM, Barash SC;
 WPI; 2003-128199/12.
 N-PSDB; ABX57759.

Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. cancer.

Claim 11; SEQ ID NO 1136; 321pp; English.

The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to sunburn by stimulating keratinocyte growth; prevents hair loss, since for family members activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodermal origin to differentiate in early embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates mammalian characteristics, such as, body height, weight, hair colour, eye colour, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery); modulates mammalian metabolism; changes mammal's metal state or physical state by influencing biorhythms, circadian rhythms, depression, tendency for violence, tolerance for pain, reproductive capabilities, hormonal or endocrine levels, appetite, libido, memory, or stress; increases or decreases storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components. This is the amino acid sequence of a novel human musculoskeletal system antigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at ftp.segdata.uspto.gov/sequence.html?DocID=20020147140

Sequence 62 AA;

Query Match 87.1%; Score 27; DB 6; Length 62;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 |||||
 Db 31 KPVFF 35

RESULT 38

ADJ28509
 ID ADJ28509 standard; protein; 62 AA.

XX AC ADJ28509;

XX DT 20-MAY-2004 (first entry)

XX DE Human musculoskeletal system-associated protein - SEQ ID 1136.

XX KW musculoskeletal system; cytostatic; osteopathic; cancer; osteoporosis;

XX KW Gene therapy; vaccine; human.

XX OS Homo sapiens.

XX PN US2004009488-A1.

XX PD 15-JAN-2004.

XX PF 13-SEP-2002; 2002US-00242515.

XX PR 31-JAN-2000; 2000US-0179065P.

XX PR 04-FEB-2000; 2000US-0180628P.

XX PR 24-FEB-2000; 2000US-0184664P.

XX PR 02-MAR-2000; 2000US-0186350P.

XX PR 16-MAR-2000; 2000US-0189874P.

XX PR 17-MAR-2000; 2000US-0190076P.

XX PR 18-APR-2000; 2000US-0198123P.

XX PR 19-MAY-2000; 2000US-0205515P.

XX PR 07-JUN-2000; 2000US-0209467P.

XX PR 28-JUN-2000; 2000US-0214086P.

XX PR 30-JUN-2000; 2000US-0215135P.

XX PR 07-JUL-2000; 2000US-0216647P.

XX PR 07-JUL-2000; 2000US-0216880P.

XX PR 11-JUL-2000; 2000US-0217487P.

XX PR 11-JUL-2000; 2000US-0217496P.

XX PR 14-JUL-2000; 2000US-0218290P.

XX PR 26-JUL-2000; 2000US-0220963P.

XX PR 14-AUG-2000; 2000US-0224518P.

XX PR 14-AUG-2000; 2000US-0224519P.

XX PR 14-AUG-2000; 2000US-0225213P.

XX PR 14-AUG-2000; 2000US-0225214P.

XX PR 14-AUG-2000; 2000US-0225266P.

XX PR 14-AUG-2000; 2000US-0225267P.

XX PR 14-AUG-2000; 2000US-0225268P.

XX PR 14-AUG-2000; 2000US-0225270P.

XX PR 14-AUG-2000; 2000US-0225447P.

XX PR 14-AUG-2000; 2000US-0225757P.

XX PR 14-AUG-2000; 2000US-0225758P.

XX PR 14-AUG-2000; 2000US-0225759P.

XX PR 18-AUG-2000; 2000US-0226279P.

XX PR 22-AUG-2000; 2000US-0226881P.

XX PR 22-AUG-2000; 2000US-0226888P.

XX PR 23-AUG-2000; 2000US-0227182P.

XX PR 23-AUG-2000; 2000US-0227009P.

XX PR 30-AUG-2000; 2000US-0228924P.

XX PR 01-SEP-2000; 2000US-0229287P.

XX PR 01-SEP-2000; 2000US-0229343P.

XX PR 01-SEP-2000; 2000US-0229344P.

XX PR 05-SEP-2000; 2000US-0229509P.

XX PR 05-SEP-2000; 2000US-0229513P.

XX PR 06-SEP-2000; 2000US-0230437P.

XX PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241828P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249219P.
PR 17-NOV-2000; 2000US-0249244P.

PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764877.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Ruben SM, Barash SC;
XX
XX WPI; 2004-090458/09.
XX N-PSDB; ADJ27486.
XX
XX New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer of musculoskeletal tissues or osteoporosis.
XX
XX Claim 11; SEQ ID NO 1136; 289pp; English.
XX
XX The invention relates to a novel isolated musculoskeletal system-associated nucleic acid molecule. The nucleic acid of the invention demonstrates cytostatic and osteopathic activities and may be useful for preparing a medicament for preventing, treating or ameliorating a medical condition such as cancer of the musculoskeletal tissues or osteoporosis, possibly via gene therapy or vaccine production. The current sequence is that of the human musculoskeletal system-associated polypeptide of the invention. The current sequence is not shown within the specification per se but is available on the USPTO web-site
XX <http://seqdata.uspto.gov/sequence.html?DocID=20040009488>.
XX
XX Sequence 62 AA;
SQ
Query Match 87.1%; Score 27; DB 8; Length 62;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 KVFVF 5
Db 31 KVFVF 35
|||||
RESULT 39
AAG00778
ID AAG00778 standard; protein; 82 AA.
XX
AC AAG00778;
XX
XX 06-OCT-2000 (first entry)
XX Human secreted protein, SEQ ID NO: 4859.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX

PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 DR N-PSDB; AAC00784.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 13; SEQ ID NO 4859; 71pp + Sequence Listing; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 SQ Sequence 82 AA;
 Query Match 87.1%; Score 27; DB 3; Length 82;
 Best Local Similarity 100.0%; Pred. NO. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFF 5
 Db 32 KVFVFF 36
 |||||
 |||||
 RESULT 40
 ABG13797
 ID ABG13797 standard; protein; 82 AA.
 XX
 AC ABG13797;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #13788.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 DR

DR N-PSDB; AAS77984.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 44156; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have application in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 82 AA;
 Query Match 87.1%; Score 27; DB 4; Length 82;
 Best Local Similarity 83.3%; Pred. NO. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFF 6
 Db 11 EFVFFFA 16
 :|||||
 |||||
 RESULT 41
 AAO12276
 ID AAO12276 standard; protein; 91 AA.
 XX
 AC AAO12276;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 26168.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN WO200164835-A2.
 XX
 PD 07-SEP-2001.
 XX
 PF 26-FEB-2001; 2001WO-US004927.
 XX
 PR 28-FEB-2000; 2000US-00515126.
 PR 18-MAY-2000; 2000US-00577409.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT;
 XX
 XX WPI; 2001-514838/56.
 DR

DR	N-PSDB; AAI92207.
XX	
PT	Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT	and treating e.g. leukemia, inflammation and immune disorders.
XX	
PS	Claim 20; SEQ ID NO 26168; 1399pp + Sequence Listing; English.
XX	
CC	The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC	the encoded proteins (AAO0010-AAO13910) that exhibit activity elating to
CC	cytokine, cell proliferation or cell differentiation or which may induce
CC	production of other cytokines in other cell populations. The
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC	peptide therapy. The polypeptides have various cytokine-like activities,
CC	e.g. stem cell growth factor activity, haematopoiesis regulating
CC	activity, tissue growth factor activity, immunomodulatory activity and
CC	activin/inhibin activity and may be useful in the diagnosis and/or
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC	inflammation. Note: The sequence data for this patent did not form part
CC	of the printed specification, but was obtained in electronic format
CC	directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
XX	Sequence 91 AA;
XX	
XX	

Query Match 87.1%; Score 27; DB 4; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	KVFF	5
Db	17	KVFF	21

RESULT 42
AAO10108
ID AAO10108 standard; protein; 99 AA.

AAO10108;

DT 06-NOV-2001 (first entry)

Human polypeptide SEQ ID NO 24000.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

PN WO200164835-A2.

07-SEP-2001.

26-FEB-2001:

PR 28-FEB-2000: 2000US-00515126.

FR 18-MAY-2000; 2000US-00577409.
XX

PA (HYSE-) HYSEQ INC.
XX

pi Tang YT, Liu C, Drmanac RT;
yy

DR WPI; 2001-514838/56.
DP N-PSDB: AAT90039

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
PT and treating e.g. leukemia, inflammation and immune disorders.

PS Claim 20; SEQ ID NO 24000; 1399pp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce

production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp:wipo.int/pub/published_pat_sequences

Sequence 99 AA;

Query Match 87.1%; Score 27; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels

Qy	1	KFVFF	5
Db	39	KFVFF	43

RESULT 43
AAE12897
ID AAE12897 standard; protein: 104 AA.

AA
AC

15-JAN-2002 (first entry)

DE Human recombinant beta-amyloid precursor protein (betaAPP) C-83.

Human; Alzheimer's disease; gamma-secretase; integral-membrane protein; beta-amyloid precursor protein; betaAPP.

OS Homo sapiens.

PN WO200175435-A2.

PD 11-OCT-2001.

30-MAR-2001; 2001WO-US010453.

PR 03-APR-2000: 2000US-0194495P.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Roberts SB, Hendrick JP, Vinitzky A, Lewis M, Smith DW, Pak R;
XX

WPI; 2001-648575/74.

DR N-PSDB; AAD20982.
XX

PT amyloid peptide.
PT capable of cleaving beta-amyloid precursor protein to produce beta amyloid peptide.
PT Novel gamma secretase protein, useful in the production of amyloids, is capable of cleaving beta-amyloid precursor protein to produce beta amyloid peptide.

PS Claim 83: Fig 3: 127pp: English.

The invention relates to the field of plaque amyloid deposits that are the hallmarks of Alzheimer's disease. In particular, the invention relates to an isolated, functionally-active protein that has gamma-secretase activity. Gamma-secretase activity is necessary for amyloid production. The present invention also relates to methods for isolating integral-membrane proteins and protein complexes, including the gamma-secretase protein of the invention. The method is useful for monitoring the cleavage of beta-amyloid precursor protein (betaAPP) by gamma-secretase. The present sequence is human recombinant betaAPP protein (C-83)

Sequence 104 AA;

Query Match 87.1%; Score 27; DB 4; Length 104;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 21 EFVFFA 26

RESULT 44
AAB93728
ID AAB93728 standard; protein; 114 AA.
AC AAB93728;
XX
XX 26-JUN-2001 (first entry)
DT
DE Human protein sequence SEQ ID NO:13358.
XX
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-00116126.
XX
XX 29-JUL-1999; 99JP-00248036.
XX
XX 27-AUG-1999; 99JP-00300253.
XX
XX 11-JAN-2000; 2000JP-00118776.
XX
XX 02-MAY-2000; 2000JP-00183767.
XX
XX 09-JUN-2000; 2000JP-00241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
XX
XX Claim 8; SEQ ID NO 13358; 2537pp + Sequence Listing; English.
XX
XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesizing polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent polynucleotides, all of which are used in the exemplification of the present invention
XX
XX Sequence 114 AA;
XX

Query Match.

87.1%; Score 27; DB 4; Length 114;

Best Local Similarity 66.7%; Pred. No. 4e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 24 KFIFFS 29

RESULT 45
ABP33134
ID ABP33134 standard; protein; 115 AA.
XX
XX AC ABP33134;
XX
XX 09-JUL-2002 (first entry)
DT
DE Human isomerase-like ORF2107 protein, SEQ ID NO:4214.
XX
XX Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; haematopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnery; KW vasotropic; antipsoriatic; antidiabetic; cytostatic; neurotropic; KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic; KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator; KW dermatological; analgesic; virucide; antibacterial; fungicide.
XX
XX Homo sapiens.
XX
XX WO200190366-A2.
XX
XX 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US017076.
XX
XX 24-MAY-2000; 2000US-0206690P.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Leach MD, Shimkets RA;
XX
XX WPI; 2002-106200/14.
XX
XX N-PSDB; ABN77160.
XX
XX Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, PT hyperproliferative disorders and disorders related to organ transplantation.
XX
XX Claim 10; Page 1311; 2508pp; English.
XX
XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN79587 represent cDNAs encoding them. The invention also encompasses CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX CC polynucleotides, the recombinant production of ORFX proteins, antibodies CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and CC polypeptides, methods of screening for modulators of ORFX expression or CC ORFX-associated disorder. The ORFX proteins of the invention have a wide CC range of biological activities, such as cytokine, cell proliferation, CC cell differentiation, immune modulation, haematopoiesis regulation, CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/ CC chemokinetic activity, haemostatic activity, thrombolytic activity, CC receptor/ligand, antiinflammatory activity, tumour inhibition activity, CC and antiinfective activity, and may also be involved in the determination

CC of bodily characteristics, fertility and behaviour. ORFX proteins,
 CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,
 CC neurological disorders such as epilepsy and Alzheimer's disease,
 CC cardiovascular diseases, immune system disorders, disorders related to
 CC organ transplantation, disorders of tissue growth and regeneration,
 CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol
 CC storage disease, and infectious diseases caused by viral, bacterial,
 CC fungal and other pathogens. ORFX nucleic acids may also be used as a
 CC source of primers and probes, in the detection of ORFX genomic sequences
 CC or transcripts, in the identification and cloning of homologous
 CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
 CC nucleic acids may additionally be used to produce transgenic animals
 CC which may be useful for studying the function and/or activity of ORFX
 CC protein, and in drug screening. The ORFX proteins may also be used as
 CC immunogens to generate specific antibodies, which are useful in the
 CC diagnosis, treatment and monitoring of ORFX-associated diseases
 XX
 XX Sequence 115 AA;

Query Match 87.1%; Score 27; DB 5; Length 115;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 |||||
 Db 67 KPVFF 71

RESULT 46

AAO02898
 ID AAO02898 standard; protein; 126 AA.

AC AAO02898;

DT 06-NOV-2001 (first entry)

DE Human polypeptide SEQ ID NO 16790.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

XX WO200164835-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US004927.

PR 28-FEB-2000; 2000US-00515126.

PR 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

DR N-PSDB; AAI82829.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 16790; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC

CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 126 AA;

Query Match 87.1%; Score 27; DB 4; Length 126;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5
 |||||
 Db 90 KPVFF 94

RESULT 47

AAO00490
 ID AAO00490 standard; protein; 132 AA.

AC AAO00490;

DT 06-NOV-2001 (first entry)

DE Human polypeptide SEQ ID NO 14382.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

OS Homo sapiens.

XX WO200164835-A2.

PD 07-SEP-2001.

PF 26-FEB-2001; 2001WO-US004927.

PR 28-FEB-2000; 2000US-00515126.

PR 18-MAY-2000; 2000US-00577409.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-514838/56.

DR N-PSDB; AAI80421.

XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX Claim 20; SEQ ID NO 14382; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO0010-AAO13910) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX

XX Sequence 132 AA;

Query Match 87.1%; Score 27; DB 4; Length 132;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFF 5
 Db 22 KVFVFF 26

RESULT 48
 ABG26562
 ID ABG26562 standard; protein; 144 AA.

XX AC ABG26562;
 XX

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #26553.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX FN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS90749.

PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 56921; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activities. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 144 AA;

Query Match 87.1%; Score 27; DB 4; Length 144;
 Best Local Similarity 66.7%; Pred. No. 5e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFF 6
 Db 111 RFIFFA 116

RESULT 49

AAO07503
 ID AAO07503 standard; protein; 146 AA.

XX AC AAO07503;

XX DT 06-NOV-2001 (first entry)

XX DE Human polypeptide SEQ ID NO 21395.

XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

XX OS Homo sapiens.

XX FN WO200164835-A2.

XX PD 07-SEP-2001.

XX PF 26-FEB-2001; 2001WO-US004927.

XX PR 28-FEB-2000; 2000US-00515126.

XX PR 18-MAY-2000; 2000US-00577409.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-514838/56.

XX DR N-PSDB; AAI87434.

PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
 PT and treating e.g. leukemia, inflammation and immune disorders.

XX PS Claim 20; SEQ ID NO 21395; 1399pp + Sequence Listing; English.

XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 146 AA;

Query Match 87.1%; Score 27; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFF 5
 Db 24 KVFVFF 28

RESULT 50

ADQ66558

ID ADQ66558 standard; protein; 148 AA.

XX ADQ66558;
 AC 07-OCT-2004 (first entry)
 DT
 XX Novel human protein sequence #1531.
 DE
 XX osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
 KW gene therapy; diagnostic marker; morbid state; osteoporosis;
 KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 XX EP1440981-A2.
 FN
 XX 28-JUL-2004.
 PD
 XX 21-JAN-2004; 2004EP-00001196.
 PF
 XX 21-JAN-2003; 2003JP-00102206.
 XX
 XX 09-MAY-2003; 2003JP-00131392.
 PR
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Nagai K, Irie R;
 FI
 XX WPI; 2004-535376/52.
 DR
 XX N-PSDB; ADQ64370.
 DR
 XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
 PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
 PT
 XX Claim 1; SEQ ID NO 3719; 2449pp; English.
 PS
 XX The invention relates to 2495 novel polynucleotides (I) and their encoded
 CC polypeptides, sequences hybridizing to these nucleotides, sequences
 CC encoding partial polypeptides and sequences having 70% or 90% identity to
 CC the nucleotide and protein sequences. The nucleotides and polypeptides
 CC are useful as diagnostic markers or therapeutic target for the diseases
 CC or morbid states. They are also useful for treating osteoporosis,
 CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
 CC dementia and various cancers. This sequence corresponds to a protein
 CC sequence of the invention.
 XX
 XX Sequence 148 AA;
 SQ
 Query Match 87.1%; Score 27; DB 8; Length 148;
 Best Local Similarity 100.0%; Pred. No. 5.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KFVFF 5
 Db 17 KFVFF 21
 RESULT 51
 AAU27710
 ID AAU27710 standard; protein; 173 AA.
 XX
 XX AAU27710;
 AC
 XX 18-DEC-2001 (first entry)
 DT
 XX Human full-length polypeptide sequence #35.
 DE
 XX Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
 KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
 KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
 KW nervous system disorder; inflammatory disorder; cell differentiation;
 KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
 KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;

KW cytostatic; antirheumatic; antiarthritic; vulnery; antiinflammatory;
 KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
 KW neuroprotective; osteopathic; antidiabetic; antiasthmatic; antiallergic;
 KW immunostimulant; analgesic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO200164834-A2.
 FN
 XX 07-SEP-2001.
 PD
 XX 26-FEB-2001; 2001WO-US004926.
 PF
 XX 28-FEB-2000; 2000US-00515126.
 XX
 XX 18-MAY-2000; 2000US-00577409.
 PR
 XX 17-JUN-2000; 2000US-00597707.
 PR
 XX 14-JUL-2000; 2000US-00616807.
 PR
 XX 19-SEP-2000; 2000US-00664641.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
 FI Drmanac R;
 FI
 XX WPI; 2001-589862/66.
 DR
 XX N-PSDB; AAS44610.
 DR
 XX Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis, treatment of cancer,
 PT neurological, inflammatory disorders and for use in arrays for detection.
 PT
 XX Claim 10; SEQ ID NO 207; 153pp; English.
 PS
 XX Sequences AAU27676-AAU28019 represent full-length polypeptides and contig
 CC polypeptides of the invention. The proteins and their associated DNA
 CC sequences are useful for the treatment, diagnosis and prevention of
 CC various types of disorder in a mammalian subject such as a human, dog,
 CC monkey, mouse, hamster or rat. The disorders include cancers such as
 CC leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as
 CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,
 CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
 CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
 CC chorea, ankyrotrophic lateral sclerosis, spinal muscular atrophy and
 CC Wernicke disease, inflammatory disorders such as nephritis, Crohn's
 CC disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory
 CC bowel disease. The sequences exhibit activity relating to angiogenesis,
 CC cell proliferation, cell differentiation, stem cell growth factor,
 CC activin or inhibin. Therefore, they can be used to manipulate stem cells
 CC in culture to give rise to neuroepithelial cells that can be used to
 CC augment or replace cells damaged by illness, accidental damage or genetic
 CC disorders. The sequences may also be used for regeneration of bone
 CC cartilage, tendons and ligaments and in tissue repair and burn healing.
 CC Note: Some sequences for this patent did not form part of the printed
 CC specification, but were obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 173 AA;
 SQ
 Query Match 87.1%; Score 27; DB 4; Length 173;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KFVFF 5
 Db 46 KFVFF 50
 RESULT 52
 AAU77842
 ID AAU77842 standard; protein; 173 AA.
 XX
 XX AAU77842;
 AC

```

XX DT 05-JUN-2002 (first entry)
XX DE Oestrogen receptor associated protein 19.03.
XX KW Oestrogen receptor associated protein 19.03; cytostatic; antiinfertility;
XX KW reproductive system; tumour; sex growth impediment.
XX OS Unidentified.
XX PN WO200212317-A1.
XX PD 14-FEB-2002.
XX PF 11-JUN-2001; 2001WO-CN000930.
XX PR 12-JUN-2000; 2000CN-00116442.
XX PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-172145/22.
XX DR N-PSDB; ABK12230.
XX KW Estrogen receptor associated protein 19.03 and encoded polynucleotide,
XX PT used in diagnosis and treatment of reproductive system tumors.
XX PS Claim 1; Page 30; 38pp; Chinese.
XX CC This invention relates to the cDNA and protein sequences of a novel
XX CC isolated protein estrogen receptor associated protein 19.03 and a method
XX CC for producing the protein by recombinant means. The protein of the
XX CC invention may have cytostatic and antiinfertility activities. The DNA and
XX CC protein sequences of the invention may be used in the diagnosis and
XX CC treatment of reproductive system tumors and sex growth impediment in the
XX CC adolescence. The present sequence represents the Estrogen receptor
XX CC associated protein 19.03 of the invention
XX SQ Sequence 173 AA;
Query Match 87.1%; Score 27; DB 5; Length 173;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFF 5
DB 46 KPVFF 50
|||||
RESULT 53
ADJ69976
ID ADJ69976 standard; protein; 173 AA.
XX AC ADJ69976;
XX DT 06-MAY-2004 (first entry)
XX DE Human heat mitochondrial protein as a therapeutic target SeqID1782.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
XX KW Huntington's disease; osteoarthritis;
XX KW Leber's hereditary optic neuropathy; LHON;
XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
XX KW osteopathic; ophthalmological; cytostatic.
XX OS Homo sapiens.
XX PN WO2003087768-A2.
XX PD 23-OCT-2003.

```

```

XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX PI Ghosh SS, Faby ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
XX PI Warnock DE;
XX WPI; 2003-845369/78.
XX DR Identifying a mitochondrial target for drug screening assays and for
XX PT treating diseases associated with altered mitochondrial function,
XX PT comprises detecting a modified polypeptide in a sample and correlating
XX PT with the disease.
XX PS Claim 1; SEQ ID NO 1782; 180pp; English.
XX CC This invention relates to novel mitochondrial targets that can be used
XX CC for therapeutic intervention in treating a disease associated with
XX CC altered mitochondrial function. Specifically, it refers to a method for
XX CC identifying proteins of the human heart mitochondrial proteome that are
XX CC useful for drug screening assays, as well as therapeutic targets. The
XX CC present invention describes a method for identifying such proteins that
XX CC can be used in the treatment of various diseases associated with altered
XX CC mitochondrial function including diabetes mellitus, Huntington's disease,
XX CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX CC compositions have neuroprotective, nootropic, antidiabetic,
XX CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX CC cytostatic activities. This polypeptide sequence is a human heart
XX CC mitochondrial protein of the invention.
XX SQ Sequence 173 AA;
Query Match 87.1%; Score 27; DB 7; Length 173;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFF 5
DB 46 KPVFF 50
|||||
RESULT 54
AAG47987
ID AAG47987 standard; protein; 184 AA.
XX AC AAG47987;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 60548.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
XX PR 05-MAR-1999; 99US-0123180P.

```

PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131443P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135622P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 21-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.

PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144864P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.

PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161933P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 184;
 Best Local Similarity 66.7%; Pred. No. 6.4e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFPA 6
 ||:|:
 Db 29 KPIFFS 34

RESULT 55
 AEB38594
 ID AEB38594 standard; protein; 186 AA.
 XX AC AEB38594;
 XX DT 08-SEP-2005 (first entry)
 XX DE L. pneumophila protein SEQ ID NO 2926.
 XX KW detection; infection; Antibacterial; Vaccine.
 XX OS Legionella pneumophila.
 XX PN W02005049642-A2.
 XX PD 02-JUN-2005.
 XX PF 23-SEP-2004; 2004WO-IB003578.
 XX PR 21-NOV-2003; 2003FR-00013687.
 XX PA (INSP) INST PASTEUR.
 XX PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 XX PA (UTLY-) UNIV LYON I BERNARD CLAUDE.
 XX PA (CNRS) CNRS CENT NAT RECH SCI.

XX Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
 XX Riunok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
 XX Jarraud S;

DR WPI; 2005-388305/40.
 XX New genome of Legionella pneumophila Paris strain and derived
 PT polypeptides, useful for detection or identification of the strain and
 PT for treatment and prevention of infections.
 XX Claim 3; SEQ ID NO 2926; 660pp; English.
 XX The invention relates to an isolated or purified nucleotide sequences (I)
 CC from Legionella pneumophila Paris strain. (I), and their related
 CC sequences or fragments, are useful as primers and probes for detection
 CC and amplification, including differentiation between the Paris and
 CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
 CC (hybrid) polypeptides (II). (II) are also useful for preparation of
 CC specific antibodies (Ab), also used for detection/identification of
 CC Legionella, and some (I), specifically those involved in synthesis of
 CC surface proteins, are targets for identification of inhibitors. (II), or
 CC vectors that contain (I), are useful as vaccines and immunogenic
 CC compositions, for treatment and prevention of infections by L.
 CC pneumophila. The present sequence represents the amino acid sequence of a
 CC L. pneumophila protein.
 XX Sequence 186 AA;
 SQ

Query Match 87.1%; Score 27; DB 9; Length 186;
 Best Local Similarity 66.7%; Pred. No. 6.4e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFPA 6
 ||:|:
 Db 7 RPIFFA 12

RESULT 56
 AAU79255
 ID AAU79255 standard; protein; 189 AA.
 XX AC AAU79255;
 XX DT 13-AUG-2002 (first entry)
 XX DE Human membrane-bound matrix metalloproteinase 1 (MT1-MMP) related protein.
 XX KW Membrane-bound matrix metalloproteinase; MT-MMP; MT1-MMP; enzyme; human;
 XX KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;
 XX KW cytostatic; antiallergic; neutropic; neuroprotective.
 XX OS Homo sapiens.
 XX PN W0200241000-A1.
 XX PD 23-MAY-2002.
 XX PF 20-NOV-2001; 2001WO-JP010136.
 XX PR 20-NOV-2000; 2000JP-00352491.
 XX PA (DAII-) DAIICHI FINE CHEM CO LTD.
 XX PI Aoki T, Yonezawa K, Fujimoto N, Ogawa M, Iwata K;
 XX WPI; 2002-435988/46.
 XX Immunoassay method for membrane-bound matrix metalloproteinase with
 PT quantitation using its antibody, applicable in diagnosis of cancer and
 PT cancer metastasis, and in drug development.
 XX Disclosure; Fig 9; 93pp; Japanese.
 XX The invention relates to a method for quantitative immunoassay of a
 CC membrane-bound matrix metalloproteinase (MT-MMP), involving using an
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane

CC among a group of MT-MMPs by using a surfactant and reductant. Such a
 CC method is for detecting a membrane-bound matrix metalloprotease with
 CC quantitation, which is applicable in diagnosis of cancer and cancer
 CC metastasis as well as in drug development, and is also used to monitor
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
 CC represents a human MT1-MMP related protein
 XX

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||
 Db 60 KVFVF 64

RESULT 57

AAU79257
 ID AAU79257 standard; protein; 189 AA.

XX AC AAU79257;

XX DT 13-AUG-2002 (first entry)

XX DE Rat membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

XX KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; rat;
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;
 KW cystostatic; antiallergic; nootropic; neuroprotective.

XX OS Rattus sp.

XX PN WO200241000-A1.

XX PD 23-MAY-2002.

XX PF 20-NOV-2001; 2001WO-JP010136.

XX PR 20-NOV-2000; 2000JP-00352491.

XX PA (DAII-) DAIICHI FINE CHEM CO LTD.

XX PI Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

XX DR WPI; 2002-435988/46.

XX PT Immunoassay method for membrane-bound matrix metalloprotease with
 PT quantitation using its antibody, applicable in diagnosis of cancer and
 PT cancer metastasis, and in drug development.

XX PS Disclosure; Fig 9; 93pp; Japanese.

XX CC The invention relates to a method for quantitative immunoassay of a
 CC membrane-bound matrix metalloprotease (MT-MMP), involving using an
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane
 CC among a group of MT-MMPs by using a surfactant and reductant. Such a
 CC method is for detecting a membrane-bound matrix metalloprotease with
 CC quantitation, which is applicable in diagnosis of cancer and cancer
 CC metastasis as well as in drug development, and is also used to monitor
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
 CC represents a rat MT1-MMP related protein
 XX

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||

Db 60 KVFVF 64

RESULT 58

AAU79258
 ID AAU79258 standard; protein; 189 AA.

XX AC AAU79258;

XX DT 13-AUG-2002 (first entry)

XX DE Rabbit membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.
 XX KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; rabbit;
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;
 KW cytostatic; antiallergic; nootropic; neuroprotective.

XX OS Oryctolagus cuniculus.

XX PN WO200241000-A1.

XX PD 23-MAY-2002.

XX PF 20-NOV-2001; 2001WO-JP010136.

XX PR 20-NOV-2000; 2000JP-00352491.

XX PA (DAII-) DAIICHI FINE CHEM CO LTD.

XX PI Aoki T, Yonezawa K, Fijimoto N, Ogawa M, Iwata K;

XX DR WPI; 2002-435988/46.

XX PT Immunoassay method for membrane-bound matrix metalloprotease with
 PT quantitation using its antibody, applicable in diagnosis of cancer and
 PT cancer metastasis, and in drug development.

XX PS Disclosure; Fig 9; 93pp; Japanese.

XX CC The invention relates to a method for quantitative immunoassay of a
 CC membrane-bound matrix metalloprotease (MT-MMP), involving using an
 CC antibody against MT-MMP selected from groups containing MT-MMPs. The
 CC method involves releasing and/or solubilising MT-MMP from a cell membrane
 CC among a group of MT-MMPs by using a surfactant and reductant. Such a
 CC method is for detecting a membrane-bound matrix metalloprotease with
 CC quantitation, which is applicable in diagnosis of cancer and cancer
 CC metastasis as well as in drug development, and is also used to monitor
 CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
 CC represents a rabbit MT1-MMP related protein
 XX

SQ Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||

Db 60 KVFVF 64

RESULT 59

AAU79256
 ID AAU79256 standard; protein; 189 AA.

XX AC AAU79256;

XX DT 13-AUG-2002 (first entry)

XX DE Murine membrane-bound matrix metalloprotease 1 (MT1-MMP) related protein.

XX KW Membrane-bound matrix metalloprotease; MT-MMP; MT1-MMP; enzyme; mouse;
 KW cancer; metastasis; rheumatoid arthritis; Alzheimer's disease;

KW cytostatic; antiallergic; nootropic; neuroprotective.

XX Mus sp.

XX WO200241000-A1.

XX 23-MAY-2002.

XX 20-NOV-2001; 2001WO-JP010136.

XX 20-NOV-2000; 2000JP-00352491.

XX (DAI-I) DAIICHI PINE CHEM CO LTD.

XX Aoki T, Yonezawa K, Fujimoto N, Ogawa M, Iwata K;

XX WPI; 2002-435988/46.

XX Immunoassay method for membrane-bound matrix metalloproteinase with
PT quantitation using its antibody, applicable in diagnosis of cancer and
PT cancer metastasis, and in drug development.

XX Disclosure; Fig 9; 93pp; Japanese.

XX The invention relates to a method for quantitative immunoassay of a
CC membrane-bound matrix metalloproteinase (MT-MMP), involving using an
CC antibody against MT-MMP selected from groups containing MT-MMPs. The
CC method involves releasing and/or solubilizing MT-MMP from a cell membrane
CC among a group of MT-MMPs by using a surfactant and reductant. Such a
CC method is for detecting a membrane-bound matrix metalloproteinase with
CC quantitation, which is applicable in diagnosis of cancer and cancer
CC metastasis as well as in drug development, and is also used to monitor
CC progress of rheumatoid arthritis and Alzheimer's disease. This sequence
CC represents a mouse MT1-MMP related protein

XX Sequence 189 AA;

Query Match 87.1%; Score 27; DB 5; Length 189;

Best Local Similarity 100.0%; Pred. No. 6.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFF 5

DB 60 KPVFF 64

RESULT 60

ABW73888

ID ABW73888 standard; protein; 197 AA.

XX ABW73888;

XX 17-OCT-2003 (first entry)

XX DNA clone originating in barley containing SNP sequence #298.

XX Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.

XX Hordeum vulgare.

XX WO2003057877-A1.

XX 17-JUL-2003.

XX 16-DEC-2002; 2002WO-IB005403.

XX 20-DEC-2001; 2001JP-00387059.

XX 20-DEC-2001; 2001JP-00387131.

XX 20-DEC-2001; 2001JP-00403299.

XX 20-DEC-2001; 2001JP-00403300.

XX 27-SEP-2002; 2002JP-00327515.

XX (UTNI-) UNIV JAPAN OKAYAMA.

XX Sato K, Takeda K, Kohara Y;

XX WPI; 2003-587127/55.

XX Single nucleotide polymorphism sites in barley varieties and DNA
PT sequences containing them for analysis and identification of barley
PT varieties and production of barley transformants with desired
PT characteristics.

XX Disclosure; SEQ ID XX; 284pp; Japanese.

XX The present invention relates to oligonucleotide clones originating in
CC barley (Hordeum vulgare) which contain single nucleotide polymorphisms
CC (SNP). The oligonucleotides may be used for analysis of SNPs among barley
CC varieties, identification of particular varieties and genotype-phenotype
CC analysis, isolation of specific genes and creation of new varieties by
CC transformation of barley varieties with them and production of new barley
CC varieties with desired properties. The present sequence represents an
CC oligonucleotide clone sequence featured in the specification. The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published-pct-sequences

XX Sequence 197 AA;

Query Match 87.1%; Score 27; DB 7; Length 197;

Best Local Similarity 66.7%; Pred. No. 6.8e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6

DB 140 KPIFYA 145

RESULT 61

ABB52559

ID ABB52559 standard; protein; 206 AA.

XX ABB52559;

XX 11-FEB-2002 (first entry)

XX Escherichia coli polypeptide SEQ ID NO 489.

XX Escherichia coli; B2/D+A-; antiinflammatory; antibacterial;
KW immunosuppressive; extra-intestinal infection; phylogeny; meningitis;
KW systemic infection; non-diarrhoeal infection; septicaemia;
KW pyelonephritis; antibiotic resistance.

XX Escherichia coli.

XX WO200166572-A2.

XX 13-SEP-2001.

XX 12-MAR-2001; 2001WO-EP003445.

XX 10-MAR-2000; 2000FR-00003145.

XX 02-FEB-2001; 2001FR-00001449.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinalay C;

XX WPI; 2001-550253/61.

XX A library of DNA fragments of Escherichia coli strains for the phylogenetic
PT determination of a given strain comprises polynucleotides of nature B2/D+
PT A-.

XX Example 6; Fig 6; 646pp; English.

CC The invention relates to a library of DNA fragments of Escherichia coli
 CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and
 CC encoded proteins (AB52459-AB52919 and AB52954-AB53094) of nature
 CC B2/D+A-. The polynucleotides have potential anti-inflammatory,
 CC antibacterial and immunosuppressive activity as part of pharmaceutical
 CC compositions used to treat, palliate or prevent extra-intestinal E. coli
 CC infections. The polypeptides are useful for determining the phylogenic
 CC group of a given E. coli strain. These polypeptides can detect and treat
 CC an undesired development of E. coli, particularly an extra-intestinal
 CC infection that include systemic and non-diarrhoeal infections such as
 CC septicemia, pyelonephritis and meningitis this is particularly
 CC advantageous as bacterial resistance is increasing with the more frequent
 CC use of broad spectrum antibiotics

XX SQ Sequence 206 AA;
 Query Match 87.1%; Score 27; DB 4; Length 206;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVF 5
 |||||
 Db 25 KVFVF 29

RESULT 62
 AEG22983
 ID AEG22983 standard; protein; 221 AA.
 XX AC AEG22983;
 XX DT 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #22974.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.
 XX FI Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX DR N-PSDB; AAS87170.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 XX PT diagnostics, forensics, gene mapping, identification of mutations
 XX PT responsible for genetic disorders or other traits and to assess
 XX PT biodiversity.
 XX PS Claim 20; SEQ ID NO 53342; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC involving aberrant protein expression or biological activity. The

CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AEG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 221 AA;
 Query Match 87.1%; Score 27; DB 4; Length 221;
 Best Local Similarity 100.0%; Pred. No. 7.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVF 5
 |||||
 Db 36 KVFVF 40

RESULT 63
 ABG06994
 ID ABG06994 standard; protein; 221 AA.
 XX AC ABG06994;
 XX DT 13-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #6985.
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX PN WO200175067-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US008631.
 XX PR 31-MAR-2000; 2000US-00540217.
 XX PR 23-AUG-2000; 2000US-00649167.
 XX PA (HYSE-) HYSEQ INC.
 XX FI Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX DR N-PSDB; AAS71181.
 XX PT New isolated polynucleotide and encoded polypeptides, useful in
 XX PT diagnostics, forensics, gene mapping, identification of mutations
 XX PT responsible for genetic disorders or other traits and to assess
 XX PT biodiversity.
 XX PS Claim 20; SEQ ID NO 37353; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 CC Sequence 221 AA;

Query Match 87.1%; Score 27; DB 4; Length 221;
 Best Local Similarity 83.3%; Pred. No. 7.6e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
 DB 11 EFVFFA 16

RESULT 64
 ADH45453
 ID ADH45453 standard; protein; 227 AA.

XX ADH45453;

XX 25-MAR-2004 (first entry)

XX Human molecule useful for disease detection and treatment, SEQ ID No 47.

XX human; molecule; disease detection; treatment; MDDT; cytostatic;
 XX antiarteriosclerotic; anti-HIV; anti-allergic; cerebroprotective;
 XX antiparkinsonian; anticonvulsant; nootropic; neuroprotective;
 XX antiinflammatory; ophthalmological; antithyroid; antiarthritic;
 XX antibacterial; virucide; protozoacide; antiparasitic; fungicide;
 XX anorectic; cardiant; hypotensive; antiinfertility; hepatotropic;
 XX gene therapy.

XX Homo sapiens.

XX WO2003093427-A2.

XX 13-NOV-2003.

XX 30-APR-2003; 2003WO-US013629.

XX 30-APR-2002; 2002US-0376988P.

XX 14-JUN-2002; 2002US-0389095P.

XX 22-AUG-2002; 2002US-0405860P.

XX 27-AUG-2002; 2002US-0406512P.

XX (INCY-) INCYTE CORP.

XX Swarnakar A, Tran UK, Khare R, Marquis JP, Hafalia AJA; Yue H;
 XX Elliott VS, Becha SD, Ramkumar J, Kable AE, Wilson AD, Jiang X;
 XX Forsythe IJ, Griffin JA, Bulloch SA, Jin P, Jiang X, Jackson AA;
 XX Mason PM, Chawla NK, Chang H, Richardson TW, Tang YT, Lee SY;
 XX Gietzen KJ, Fu GK;

XX WPI; 2004-022653/02.

XX N-PSDB; ADH45507.

XX New human molecules for disease detection and treatment (MDDT) and
 XX encoding polynucleotides, useful for diagnosing, preventing or treating
 XX diseases associated with aberrant MDDT expression, e.g. cancer, stroke,
 XX obesity or AIDS.

XX Claim 1; SEQ ID NO 47; 267pp; English.

XX The invention relates to human molecules useful for disease detection and
 XX treatment (MDDT) and also the polynucleotides which encode and identify
 XX and encode MDDT. The MDDT polypeptides and encoding polynucleotides have

CC the following activities: cytostatic, antiarteriosclerotic, anti-HIV,
 CC anti-allergic, cerebroprotective, antiparkinsonian, anticonvulsant,
 CC nootropic, neuroprotective, antiinflammatory, ophthalmological,
 CC antithyroid, antiarthritic, antibacterial, virucide, protozoacide,
 CC antiparasitic, fungicide, anorectic, cardiant, hypotensive,
 CC antiinfertility, and hepatotropic. The MDDT polynucleotide may be used in
 CC gene therapy to treat disorders. The polypeptides and polynucleotides are
 CC useful in diagnosing, preventing or treating diseases or conditions
 CC associated with the decreased expression or overexpression of MDDT, such
 CC as autoimmune/inflammatory disorders (AIDS, allergies, atopic dermatitis,
 CC arthritis or thyroiditis), infections (e.g. bacterial, viral, parasitic,
 CC protozoal or fungal), metabolic disorders (e.g. obesity), reproductive
 CC disorders (e.g. infertility), neurological disorders (Parkinson's
 CC disease, Alzheimer's disease, stroke, epilepsy), cardiovascular disorders
 CC (e.g. myocardial infarction or hypertension), eye disorders, or cell
 CC proliferative diseases (e.g. cancer, atherosclerosis, hepatitis). These
 CC are also useful in assessing the effects of exogenous compounds on the
 CC expression of nucleic acid and amino acid sequences of MDDT. The MDDT or
 CC its fragments are useful in screening compounds for effectiveness as
 CC agonist or antagonist of the polypeptides, or in altering the expression
 CC of the target polynucleotide and compounds that specifically bind to or
 CC modulate the activity of the polypeptide. The microarray of the invention
 CC is useful in monitoring or measuring protein-protein interactions, drug-
 CC target interactions, and gene expression profiles. This sequence
 CC represents an MDDT polypeptide of the invention.

XX Sequence 227 AA;

Query Match 87.1%; Score 27; DB 8; Length 227;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
 DB 32 KVFVFF 36

RESULT 65

ABM91660

ID ABM91660 standard; protein; 238 AA.

XX ABM91660;

XX 02-JUN-2005 (first entry)

XX M. xanthus protein sequence, seq id 10859.

XX Transgenic plant; DNA replication; gene regulation; gene expression.

XX Myxococcus xanthus.

XX US6833447-B1.

XX 21-DEC-2004.

XX 10-JUL-2001; 2001US-00902540.

XX 10-JUL-2000; 2000US-0217883P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Goldman BS, Hinkle GJ, Slater SC, Wiegand RC;

XX WPI; 2005-028716/03.

XX New substantially purified Myxococcus xanthus nucleic acid molecule
 XX encoding a nitrite reductase, useful for determining gene expression,
 XX identifying mutations in a gene of interest, and for constructing
 XX mutations in a gene of interest.

XX Example 2; SEQ ID NO 10859; 25pp; English.

XX The invention relates to a substantially purified nucleic acid molecule

CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent
CC a group of 7134 *Mycococcus xanthus* proteins and peptides. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
XX
SQ Sequence 238 AA;

Query Match 87.1%; Score 27; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
DB 132 KVFVFF 136

RESULT 66
ABP40600
ID ABP40600 standard; protein; 240 AA.
XX
AC ABP40600;
XX
DT 24-JUL-2002 (first entry)
XX
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5445.
XX
KW Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
KW antibacterial; gene therapy.
XX
OS Staphylococcus epidermidis.
XX
PN US6380370-B1.
XX
PD 30-APR-2002.
XX
PF 13-AUG-1998; 98US-00134001.
XX
PR 14-AUG-1997; 97US-00557739P.
PR 08-NOV-1997; 97US-0064964P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Doucette-Stamm LA, Bush D;
XX
DR WPI; 2002-381255/41.
DR N-PSDB; ABN93145.
XX
PT Novel isolated nucleic acid encoding a Staphylococcus epidermis
PT polypeptide, useful for diagnosing and treating bacterial infections.
XX
PS Disclosure; SEQ ID NO 5445; 267pp; English.
XX
CC ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
CC antibacterial activity and can be used in gene therapy. The sequences can
CC also be used in the diagnosis and treatment of bacterial infections,
CC particularly S. epidermidis infections. The sequences can be used to
CC screen for compounds able to interfere with the S. epidermidis life cycle
CC or inhibit S. epidermidis infection. N.B. The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site
XX
SQ Sequence 240 AA;

Query Match 87.1%; Score 27; DB 5; Length 240;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CC encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC recombinant DNA construct for expression of a nitrite reductase gene in a
CC plant cell, and a plant cell comprising the recombinant DNA construct.
CC The nucleic acid is useful for determining gene expression, identifying
CC mutations in a gene of interest, and for constructing mutations in a gene
CC of interest. Sequences given in records for SEQ IDs 9692-16825 represent
CC a group of 7134 *Mycococcus xanthus* proteins and peptides. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
XX
SQ Sequence 238 AA;

Query Match 87.1%; Score 27; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 6
DB 168 QVFVFF 173

RESULT 67
ADS07805
ID ADS07805 standard; protein; 240 AA.
XX
AC ADS07805;
XX
DT 04-NOV-2004 (first entry)
XX
DE Staphylococcus epidermis polypeptide seqid 7100.
XX
KW antibacterial; vaccine; antisense therapy; Staphylococcus epidermidis;
KW recombinant expression vector; infection; computer readable medium;
KW computer based system.
XX
OS Staphylococcus epidermidis.
XX
PN US2004147734-A1.
XX
PD 29-JUL-2004.
XX
PF 01-DEC-2003; 2003US-00724972.
XX
PR 08-NOV-1997; 97US-0064964P.
PR 13-AUG-1998; 98US-00134001.
PR 29-NOV-1999; 99US-00450969.
XX
PA (DOUC/) DOUCETTE-STAMM L.
PA (BUSH/) BUSH D.
XX
PI Doucette-Stamm L, Bush D;
XX
DR WPI; 2004-580138/56.
DR N-PSDB; ADS04033.
XX
PT New isolated polypeptide and encoding nucleic acid derived from
PT Staphylococcus epidermidis, useful for diagnosing, preventing and/or
PT treating an S. epidermidis bacterial infection.
XX
PS Claim 17; SEQ ID NO 7100; 741pp; English.
XX
CC The invention describes an isolated nucleic acid comprising a nucleotide
CC sequence with any of 3772 fully defined nucleotide sequences (SEQ ID NO:
CC 1-3772) and encoding an Staphylococcus epidermidis polypeptide with any
CC of 3772 fully defined amino acid sequences (SEQ ID NO: 3772-7544) as
CC given in the specification. Also described are: a recombinant expression
CC vector; a cell comprising a recombinant expression vector of (1);
CC producing an S. epidermidis polypeptide; an isolated nucleic acid
CC comprising a nucleotide sequence of at least 8 nucleotides in length; a
CC vaccine composition for prevention or treatment of an S. epidermidis
CC infection, comprising a nucleic acid cited above and a carrier; treating
CC a subject for S. epidermidis infection; a recombinant or substantially
CC pure preparation of an S. epidermidis polypeptide or its fragment; a
CC vaccine composition for prevention or treatment of an S. epidermidis
CC infection; detecting the presence of a Staphylococcus nucleic acid in a
CC sample; a computer readable medium having recorded in it the nucleotide
CC sequences with SEQ ID NO: 1-3772 or its fragments; a computer based
CC system for identifying fragments of the Staphylococcus genome of
CC commercial importance; a computer based system for identifying fragments
CC of the Staphylococcus plasmids of commercial importance; identifying
CC commercially important nucleic acid fragments of the Staphylococcus
CC genome and/or plasmids; and identifying an expression modulating fragment
CC of the Staphylococcus genome and/or plasmids. The methods and
CC compositions of the present invention are useful for the diagnosis,
CC prevention and/or treatment of an Staphylococcus epidermidis bacterial
CC infection. This is the amino acid sequence of a S. epidermidis protein of
CC the invention.
XX

```
SQ Sequence 240 AA;
Query Match 87.1%; Score 27; DB 8; Length 240;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KVFVFA 6
Db 168 QVFVFA 173

RESULT 68
AAG10914
ID AAG10914 standard; protein; 248 AA.
XX
AC AAG10914;
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9429.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
```

```
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149923P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151439P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152263P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155133P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158023P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159639P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
PR 29-OCT-1999; 99US-0162143P.

Query Match      87.1%; Score 27; DB 3; Length 248;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVFFA 6
```

```
Db      206 KPIEVA 211
RESULT 69
AAG10913
ID AAG10913 standard; protein; 252 AA.
XX
AC AAG10913;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 9428.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 14-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
```


PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139753P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 08-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142377P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 20-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144684P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 08-AUG-1999; 99US-0147433P.
PR 08-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.

PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149428P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156598P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0158293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 252;
Best Local Similarity 66.7%; Pred. No. 8.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVVFFA 6
|||:|:
Db 210 KFIFYA 215

RESULT 70
AAG10912
ID AAG10912 standard; protein; 270 AA.

XX AC AAG10912; 18-JUN-1999; 99US-0139462P.
XX DT 17-OCT-2000 (first entry) 18-JUN-1999; 99US-0139463P.
XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 9427. 18-JUN-1999; 99US-0139750P.
XX KW Protein identification; signal transduction pathway; metabolic pathway; 18-JUN-1999; 99US-0139763P.
XX KW hybridisation assay; genetic mapping; gene expression control; promoter; 21-JUN-1999; 99US-0139817P.
XX KW termination sequence. 22-JUN-1999; 99US-0139899P.
XX OS Arabidopsis thaliana. 23-JUN-1999; 99US-0140353P.
XX PN EP1033405-A2. 23-JUN-1999; 99US-0140354P.
XX PD 06-SEP-2000. 24-JUN-1999; 99US-0140695P.
XX PF 25-FEB-2000; 200EP-00301439. 28-JUN-1999; 99US-0140823P.
PR 25-FEB-1999; 99US-0121825P. 29-JUN-1999; 99US-0140931P.
PR 05-MAR-1999; 99US-0123180P. 30-JUN-1999; 99US-0141287P.
PR 09-MAR-1999; 99US-0123548P. 01-JUL-1999; 99US-0141842P.
PR 23-MAR-1999; 99US-0125788P. 01-JUL-1999; 99US-0142154P.
PR 25-MAR-1999; 99US-0126264P. 02-JUL-1999; 99US-0142055P.
PR 29-MAR-1999; 99US-0126785P. 06-JUL-1999; 99US-0142390P.
PR 01-APR-1999; 99US-0127462P. 08-JUL-1999; 99US-0142803P.
PR 06-APR-1999; 99US-0128234P. 09-JUL-1999; 99US-0142920P.
PR 08-APR-1999; 99US-0128714P. 12-JUL-1999; 99US-0142977P.
PR 16-APR-1999; 99US-0129845P. 13-JUL-1999; 99US-0143542P.
PR 19-APR-1999; 99US-0130077P. 14-JUL-1999; 99US-0143624P.
PR 21-APR-1999; 99US-0130449P. 15-JUL-1999; 99US-0144005P.
PR 23-APR-1999; 99US-0130510P. 16-JUL-1999; 99US-0144086P.
PR 28-APR-1999; 99US-0131449P. 19-JUL-1999; 99US-0144331P.
PR 30-APR-1999; 99US-0132048P. 19-JUL-1999; 99US-0144332P.
PR 04-MAY-1999; 99US-0132407P. 19-JUL-1999; 99US-0144333P.
PR 05-MAY-1999; 99US-0132484P. 19-JUL-1999; 99US-0144334P.
PR 06-MAY-1999; 99US-0132485P. 20-JUL-1999; 99US-0144335P.
PR 06-MAY-1999; 99US-0132486P. 20-JUL-1999; 99US-0144632P.
PR 06-MAY-1999; 99US-0132487P. 21-JUL-1999; 99US-0144884P.
PR 07-MAY-1999; 99US-0132863P. 21-JUL-1999; 99US-0144814P.
PR 11-MAY-1999; 99US-0134256P. 21-JUL-1999; 99US-0145086P.
PR 14-MAY-1999; 99US-0134218P. 21-JUL-1999; 99US-0145088P.
PR 14-MAY-1999; 99US-0134219P. 22-JUL-1999; 99US-0145085P.
PR 14-MAY-1999; 99US-0134221P. 22-JUL-1999; 99US-0145087P.
PR 14-MAY-1999; 99US-0134370P. 22-JUL-1999; 99US-0145089P.
PR 18-MAY-1999; 99US-0134768P. 22-JUL-1999; 99US-0145192P.
PR 19-MAY-1999; 99US-0134941P. 23-JUL-1999; 99US-0145145P.
PR 20-MAY-1999; 99US-0135124P. 23-JUL-1999; 99US-0145218P.
PR 21-MAY-1999; 99US-0135353P. 23-JUL-1999; 99US-0145224P.
PR 24-MAY-1999; 99US-0135629P. 26-JUL-1999; 99US-0145276P.
PR 25-MAY-1999; 99US-0136021P. 27-JUL-1999; 99US-0145913P.
PR 27-MAY-1999; 99US-0136392P. 27-JUL-1999; 99US-0145918P.
PR 28-MAY-1999; 99US-0136782P. 27-JUL-1999; 99US-0145919P.
PR 01-JUN-1999; 99US-0137222P. 28-JUL-1999; 99US-0145951P.
PR 03-JUN-1999; 99US-0137528P. 02-AUG-1999; 99US-0146386P.
PR 04-JUN-1999; 99US-0137502P. 02-AUG-1999; 99US-0146388P.
PR 07-JUN-1999; 99US-0137724P. 02-AUG-1999; 99US-0146389P.
PR 08-JUN-1999; 99US-0138094P. 03-AUG-1999; 99US-0147038P.
PR 10-JUN-1999; 99US-0138540P. 04-AUG-1999; 99US-0147204P.
PR 10-JUN-1999; 99US-0138847P. 04-AUG-1999; 99US-0147302P.
PR 14-JUN-1999; 99US-0139119P. 05-AUG-1999; 99US-0147192P.
PR 16-JUN-1999; 99US-0139452P. 06-AUG-1999; 99US-0147260P.
PR 16-JUN-1999; 99US-0139453P. 06-AUG-1999; 99US-0147303P.
PR 17-JUN-1999; 99US-0139492P. 06-AUG-1999; 99US-0147416P.
PR 18-JUN-1999; 99US-0139454P. 09-AUG-1999; 99US-0147493P.
PR 18-JUN-1999; 99US-0139455P. 09-AUG-1999; 99US-0147935P.
PR 18-JUN-1999; 99US-0139456P. 10-AUG-1999; 99US-0148171P.
PR 18-JUN-1999; 99US-0139457P. 11-AUG-1999; 99US-0148319P.
PR 18-JUN-1999; 99US-0139458P. 12-AUG-1999; 99US-0148341P.
PR 18-JUN-1999; 99US-0139459P. 13-AUG-1999; 99US-0148565P.
PR 18-JUN-1999; 99US-0139460P. 13-AUG-1999; 99US-0148684P.
PR 18-JUN-1999; 99US-0139461P. 16-AUG-1999; 99US-0149368P.
PR 18-JUN-1999; 99US-0139462P. 17-AUG-1999; 99US-0149175P.
PR 18-JUN-1999; 99US-0149426P. 18-AUG-1999; 99US-0149426P.
PR 18-JUN-1999; 99US-0149722P. 20-AUG-1999; 99US-0149722P.
PR 18-JUN-1999; 99US-0149723P. 20-AUG-1999; 99US-0149723P.
PR 18-JUN-1999; 99US-0149923P. 20-AUG-1999; 99US-0149923P.
PR 18-JUN-1999; 99US-0149902P. 23-AUG-1999; 99US-0149902P.
PR 18-JUN-1999; 99US-0149930P. 23-AUG-1999; 99US-0149930P.

PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153758P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154039P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0156559P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156596P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157753P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158029P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158369P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159584P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160989P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161922P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 270;
 Best Local Similarity 66.7%; Pred. No. 9.2e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFPA 6
 Db 228 KFIFYA 233

RESULT 71
 AAU80872
 ID AAU80872 standard; protein; 297 AA.
 AC AAU80872;
 XX
 DT 26-MAR-2002 (first entry)
 XX Human CLAN NACHT.
 DE
 XX

KW Caspase recruitment domain; CARD; NB-ARC, ANGIO-R; LRR; SAM;
 KW abnormal cell proliferation; cancer; abnormal cell death; apoptosis;
 KW autoimmune disease; inflammation; keratinocyte hyperplasia;
 KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
 KW balloon angioplasty; restenosis; glioma; carcinoma; sarcoma; melanoma;
 KW leukaemia; allergy; arthritis; lupus; Schrogen's syndrome;
 KW Crohn's disease; graft-versus-host disease; stroke;
 KW myocardial infarction; heart failure; neurodegenerative disease;
 KW Parkinson's disease; Alzheimer's disease; HIV;
 KW human immunodeficiency virus infection.
 XX Homo sapiens.
 OS WO200190156-A2.
 PN 29-NOV-2001.
 PD 24-MAY-2001; 2001WO-US017158.
 PF 24-MAY-2000; 2000US-00579240.
 PR 10-OCT-2000; 2000US-00686347.
 PR 14-MAR-2001; 2001US-0275980P.
 PR 23-MAY-2001; 2001US-00864921.
 XX (BURN-) BURNHAM INST.
 PI Reed JC, Pio PF, Godzik A, Stehlik C, Damiano JS, Lee SH;
 PI Oliveira VAM, Hayashi H, Pawlowski K;
 XX WPI; 2002-083086/11.
 DR N-PSDB; ABK22766.
 PT New caspase recruitment domain (CARD)-containing polypeptides and
 PT encoding nucleic acids, useful for treating abnormal cell proliferation
 PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
 PT arthritis or stroke.
 XX Claim 9; Page 201-202; 216pp; English.
 XX The invention relates to an isolated caspase recruitment domain (CARD) -
 CC containing polypeptide, or a CARD, NB-ARC, ANGIO-R, LRR or SAM domain
 CC from it, and the polynucleotides encoding them. Also included are a
 CC recombinant vector comprising the polynucleotide, recombinant cells
 CC containing the vector (e.g. bacteria, yeast, plant, animal, mammalian and
 CC insect cells) and an anti-CARD antibody. The CARD-containing polypeptide
 CC and CARD-encoding nucleic acid are useful for treating a pathology
 CC characterised by abnormal cell proliferation (e.g. cancer), abnormal cell
 CC death (apoptosis), autoimmune diseases or inflammation. In particular,
 CC the polypeptide and nucleic acid are useful for treating keratinocyte
 CC hyperplasia, inflammatory hyperplasia, fibrosis, smooth muscle cell
 CC proliferation in arteries following balloon angioplasty (restenosis),
 CC gliomas, carcinomas, sarcomas, melanomas, leukaemias, allergies,
 CC arthritis, lupus, Schrogen's syndrome, Crohn's disease, graft-versus-host
 CC disease, stroke, myocardial infarction, heart failure, neurodegenerative
 CC diseases (e.g. Parkinson's disease or Alzheimer's disease) or
 CC immunodeficiency associated disease (e.g. human immunodeficiency virus
 CC (HIV) infection). The nucleic acids are useful in a variety of diagnostic
 CC applications. The present sequence is a CARD domain containing protein
 XX
 SQ Sequence 297 AA;

Query Match 87.1%; Score 27; DB 5; Length 297;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFPA 5
 Db 38 KFVFPA 42

RESULT 72
 ABU81731
 ID ABU81731 standard; protein; 297 AA.

XX ABU81731;
XX
XX
XX 26-JUN-2003 (first entry)
XX
XX Human caspase recruitment domain-containing polypeptide #15.
XX
XX Human; caspase recruitment domain-containing polypeptide; CARD; NB-ARC;
KW ANGIO-R; leucine rich repeat; LRR; S-adenosyl methionine domain;
KW apoptosis; NF-kappaB induction; cytokine processing; SAM; transcription;
KW cJun N-terminal kinase induction; caspase-mediated proteolysis; cancer;
KW inflammation; cell adhesion; cell proliferation; abnormal cell death;
KW keratinocyte hyperplasia; neoplasia; benign prostatic hypertrophy; lupus;
KW inflammatory hyperplasia; fibrosis; smooth muscle cell proliferation;
KW angioplasty; artery; keloid; restenosis; autoimmune disease; allergy;
KW arthritis; Sjogren's syndrome; Crohn's disease; ulcerative colitis;
KW allograft rejection; graft versus host disease; myocardial infarction;
KW heart failure; neurodegenerative disease; stroke; HIV.
XX
XX Homo sapiens.
XX
XX US2002176853-A1.
XX
XX 28-NOV-2002.
XX
XX 23-MAY-2001; 2001US-00864921.
XX
XX 24-MAY-2000; 2000US-0325756P.
XX 10-OCT-2000; 2000US-0367337P.
XX 14-MAR-2001; 2001US-0275980P.
XX
XX (REED/) REED J C.
PA (PIOF/) PIO F F.
PA (GODZ/) GODZIK A.
PA (STEH/) STEHLIK C.
PA (DAMI/) DAMIANO J S.
PA (LEES/) LEE S H.
PA (OLIV/) OLIVEIRA V A.
PA (HAYA/) HAYASHI H.
PA (PAWL/) PAWLOWSKI K.
XX
XX Reed JC, Pio FF, Godzik A, Stehlik C, Damiano JS, Lee SH;
PI Oliveira VA, Hayashi H, Pawlowski K;
XX
XX WPI; 2002-083086/11.
XX N-PSDB; ACA68180.
XX
XX New caspase recruitment domain (CARD)-containing polypeptides and
PT encoding nucleic acids, useful for treating abnormal cell proliferation
PT or cell death, autoimmune diseases or inflammation, e.g. carcinomas,
PT arthritis or stroke.
XX
XX Claim 1; Page 85-86; 106pp; English.
XX
XX The invention relates to an isolated caspase recruitment domain (CARD)-
XX containing polypeptide, or its CARD, NB-ARC, ANGIO-R, leucine rich repeat
CC (LRR) or S-adenosyl methionine (SAM) domain, and its associated
CC polynucleotide. The DNA is useful for altering the level of a biochemical
CC process (including apoptosis, NF-kappaB induction, cytokine processing,
CC cJun N-terminal kinase induction, caspase-mediated proteolysis,
CC transcription, inflammation and cell adhesion) modulated by the DNA. The
CC sequences are useful for treating a pathology characterised by abnormal
CC cell proliferation, abnormal cell death or inflammation. The treatable
CC diseases include cancer, keratinocyte hyperplasia, neoplasia, keloids,
CC benign prostatic hypertrophy, inflammatory hyperplasia, fibrosis, smooth
CC muscle cell proliferation in arteries following angioplasty, restenosis,
CC autoimmune diseases including allergies, inflammatory diseases including
CC arthritis, lupus, Sjogren's syndrome, Crohn's disease, ulcerative
CC colitis, allograft rejection such as graft versus host disease, stroke,
CC myocardial infarction, heart failure, neurodegenerative diseases such as
CC Parkinson's disease and Alzheimer's disease and immunodeficiency
CC associated diseases such as human immunodeficiency virus (HIV) infection.
XX Sequences ABU81714-ABU81735 represent human CARD-containing polypeptides

CC of the invention
XX
XX SQ Sequence 297 AA;
XX
XX Query Match 87.1%; Score 27; DB 5; Length 297;
XX Best Local Similarity 100.0%; Pred. No. 1.e+03;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KVFVF 5
XX Db 38 KVFVF 42
XX
XX RESULT 73
XX ADP47907
XX ID ADP47907 standard; protein; 312 AA.
XX
XX AC ADP47907;
XX
XX DT 12-AUG-2004 (first entry)
XX
XX DE Human CATERPILLER Ipa nucleotide binding domain (NBD) protein.
XX
XX KW Monarch-1; CATERPILLER 11.2; caspase recruitment domain;
KW CARD, transcription enhancer, R-binding, pyrin, lots of leucine repeat;
KW CATERPILLER 11.3; CATERPILLER 16.1; CATERPILLER 16.2; CIAS1;
KW cold-induced autoinflammatory syndrome 1; antiinflammatory; cytostatic;
KW inflammatory disease; cancer; gene therapy; human; purine;
KW nucleotide binding domain; NBD; IpaF.
XX
XX OS Homo sapiens.
XX
XX FN WO2004034093-A2.
XX
XX PD 22-APR-2004.
XX
XX PF 30-APR-2003; 2003WO-US013562.
XX
XX PR 30-APR-2002; 2002US-0376626P.
XX
XX PA (UTNC-) UNIV NORTH CAROLINA.
XX
XX PI Ting JY, Linhoff MW, Harton JA, Williams KL, Lich J, O'Connor W;
PI Moore CB, Davis B, Brickey J, Conti B, Zhang J, Zhu X;
XX
XX DR WPI; 2004-348215/32.
XX
XX PT New nucleic acid encoding Monarch-1, CATERPILLER 11.2, CATERPILLER 11.3,
XX CATERPILLER 16.1, CATERPILLER 16.2 or CIAS1 polypeptide, useful in
XX preparing a composition for treating inflammatory disease or cancer.
XX
XX PS Example 1; Fig 3; 205pp; English.
XX
XX CC The invention relates to a novel isolated nucleic acid encoding a Monarch
XX -1, CATERPILLER (CARD [caspase recruitment domain], transcription
XX enhancer, R(purine)-binding, pyrin, lots of leucine repeats) 11.2,
XX CATERPILLER 11.3, CATERPILLER 16.1, CATERPILLER 16.2 or CIAS1 (cold-
XX induced autoinflammatory syndrome 1) polypeptide comprising the amino
XX acids encoded by exon 6 and lacking the amino acids encoded by exon 4 or
XX its fragment. The nucleic acid of the invention demonstrates
XX antiinflammatory and cytostatic activities and may be useful in preparing
XX a composition for treating an inflammatory disease or cancer, possibly
XX via gene therapy. The current sequence is that of a human CATERPILLER
XX nucleotide binding domain (NBD) protein of the invention.
XX
XX SQ Sequence 312 AA;
XX
XX Query Match 87.1%; Score 27; DB 8; Length 312;
XX Best Local Similarity 100.0%; Pred. No. 1.1e+03;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KVFVF 5
XX
XX

Db 51 KPVFP 55

RESULT 74
AAG33404
ID AAG33404 standard; protein; 313 AA.
XX
AC AAG33404;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 40468.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PP 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 13-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132563P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134370P.
PR 19-MAY-1999; 99US-0134768P.
PR 20-MAY-1999; 99US-0134941P.
PR 21-MAY-1999; 99US-0135124P.
PR 24-MAY-1999; 99US-0135353P.
PR 25-MAY-1999; 99US-0135629P.
PR 27-MAY-1999; 99US-0136021P.
PR 28-MAY-1999; 99US-0136382P.
PR 01-JUN-1999; 99US-0136782P.
PR 03-JUN-1999; 99US-0137222P.
PR 04-JUN-1999; 99US-0137528P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 22-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.

PR 18-AUG-1999; 99US-0149426P.
 PR 20-AUG-1999; 99US-0149722P.
 PR 20-AUG-1999; 99US-0149723P.
 PR 20-AUG-1999; 99US-0149929P.
 PR 23-AUG-1999; 99US-0149902P.
 PR 23-AUG-1999; 99US-0149930P.
 PR 25-AUG-1999; 99US-0150566P.
 PR 26-AUG-1999; 99US-0150884P.
 PR 27-AUG-1999; 99US-0151065P.
 PR 27-AUG-1999; 99US-0151066P.
 PR 27-AUG-1999; 99US-0151080P.
 PR 30-AUG-1999; 99US-0151303P.
 PR 31-AUG-1999; 99US-0151438P.
 PR 01-SEP-1999; 99US-0151930P.
 PR 07-SEP-1999; 99US-0152363P.
 PR 10-SEP-1999; 99US-0153070P.
 PR 13-SEP-1999; 99US-0153759P.
 PR 15-SEP-1999; 99US-0154018P.
 PR 16-SEP-1999; 99US-0154033P.
 PR 20-SEP-1999; 99US-0154779P.
 PR 22-SEP-1999; 99US-0155139P.
 PR 23-SEP-1999; 99US-0155486P.
 PR 24-SEP-1999; 99US-0155659P.
 PR 28-SEP-1999; 99US-0156458P.
 PR 29-SEP-1999; 99US-0156598P.
 PR 04-OCT-1999; 99US-0157117P.
 PR 05-OCT-1999; 99US-0157533P.
 PR 06-OCT-1999; 99US-0157865P.
 PR 07-OCT-1999; 99US-0158023P.
 PR 08-OCT-1999; 99US-0158232P.
 PR 12-OCT-1999; 99US-0158363P.
 PR 13-OCT-1999; 99US-0159293P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 13-OCT-1999; 99US-0159294P.
 PR 14-OCT-1999; 99US-0159295P.
 PR 14-OCT-1999; 99US-0159329P.
 PR 14-OCT-1999; 99US-0159330P.
 PR 14-OCT-1999; 99US-0159331P.
 PR 14-OCT-1999; 99US-0159637P.
 PR 14-OCT-1999; 99US-0159638P.
 PR 18-OCT-1999; 99US-0159638P.
 PR 21-OCT-1999; 99US-0160741P.
 PR 21-OCT-1999; 99US-0160767P.
 PR 21-OCT-1999; 99US-0160768P.
 PR 21-OCT-1999; 99US-0160770P.
 PR 21-OCT-1999; 99US-0160814P.
 PR 21-OCT-1999; 99US-0160815P.
 PR 22-OCT-1999; 99US-0160980P.
 PR 22-OCT-1999; 99US-0160981P.
 PR 22-OCT-1999; 99US-0160982P.
 PR 25-OCT-1999; 99US-0161404P.
 PR 25-OCT-1999; 99US-0161405P.
 PR 25-OCT-1999; 99US-0161406P.
 PR 26-OCT-1999; 99US-0161359P.
 PR 26-OCT-1999; 99US-0161360P.
 PR 26-OCT-1999; 99US-0161361P.
 PR 28-OCT-1999; 99US-0161920P.
 PR 28-OCT-1999; 99US-0161992P.
 PR 28-OCT-1999; 99US-0161993P.
 PR 29-OCT-1999; 99US-0162142P.
 PR 29-OCT-1999; 99US-0162142P.

Query Match 87.1%; Score 27; DB 3; Length 313;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
 Db 86 KVFVF 90

RESULT 75
 ID ADT58396 standard; protein; 335 AA.
 XX

AC ADT58396;
 XX 13-JAN-2005 (first entry)
 DT XX Plant polypeptide, SEQ ID 8473.
 DE XX
 DE XX Plant; transgenic; cold tolerance; growth rate; drought tolerance;
 KW disease resistance; galactomannan production; plant growth regulator;
 KW heat tolerance; herbicide tolerance; lignin production;
 KW extreme osmotic condition tolerance; pathogens resistance;
 KW pest resistance; yield improvement; seed oil yield; seed protein yield.
 XX Viridiplantae.
 OS
 XX US2004216190-A1.
 FN
 XX 28-OCT-2004.
 PD
 XX 18-DEC-2003; 2003US-00739930.
 PF
 XX 28-APR-2003; 2003US-00424599.
 PR 28-APR-2003; 2003US-00425115.
 XX (KOVA/) KOVALIC D K.
 PA
 XX Kovalic DK;
 FI
 XX WPI; 2004-757369/74.
 DR
 XX New recombinant DNA constructs useful in the field of biochemistry and
 PT genetics, and in particular for producing transgenic plants with improved
 PT biological characteristics.
 XX
 PS Claim 2; SEQ ID NO 8473; 14pp; English.
 PS
 XX The invention relates a recombinant DNA construct comprising a
 CC polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
 CC 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
 CC (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
 CC Arabidopsis, wheat and rape but the specification does not indicate which
 CC sequences is derived from which organism. Also included is a method of
 CC producing a plant having an improved property, comprising transforming a
 CC plant with a recombinant DNA construct comprising a promoter region
 CC functional in a plant cell operably joined to a polynucleotide encoding a
 CC polypeptide associated with the property, and growing the transformed
 CC plant. The property is selected from improving plant cold tolerance, for
 CC manipulating growth rate in plant cells by modification of the cell cycle
 CC pathway, for improving plant drought tolerance, for providing increased
 CC resistance to plant disease, for galactomannan production, for production
 CC of plant growth regulators, for improving plant heat tolerance, for
 CC improving plant tolerance to herbicides, for increasing the rate of
 CC homologous recombination in plants, for lignin production, for improving
 CC plant tolerance to extreme osmotic conditions, for improving plant
 CC tolerance to pathogens or pests, for yield improvement by modification of
 CC photosynthesis, for modifying seed oil yield and/or content, for
 CC modifying seed protein yield and/or content, for yield improvement by
 CC modification of carbohydrate, nitrogen or phosphorus use and/or uptake
 CC and for yield improvement by providing improved plant growth and
 CC development under at least one stress condition. The polynucleotide may
 CC also encode a plant transcription factor. The methods and compositions of
 CC the present invention are useful in the field of biochemistry and
 CC genetics, in particular for producing transgenic plants with improved
 CC biological characteristics such as increased yield, improved nitrogen
 CC flow, increasing plant tolerance to cold or heat, improving plant
 CC tolerance to extreme osmotic and drought conditions, and improving plant
 CC tolerance to plant pests or pathogens. They can also be used in physical
 CC arrays of molecules, plant breeding markers, computer-based storage and
 CC analysis systems. The present sequence is one of the 5544 plant protein
 CC sequences of the invention. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20040216190.

SQ Sequence 335 AA;

Query Match 87.1%; Score 27; DB 8; Length 335;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KPVFFA 6
 || ||
 Db 80 KPAFFA 85

Search completed: December 29, 2005, 17:33:39
 Job time : 82.7742 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-10

Perfect score: 29

Sequence: 1 KIVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	164	Q73N39	TREDE
2	29	100.0	387	Q81FHS	BACCR
3	29	100.0	450	Q4TRF8	erythroba
4	29	100.0	464	Q4S4T5	TETNG
5	29	100.0	606	Q91VU5	MOUSE
6	29	100.0	663	Q6RUU2	MOUSE
7	29	100.0	690	Q83IB2	TROW8
8	29	100.0	698	Q83GW3	TROWT
9	29	100.0	1265	Q6ZQ91	MOUSE
10	29	100.0	1412	Q5F3M1	CHICK
11	28	96.6	88	Q4LRQ8	SODGL
12	28	96.6	183	Q9RQ09	BACTN
13	28	96.6	186	GL19	ORYSA
14	28	96.6	231	Q8C6V8	MOUSE
15	28	96.6	231	Q61C67	CABBR
16	28	96.6	315	Q4HSJ7	CAMUP
17	28	96.6	362	Q6D7U3	ERWCT
18	28	96.6	372	Q6D7U3	ERWCT
19	28	96.6	373	Q7M9N5	WOLLSU
20	28	96.6	382	Q9V7J0	DROME
21	28	96.6	387	Q9K110	BACCE
22	28	96.6	387	Q4MT39	BACCE
23	28	96.6	387	Q63DD4	BACCC
24	28	96.6	387	Q6HKU6	BACCH
25	28	96.6	387	Q73AP3	BACCL
26	28	96.6	387	Q81SK9	BACAN
27	28	96.6	410	Q6L2B4	PICTO
28	28	96.6	410	Q8C5T3	MOUSE
29	28	96.6	442	Q9PHV5	CAMJE
30	28	96.6	447	Q59243	PYRHO
31	28	96.6	556	Q95S93	DROME

32	28	96.6	556	2	Q9V7I9	DROME
33	28	96.6	703	2	Q5HYE1	HUMAN
34	28	96.6	721	2	Q6AG25	LEIIXX
35	28	96.6	785	2	Q9GQ82	DROME
36	28	96.6	925	2	Q95786	HUMAN
37	28	96.6	925	2	Q5VY71	HOMO SAPIEN
38	28	96.6	926	2	Q6Q899	MUSCULU
39	28	96.6	940	2	Q9GLV6	PIG
40	28	96.6	1144	1	NOS2	MOUSE
41	28	96.6	1144	2	Q5SXT3	MOUSE
42	28	96.6	1145	2	Q8R410	MOUSE
43	28	96.6	1145	2	Q6P6A0	MOUSE
44	28	96.6	1384	2	Q68K27	CHLRE
45	28	96.6	1408	2	Q7QEP0	ANOGA
46	28	96.6	1443	2	Q9VPR0	DROME
47	28	96.6	1458	2	Q5BI64	DROME
48	28	96.6	1503	2	Q7KT24	DROME
49	28	96.6	1676	2	Q8A6R7	BACTN
50	27	93.1	33	2	Q9UC33	HUMAN
51	27	93.1	42	2	Q5GJ36	GRAGR
52	27	93.1	42	2	Q5GJ37	TURTR
53	27	93.1	42	2	Q7M088	CAVPO
54	27	93.1	52	2	Q8WZ99	HUMAN
55	27	93.1	57	1	A4	URSWA
56	27	93.1	58	1	A4	CANFA
57	27	93.1	58	1	A4	RABIT
58	27	93.1	58	1	A4	SHEEP
59	27	93.1	59	1	A4	BOVIN
60	27	93.1	79	2	Q35463	CRIGR
61	27	93.1	113	2	Q8JH58	CHESE
62	27	93.1	137	2	Q7UPR1	RHOBA
63	27	93.1	152	2	Q9STZ9	ARATH
64	27	93.1	203	2	Q6AKB9	DESFS
65	27	93.1	218	2	Q8BPV5	MOUSE
66	27	93.1	229	2	Q8VY56	ARATH
67	27	93.1	231	2	Q9SV79	ARATH
68	27	93.1	352	2	Q9XGY6	SIMCH
69	27	93.1	357	2	Q8U460	PYRPU
70	27	93.1	357	2	Q8UUI8	BRARE
71	27	93.1	366	2	Q8PPL1	XANAC
72	27	93.1	380	2	Q67225	AQUAE
73	27	93.1	384	2	Q8BPC7	MOUSE
74	27	93.1	391	2	Q4NSU7	THEPA
75	27	93.1	399	2	Q5WPU9	LUTLO
76	27	93.1	403	2	Q5L117	GEOKA
77	27	93.1	404	2	Q4VYS5	XANCP
78	27	93.1	404	2	Q8P597	XANCP
79	27	93.1	428	2	Q9M1Q8	ARATH
80	27	93.1	461	2	Q89329	9POTV
81	27	93.1	470	2	Q7T910	9POTV
82	27	93.1	472	2	Q8UUS0	BRARE
83	27	93.1	488	2	Q52NV6	9POTV
84	27	93.1	490	2	Q7T911	9POTV
85	27	93.1	490	2	Q7T912	9POTV
86	27	93.1	493	2	Q5K4D4	9POTV
87	27	93.1	493	2	Q5K4D5	9POTV
88	27	93.1	508	2	Q5GVS5	XANOR
89	27	93.1	534	2	Q93296	CHICK
90	27	93.1	569	2	Q9PVL1	CHICK
91	27	93.1	612	2	Q919E7	BRARE
92	27	93.1	615	2	Q50285	ENTHI
93	27	93.1	623	2	Q4WBU2	ASFPF
94	27	93.1	630	2	Q5B2V4	EMENI
95	27	93.1	638	2	Q5B2V4	EMENI
96	27	93.1	678	2	Q7Z2T1	BRARE
97	27	93.1	693	2	Q98SG0	XENLA
98	27	93.1	695	2	Q5R477	PONPY
99	27	93.1	695	2	Q6RH29	CANFA
100	27	93.1	695	2	Q56JK3	CANFA
101	27	93.1	695	2	Q6GR78	MOUSE
102	27	93.1	695	2	Q9DGJ8	CHICK
103	27	93.1	695	2	Q98SF9	XENLA
104	27	93.1	695	2	Q7ZXQ0	XENLA

Q9V7I9	drosofila
Q5hye1	homo sapien
Q6sg25	leifsonia x
Q9GQ82	drosofila
Q5vvt1	homo sapien
Q6Q899	mus musculus
Q9GLV6	sus scrofa
P29477	mus musculus
Q8R410	mus musculus
Q6P6A0	mus musculus
Q68K27	chlamydomon
Q7QEP0	anopheles g
Q9VPR0	drosofila
Q5BI64	drosofila
Q7KT24	drosofila
Q8A6R7	bacteroides
Q9UC33	homo sapien
Q5GJ36	grampus gri
Q5GJ37	tursiops tr
Q7M088	cavia porce
Q8WZ99	homo sapien
Q29149	u alzheimer
Q28280	c alzheimer
Q28748	o alzheimer
Q28757	o alzheimer
Q28053	b alzheimer
Q35463	cricetulus
Q8JH58	chelydra se
Q7UPR1	rhodopirell
Q9STZ9	arabidopsis
Q6AKB9	desulfotale
Q8BPV5	mus musculus
Q8VY56	arabidopsis
Q9SV79	arabidopsis
Q9XGY6	simmondsia
Q8U460	pyrococcus
Q8UUI8	brachydanio
Q8PPL1	xanthomonas
Q67225	aquifex aeo
Q8BPC7	mus musculus
Q4NSU7	theileria p
Q5WPU9	lutomyia l
Q5L117	geobacillus
Q4VYS5	xanthomonas
Q8P597	xanthomonas
Q9M1Q8	arabidopsis
Q89329	zucchini ye
Q7T910	zucchini ye
Q8UUS0	brachydanio
Q52NV6	zucchini ye
Q7T911	zucchini ye
Q7T912	zucchini ye
Q5K4D4	soybean mos
Q5K4D5	soybean mos
Q5GVS5	xanthomonas
Q93296	gallus gall
Q9PVL1	gallus gall
Q919E7	brachydanio
Q50285	entamoeba h
Q4WBU2	aspergillus
Q5K7B5	cryptococcu
Q5B2V4	aspergillus
Q7Z2T1	brachydanio
Q98SG0	xenopus lae
Q5R477	pongo pygma
Q6RH29	canis fami
Q56JK3	canis fami
Q6GR78	mus musculus
Q9DGJ8	gallus gall
Q98SF9	xenopus lae
Q7ZXQ0	xenopus lae

105	27	93.1	714	2	Q56JK4 CANFA	Q56jk4	canis famil	178	26	89.7	248	2	Q813W8 PLAF7	Q813w8	plasmodium
106	27	93.1	733	2	Q6P6Q5 RAT	Q6p6q5	rattus norv	179	26	89.7	253	2	Q9KL60 VIBCH	Q9kl60	vibrio chol
107	27	93.1	737	1	A4 FUGRU	Q93279	fugu rubrip	180	26	89.7	270	2	Q7MV75 PORGI	Q7mv75	porphyronon
108	27	93.1	738	1	Q6NUZ1 BRARE	Q6nuz1	brachydanio	181	26	89.7	279	2	Q4ILF1 GIBZE	Q4ilf1	gibberella
109	27	93.1	738	2	Q90W28 BRARE	Q90w28	brachydanio	182	26	89.7	281	2	Q51ZJ1 MAGGR	Q51zj1	magnaporthe
110	27	93.1	747	2	Q31963 9P1P1	Q31963	xenopus. ap	183	26	89.7	281	2	Q4XS11 PLACH	Q4xsl1	plasmodium
111	27	93.1	749	2	Q56JK2 STECO	Q56jk2	strenella co	184	26	89.7	284	2	Q4ZX22 PSSES	Q4zx22	pseudomonas
112	27	93.1	749	2	Q6NR11 XENLA	Q6nr11	xenopus lae	185	26	89.7	292	2	Q4WK19 ASPFU	Q4wk19	aspergillus
113	27	93.1	750	2	Q6DJB6 XENTR	Q6djb6	xenopus tro	186	26	89.7	300	2	Q9XU61 CAEPF	Q9xu61	caenorhabdi
114	27	93.1	751	1	A4 SAJSC	Q95241	s amyloid b	187	26	89.7	301	2	Q5B613 XEMI	Q5b613	aspergillus
115	27	93.1	751	2	Q6SC00 HUMAN	Q6sc00	homo sapien	188	26	89.7	306	2	Q68RL2 XHENI	Q68rl2	glycaepis b
116	27	93.1	751	2	Q6RH28 CANFA	Q6rn28	canis famil	189	26	89.7	312	2	Q9ZZU4 XCAEN	Q9zzu4	littorina s
117	27	93.1	751	2	Q56JK5 CANFA	Q56jk5	canis famil	190	26	89.7	321	1	Y189 RICPR	Q5zdx5	rickettsia
118	27	93.1	751	2	Q4R4R8 MACFA	Q4r4r8	macaca fasc	191	26	89.7	333	2	Q6TG00 HELZE	Q6tg00	heliothis z
119	27	93.1	751	2	Q9DQJ7 CHICK	Q9dqj7	gallus gall	192	26	89.7	336	1	RSMC BUCAP	Q8k9l5	buchera ap
120	27	93.1	754	2	Q4RY33 TETNG	Q4ry33	tetraodon n	193	26	89.7	337	2	Q54NZ2 DICDI	Q54nz2	dictyosteli
121	27	93.1	754	2	Q4S0J4 TETNG	Q4s0j4	tetraodon n	194	26	89.7	347	2	Q87PM3 VIBPA	Q87pm3	vibrio para
122	27	93.1	760	2	Q55HW1 CRYNE	Q55hw1	cryptococcu	195	26	89.7	349	2	Q9XU59 CAEBL	Q9xu59	caenorhabdi
123	27	93.1	770	1	A4 CAVPO	Q60495	c amyloid b	196	26	89.7	352	2	O8YUK9 ANASP	Q8yuk9	anabaena sp
124	27	93.1	770	1	A4 HUMAN	P05067	h amyloid b	197	26	89.7	360	2	Q7NM29 GLOVI	Q7nm29	gloeobacter
125	27	93.1	770	1	A4 MACFA	P53601	m amyloid b	198	26	89.7	366	2	Q8DI25 SYNEL	Q8di25	synechococc
126	27	93.1	770	1	A4 MOUSE	P12023	m amyloid b	199	26	89.7	380	2	Q7VJCL HELHP	Q7vjc1	helicobacte
127	27	93.1	770	1	A4 PANTR	Q51s80	p amyloid b	200	26	89.7	382	2	Q9KDE2 BACHD	Q9kde2	bacillus ha
128	27	93.1	770	1	A4 PIG	P79307	s amyloid b	201	26	89.7	390	2	Q5WLG1 BACSK	Q5wlg1	bacillus cl
129	27	93.1	770	1	A4 RAT	P08592	r amyloid b	202	26	89.7	391	2	Q8A2G6 BACTN	Q8a2g6	bacteroides
130	27	93.1	770	2	Q6RH30 CANFA	Q6rh30	canis famil	203	26	89.7	400	2	Q7PXH6 ANOGA	Q7pxh6	anopheles g
131	27	93.1	770	2	Q56JK6 CANFA	Q56jk6	canis famil	204	26	89.7	402	2	Q9ZIT8 ECOLI	Q9zit8	escherichia
132	27	93.1	770	2	Q53ZT3 MOUSE	Q53zt3	mus musculu	205	26	89.7	402	2	Q7DB96 SCOS7	Q7db96	escherichia
133	27	93.1	770	2	Q547B7 RAT	Q547b7	rattus norv	206	26	89.7	402	2	Q83PPI SHIFL	Q83ppi	shigella fl
134	27	93.1	780	1	A4 TERFL	Q73683	tetraodon f	207	26	89.7	405	1	SYI BORBU	Q51343	borrelia bu
135	27	93.1	955	2	Q80R22 9POTV	Q80r22	calla lily	208	26	89.7	405	2	Q661P9 BORGA	Q661p9	borrelia ga
136	27	93.1	962	2	QANTK2 9DELT	Q4ntk2	anaeromykob	209	26	89.7	421	2	Q9LH60 ARATH	Q9lh60	arabidopsis
137	27	93.1	1016	2	Q05912 9POTV	Q05912	zuccchini ye	210	26	89.7	468	2	Q616J7 CAEBR	Q616j7	caenorhabdi
138	27	93.1	1056	2	Q6FKH6 CANGA	Q6fkh6	candida gla	211	26	89.7	472	2	Q4WEZ5 ASPFU	Q4wez5	aspergillus
139	27	93.1	1655	2	Q4Q5Q4 LEIMA	Q4q5q4	leishmania	212	26	89.7	479	2	Q9QDL5 9POTV	Q9qdl5	sarcophilus
140	27	93.1	140	2	Q8QKU4 9POTV	Q8qku4	zuccchini ye	213	26	89.7	479	2	Q4F979 9POTV	Q4f979	eustrephus
141	27	93.1	3080	1	POLG ZYMVC	P18479	z genome po	214	26	89.7	480	2	Q4N8N8 THEPA	Q4n8n8	theileria p
142	27	93.1	3080	2	Q6WN47 9POTV	Q6wn47	zuccchini ye	215	26	89.7	496	2	Q5K4D0 9POTV	Q5k4d0	dasheen mos
143	27	93.1	3080	2	Q6WN48 9POTV	Q6wn48	zuccchini ye	216	26	89.7	502	2	Q5L1S5 GEOKA	Q5l1s5	geobacillus
144	27	93.1	3080	2	Q6WN49 9POTV	Q6wn49	zuccchini ye	217	26	89.7	522	2	Q4XPM5 PLACH	Q4xpm5	plasmodium
145	27	93.1	3080	2	Q5Y2U7 9POTV	Q6y2u7	zuccchini ye	218	26	89.7	524	2	Q912R1 9POTV	Q912r1	dasheen mos
146	27	93.1	3080	2	Q7T908 9POTV	Q7t908	zuccchini ye	219	26	89.7	539	2	Q9QP99 9POTV	Q9qp99	dasheen mos
147	27	93.1	3080	2	Q7T914 9POTV	Q7t914	zuccchini ye	220	26	89.7	557	2	Q4UGZ4 THEAN	Q4ugz4	theileria a
148	27	93.1	3083	1	POLG ZYMVS	Q36979	z genome po	221	26	89.7	598	2	Q644G8 9SALA	Q644g8	gyrinophilu
149	27	93.1	3105	2	Q70XR2 9POTV	Q70xr2	soybean mos	222	26	89.7	604	2	Q645P2 9SALA	Q645f2	stereochilu
150	26	89.7	40	2	Q1FF3 IRV6	Q91ff3	chilo iride	223	26	89.7	606	2	Q8SJ19 URSAM	Q8sji9	ursus ameri
151	26	89.7	66	2	Q728F0 DESVH	P728f0	desulfovibr	224	26	89.7	607	2	Q644P6 9SALA	Q644p6	thorius n.
152	26	89.7	74	1	Y131 MYCGE	P47377	mycoplasma	225	26	89.7	611	2	Q6ZLV9 9TELE	Q6zlv9	ophiurus m
153	26	89.7	81	2	Q6D3D0 ERWCT	Q6d3d0	erwinia car	226	26	89.7	611	2	Q6ZLV9 9TELE	Q6zlv9	ophiurus m
154	26	89.7	89	2	Q83VF2 LACLC	Q83vf2	lactococcus	227	26	89.7	613	2	Q4ZGG0 9TELE	Q4zgg0	scleropages
155	26	89.7	105	2	Q64CV5 9ARCH	Q64cv5	uncultured	228	26	89.7	620	2	Q29198 ARCFU	Q29198	archaeoglob
156	26	89.7	109	2	Q9X292 THEMA	Q9x292	thermotoga	229	26	89.7	624	2	Q6FRJ6 ACIAD	Q6fjb6	acinetobact
157	26	89.7	145	2	Q5USA9 9PEZI	Q5usa9	monacrospor	230	26	89.7	685	1	MDL1 CANAL	Q8rm01	acinetobact
158	26	89.7	156	2	Q8DN20 STRR6	Q8dn20	streptococc	231	26	89.7	685	2	Q5A951 CANAL	P97998	candida alb
159	26	89.7	156	2	Q8N292 STYRN	Q8n292	streptococc	232	26	89.7	726	2	Q4Y7D6 PLACH	Q4y7d6	plasmodium
160	26	89.7	164	2	Q81Y15 BACAN	Q81y15	bacillus an	233	26	89.7	738	2	Q5A445 CANAL	Q5a445	candida alb
161	26	89.7	190	2	Q92WB8 RHIME	Q92wb8	rhizobium m	234	26	89.7	743	2	Q6BM34 DEBHA	Q6bm34	debaryomyce
162	26	89.7	194	2	Q87G46 CLOAB	Q87g46	clostridium	235	26	89.7	771	2	Q4SDLA TETNG	Q4sdl4	tetradodon n
163	26	89.7	196	2	Q8HVS9 BACAN	Q6hvs9	bacillus an	236	26	89.7	774	2	Q64777 ARATH	Q64777	arabidopsis
164	26	89.7	202	2	Q7P578 FUSVN	Q7p578	fusobacteri	237	26	89.7	787	2	Q4XMD0 PLACH	Q4xmd0	plasmodium
165	26	89.7	202	2	Q8REI9 FUSNN	Q8re19	fusobacteri	238	26	89.7	804	2	Q64770 ARATH	Q64770	arabidopsis
166	26	89.7	218	2	Q5CYB3 CRYPV	Q5cyb3	cryptospori	239	26	89.7	881	2	Q6BM22 DEBHA	Q6bm22	debaryomyce
167	26	89.7	218	2	Q5CIV9 CRYHO	Q5civ9	cryptospori	240	26	89.7	911	2	Q6MUP5 MYCMS	Q6muf5	mycoplasma
168	26	89.7	220	2	Q5ZIT4 PEMVM	Q5z4t4	peanut mott	241	26	89.7	957	2	Q7T3T7 OREMO	Q7t3t7	oreochromis
169	26	89.7	230	2	Q7RDM9 PLAYO	Q7rdm9	plasmodium	242	26	89.7	969	2	Q71953 9POTV	Q71953	dasheen mos
170	26	89.7	231	2	Q637W5 BACCZ	Q637w5	bacillus ce	243	26	89.7	973	2	Q9VTH1 DROME	Q9vth1	drosophila
171	26	89.7	241	2	Q4XAZ2 PLACH	Q4xaz2	plasmodium	244	26	89.7	1094	2	Q4Q4Z7 LEIMA	Q4q4z7	leishmania
172	26	89.7	241	2	Q4MXQ0 BACCZ	Q4mxq0	bacillus ce	245	26	89.7	1119	2	Q9LM79 ARATH	Q9lm79	arabidopsis
173	26	89.7	241	2	Q638P6 BACCZ	Q638p6	bacillus ce	246	26	89.7	1273	2	Q9LM82 ARATH	Q9lm82	arabidopsis
174	26	89.7	241	2	Q6HG76 BACHK	Q6hg76	bacillus th	247	26	89.7	3099	1	POLG PEMVM	Q56075	p genome po
175	26	89.7	241	2	Q734P7 BACCI	Q734p7	bacillus ce	248	26	89.7	3191	2	Q912R2 9POTV	Q912r2	dasheen mos
176	26	89.7	241	2	Q81B59 BACCR	Q81b59	bacillus ce	249	26	89.7	3381	2	Q81DK4 PLAF7	Q81dk4	plasmodium
177	26	89.7	241	2	Q81N30 BACAN	Q81n30	bacillus an	250	25	86.2	20	2	Q8CYA3 STRR6	Q8cya3	streptococc

251 25 86.2 26 2 Q4XGP1 PLASMODIUM
252 25 86.2 46 2 Q4Y2T9 PLASMODIUM
253 25 86.2 47 2 Q8EXM4 LEPTOSPIRA
254 25 86.2 46 2 Q8QGY9 FUGU RUBRIP
255 25 86.2 49 2 Q8XA79 PLASMODIUM
256 25 86.2 51 2 Q7RF81 PLASMODIUM
257 25 86.2 51 2 Q4YGS7 PLASMODIUM
258 25 86.2 55 2 Q8YV98 NITROSPHONIA
259 25 86.2 59 2 Q4YGP8 PLASMODIUM
260 25 86.2 62 1 Y078 HELPY
261 25 86.2 62 1 Y085 HELPY
262 25 86.2 62 2 Q64S36 BACFR
263 25 86.2 72 2 Q4HSS4 CANUP
264 25 86.2 77 2 Q5K6Q9 CRAGI
265 25 86.2 79 2 Q5WJL8 BACSK
266 25 86.2 81 1 MOAD ECOLI
267 25 86.2 81 2 Q9APF7 9BACT
268 25 86.2 81 2 Q57RF2 SALCH
269 25 86.2 81 2 Q6STT0 MANSIM
270 25 86.2 81 2 Q7N6P4 PHOIL
271 25 86.2 81 2 Q8D897 VIBVU
272 25 86.2 81 2 Q9KT78 VIBCH
273 25 86.2 81 2 Q83S38 SHIFL
274 25 86.2 81 2 Q7NM72 VIBVU
275 25 86.2 81 2 Q8X807 ESCHERICHA
276 25 86.2 83 2 Q8CLV3 YERSINIA PE
277 25 86.2 83 2 Q5PG40 SALPA
278 25 86.2 83 2 Q8Z886 SALTI
279 25 86.2 83 2 Q8ZQ00 SALTY
280 25 86.2 85 2 Q87MY3 VIBRIO PARA
281 25 86.2 108 1 Y3403 METUA
282 25 86.2 109 2 Q6YVX4 ORYZA SATIV
283 25 86.2 111 2 Q9AI26 ECOLI
284 25 86.2 116 2 Q49347 MYCGE
285 25 86.2 121 2 Q4VBR3 BRARE
286 25 86.2 128 2 Q6DUB9 PSRFL
287 25 86.2 128 2 Q4KBR9 PSEUDOMONAS
288 25 86.2 130 1 Y613 PASMO
289 25 86.2 131 2 Q6BXU4 DEBHA
290 25 86.2 135 2 Q9LIH4 ARATH
291 25 86.2 141 2 Q5LGT9 BACFN
292 25 86.2 141 2 Q67684 AQUAE
293 25 86.2 141 2 Q64XP1 BACFR
294 25 86.2 143 1 COPI YEAST
295 25 86.2 143 2 Q6BWX4 DEBHA
296 25 86.2 143 2 Q6CQ22 KLJULA
297 25 86.2 143 2 Q6FV81 CANGA
298 25 86.2 143 2 Q9HF97 ZYGRO
299 25 86.2 143 2 Q759P0 ASHGO
300 25 86.2 143 2 Q8EMC6 OCEITH

ALIGNMENTS

RESULT 1
Q73N39 TREDE PRELIMINARY; PRT; 164 AA.
AC Q73N39;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Membrane protein, putative.
GN OrderedLocuNames=TDE1317;
OS Treponema denticola.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=158;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 35405 / DSM 14222;
RA PubMed=15064399; DOI=10.1073/pnas.0307639101;
RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,
RA Dodson R.J., Davidse T.M., DeBoy R.T., Fouts D.E., Haft D.H.,

RA Selenget J., Ren Q., Brinkac L.M., Madupu R., Kolonay J.F.,
RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,
RA Gebregoriss E., Geer K., Tsagaye G., Malek J.A., Ayodeji B.,
RA Shatsman S., McLeod M.P., Smajls D., Howell J.K., Fal S., Amin A.,
RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,
RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;
RT "Comparison of the genome of the oral pathogen Treponema denticola
with other spirochete genomes";
RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).
DR EMBL; AE017250; AAS11834.1; -; Genomic_DNA.
DR TIGR; TDE1317; -;
SQ Complete proteome.
KW SEQUENCE 164 AA; 18968 MW; 27B92778DDA9117C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 164;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|||
Db 50 KIVFFA 55

RESULT 2

Q81FH5 BACCR PRELIMINARY; PRT; 387 AA.
ID Q81FH5; AC Q81FH5;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Na+/H+ antiporter NAPA (Inosine-dependent germination).
GN OrderedLocuNames=BC1612;
OC Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candellon B.,
RA Kapral V., Bhattacharya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goldsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis";
RL Nature 423:87-91(2003).
DR EMBL; AE017003; AAP08591.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRfams; TIGR00932; 2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41037 MW; 907C03B6BA150B4A CRC64;

Query Match 100.0%; Score 29; DB 2; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.1e-02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|||
Db 184 KIVFFA 189

RESULT 3

Q4TRF8_9SPHN PRELIMINARY; PRT; 450 AA.
ID Q4TRF8_9SPHN

FT	NON_TER	464	464	
SQ	SEQUENCE	464 AA;	53213 MW;	0F9FF81DB193CE5C CRC64;
Query Match	100.0%;	Score 29;	DB 2;	Length 464;
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;		
Matches	6;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 KIVFFA 6			
DB	304 KIVFFA 309			
RESULT 5				
Q91VU5_MOUSE				
ID	Q91VU5_MOUSE PRELIMINARY;	PRT;	606 AA.	
AC	Q91VU5			
DT	01-DEC-2001 (TrEMBLrel. 19, Created)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Wdct2 protein.			
GN	Name=AI661311; Synonyms=Wdct2;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;			
OC	Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAN=129; TISSUE=Mammary tumor. Brcal-/fl;			
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Heich F.,			
RA	Diatchenko L., Marudina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hate S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Vallalon D.J., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,			
RA	Schmurch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAN=129; TISSUE=Mammary tumor. Brcal-/fl;			
RG	NIH MGC Project;			
RL	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.			
RL	EMBL: BC009019; AAH09019.1; -; mRNA.			
DR	Ensembl; ENSMUSG0000024169; Mus musculus.			
DR	Mgi; MGI:2146906; AI661311.			
DR	GO; GO:0005488; F:binding; IEA.			
DR	InterPro; IPR011990; TPR-like helical.			
SQ	SEQUENCE 606 AA; 70992 MW; 4BB6057E07ADAl6C CRC64;			
Query Match	100.0%;	Score 29;	DB 2;	Length 606;
Best Local Similarity	100.0%;	Pred. No. 3e+02;		
Matches	6;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1 KIVFFA 6			
DB	376 KIVFFA 381			
RESULT 6				
Q6RUU2_MOUSE				

```

ID QGRU2_MOUSE PRELIMINARY; PRT; 663 AA.
AC QGRU2_MOUSE PRELIMINARY; PRT; 663 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bratwaite M., Waelz P., Dudekula D., Nagaraja R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RE EMBL; AY491413; AAS21643.1; -; Genomic_DNA.
FW Hypothetical protein.
KT NON TER 1
SQ SEQUENCE 663 AA; 77192 MW; CEB02E3EED0356F1C CRC64;

Query Match 100.0%; Score 29; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 433 KIVFFA 438

RESULT 7
ID Q831B2_TROW8 PRELIMINARY; PRT; 690 AA.
AC Q831B2_TROW8 PRELIMINARY; PRT; 690 AA.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative helicase regulator.
GN OrderedLocNames=TW130;
OS Tropheryma whipplei (strain TW08/27) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=218496;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bentley S.D., Mairwald M., Murphy L.D., Pallen M.J., Yeats C.A.,
RA Dover L.G., Norbertczak H.T., Besra G.S., Quail M.A., Harris D.E.,
RA von Herbay A., Goble A., Rutter S., Squares R., Squares S.,
RA Barrall B.G., Parkhill J., Reiman D.A.;
RT "Sequencing and analysis of the genome of the Whipple's disease
bacterium Tropheryma whipplei."
RL Lancet 361:637-644(2003).
DR EMBL; BX251410; CAD66810.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome.
SQ SEQUENCE 690 AA; 76266 MW; CD3633B94B669E32 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 526 KIVFFA 531

```

```

RESULT 8
ID Q83GW3_TROWT PRELIMINARY; PRT; 698 AA.
AC Q83GW3_TROWT PRELIMINARY; PRT; 698 AA.
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DNA helicase.
GN OrderedLocNames=TW118;
OS Tropheryma whipplei (strain Twist) (Whipple's bacillus).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Cellulomonadaceae; Tropheryma.
OX NCBI_TaxID=203267;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Raoult D., Ogata H., Audic S., Robert C., Suhr K., Drancourt M.,
RA Claverie J.-M.;
RT "Tropheryma whipplei Twist: a human pathogenic Actinobacteria with a
reduced genome."
RL Genome Res. 13:1800-1809(2003).
DR EMBL; AE016850; AAO44215.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004386; F:Helicase activity; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Complete proteome; Helicase.
SQ SEQUENCE 698 AA; 77193 MW; 6D104BF533CDDE72 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 534 KIVFFA 539

RESULT 9
ID Q6ZQ91_MOUSE PRELIMINARY; PRT; 1265 AA.
AC Q6ZQ91_MOUSE PRELIMINARY; PRT; 1265 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MKIAA0590 protein (Fragment).
GN Name=mkIAA0590;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Saga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
III. the complete nucleotide sequences of 500 mouse KIAA-homologous
cDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries."
RL DNA Res. 10:167-180(2003).
RE EMBL; AK129167; BAC97977.1; -; mRNA.

```

```

FT NON_TER 1 1
SQ SEQUENCE 1265 AA; 143403 MW; C9C157ABE80FF928 CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 1265;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1081 KIVFFA 1086

RESULT 10
Q5F3M1 CHICK
ID Q5F3M1 CHICK PRELIMINARY; PRT; 1412 AA.
AC Q5F3M1
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
GN ORFNames=RCJMB04.13m2;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M.,
RA Flachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
RT "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis.";
RL Genome Biol. 6:R6-R6(2005).
DR EMBL; AJ851629; CAH5263.1; -; mRNA.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 4.
DR PROSITE; PS50082; WD_REPEATS_2; 1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein.
SQ SEQUENCE 1412 AA; 158448 MW; FA0050885B274747 CRC64;

Query Match
Best Local Similarity 100.0%; Score 29; DB 2; Length 1412;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 1225 KIVFFA 1230

RESULT 11
Q4LBQ8 SODGL
ID Q4LBQ8 SODGL PRELIMINARY; PRT; 88 AA.
AC Q4LBQ8
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chey protein.
GN Name=cheY;
OS Sodalis glossinidius.
OG Plasmid pSG4.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Sodalis.
OX NCBI_TaxID=63612;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC PLASMID=pSG4;
RA Darby A.C., Lagnel J., Matthew C.Z., Bourtzis K., Maudlin I.,
RA Welburn S.C.;
RT "Extrachromosomal DNA of the symbiont Sodalis glossinidius.";

```

```

RL J. Bacteriol. 187:5003-5007(2005).
DR EMBL; AJ868439; CAI59440.1; -; Genomic DNA.
DR EMBL; AJ868438; CAI59427.1; -; Genomic_DNA.
KW Plasmid.
SQ SEQUENCE 88 AA; 10177 MW; F4168F2A56B8D0AC CRC64;

Query Match
Best Local Similarity 96.6%; Score 28; DB 2; Length 88;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 42 KIVFFA 47

RESULT 12
Q9RQ09 BACTN
ID Q9RQ09 BACTN PRELIMINARY; PRT; 183 AA.
AC Q9RQ09; Q7C422;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE RNA polymerase sigma factor SigZ-like protein (RNA polymerase ECF-type
DE sigma factor).
GN Name=sigZ; OrderedLocusNames=BT1278;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482;
RX MEDLINE=93380605; PubMed=10449780; DOI=10.1073/pnas.96.17.9833;
RA Hooper L.V., Xu J., Falk P.G., Midtvedt T., Gordon J.I.;
RT "A molecular sensor that allows a gut commensal to control its
RT nutrient foundation in a competitive ecosystem.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:9833-9838(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.10800029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AF137263; AAF01488.1; -; Genomic DNA.
DR EMBL; AE016931; AA076385.1; -; Genomic_DNA.
DR GO; GO:0016987; P:sigma factor activity; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR GO; GO:0006352; P:transcription initiation; IEA.
DR InterPro; IPR007627; Sigma70_r2.
DR InterPro; IPR011991; Wing_hlx_DNA_bd.
DR Pfam; PF04542; Sigma70_r2; 1.
KW Complete proteome; DNA-binding; DNA-directed RNA polymerase;
KW Nucleotidyltransferase; Sigma factor; Transcription;
KW Transcription regulation; Transference.
SQ SEQUENCE 183 AA; 22042 MW; 6B24DABC99BEC643 CRC64;

Query Match
Best Local Similarity 96.6%; Score 28; DB 2; Length 183;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
Db 172 KIVFFA 177

RESULT 13
GL19 ORYSA
ID GL19 ORYSA STANDARD; PRT; 186 AA.
AC P29835;
DT 01-APR-1993 (Rel. 25, Created)

```

DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE 19 kDa globulin precursor (Alpha-globulin).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=cv. Japonica / Nipponbare; TISSUE=Endosperm;
 RC MEDLINE=92119226; PubMed=1731968;
 RX Shorrosh B.S., Wen L., Zen K.C., Huang J.K., Pan J.S., Hermodson M.A.,
 RA Tanaka K., Muthukrishnan S., Reek G.R.;
 RA "A novel cereal storage protein: molecular genetics of the 19 kDa
 RT globulin of rice."
 RL Plant Mol. Biol. 18:151-154(1992).
 RN [2]
 RP NUCLEOTIDE SEQUENCE OF 5-186
 RC STRAIN=cv. Japonica / Lemont; TISSUE=Endosperm;
 RX MEDLINE=93277591; PubMed=8503935;
 RA Krishnan H.B., Pueppke S.G.;
 RA "Nucleotide sequence of an abundant rice seed globulin: homology with
 RT the high molecular weight glutelins of wheat, rye and triticale."
 RL Biochem. Biophys. Res. Commun. 193:460-466(1993).
 CC -!- FUNCTION: Seed storage protein.
 CC -!- SIMILARITY: Belongs to the 2S seed storage albumins family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; X63990; CAA45400.1; -; mRNA.
 DR EMBL; L12252; AAY2362.1; ALT_INIT; mRNA.
 DR FIR; S20024; WNRZ19.
 DR HSSP; P24565; 1PNE.
 DR Gramene; P29835; -.
 DR InterPro; IPR001419; Glutenin.
 DR PANTHER; PTHR14054; Glutenin; 1.
 DR Pfam; PF00234; Tryp_alpha_aml; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 KW Direct protein sequencing; Seed storage protein; Signal;
 KM Storage protein.
 FT SIGNAL 1 22 Potential.
 FT CHAIN 23 186 19 kDa globulin.
 SQ SEQUENCE 186 AA; 21050 MW; 9E09BA74CB0B6810 CRC64;
 Query Match 96.6%; Score 28; DB 1; Length 186;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVEFFA 6
 Db 4 KVVFFA 9
 RESULT 14
 P93414 ORYSA
 ID P93414 ORYSA PRELIMINARY; PRT; 186 AA.
 AC P93414;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE 26 kDa globulin (Alpha-globulin).
 DE Name=P0010D04.16; Synonyms=QJ1057 B02.5;
 GN Oryza sativa (japonica cultivar-group).
 OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=39947;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=Endosperm;
 RX MEDLINE=96235139; PubMed=8666249; DOI=10.1016/0378-1119(95)00887-X;
 RA Nakase M., Hotta H., Adachi T., Aoki N., Nakamura R., Masumura T.,
 RA Tanaka K., Matsuda T.;
 RA "Cloning of the rice seed alpha-globulin-encoding gene: sequence
 RT similarity of the 5'-flanking region to those of the genes encoding
 RT wheat high molecular-weight glutenin and barley D hordein."
 RL Gene 170:223-226(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Chow T.-Y., Haing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Chow T.-Y., Haing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RT "Oryza sativa BAC QJ1057 B02 genomic sequence."
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; P50643; BAA09308.1; -; Genomic DNA.
 DR EMBL; AC130605; AAT44292.1; -; Genomic DNA.
 DR EMBL; AC113332; AAT93857.1; -; Genomic DNA.
 DR FIR; JC4784; JC4784.
 DR HSSP; P24565; 1PNE.
 DR Gramene; P93414; -.
 DR GO; GO:0045735; P.nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001419; Glutenin.
 DR Pfam; PF00234; Tryp_alpha_aml; 1.
 DR PRINTS; PR00210; GLUTENIN.
 DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 186 AA; 21055 MW; AE2B8F1107C8BC94 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 186;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVEFFA 6
 Db 4 KVVFFA 9
 RESULT 15
 Q8C6Y8 MOUSE
 ID Q8C6Y8_MOUSE PRELIMINARY; PRT; 231 AA.
 AC Q8C6Y8;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched
 DE library, clone: D830015B12 product: hypothetical DEAD/DEAD box helicase
 DE containing protein, full insert sequence. (Fragment).
 DE Name=Ddx58;
 GN Names=Ddx58;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=C57BL/6J; TISSUE=Heart;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RX

RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayateu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK052871; BAC35183.1; -; mRNA.
 DR MGI; MGI:2442858; Ddx58.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0004386; P:helicase activity; IEA.
 DR GO; GO:0003676; P:nucleic acid binding; IEA.
 DR InterPro; IPR011545; DEAD/DEAH_N.
 DR Pfam; PF00270; DEAD; 1.
 DR SMART; SM00487; DEXDC; 1.
 KW Helicase; Hypothetical protein.
 FT NON_TER 231 231
 SQ SEQUENCE 231 AA; 25524 MW; 1D191607390D7FBB CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 231;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 145 KIVFFA 150
 RESULT 16
 Q61C67 CAEBR PRELIMINARY; PRT; 315 AA.
 ID Q61C67 CAEBR PRELIMINARY; PRT; 315 AA.
 AC Q61C67;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG13055 (Fragment).
 GN Name=CBG13055;
 OS Caenorhabditis briggsae.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6238;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RG The C.briggsae Sequencing Consortium;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CAAC01000061; CAB67532.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004872; P:receptor activity; IEA.
 DR GO; GO:0001584; P:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Hypothetical protein; Receptor;
 KW Transducer; Transmembrane.
 FT NON_TER 1 1
 FT NON_TER 315 315
 SQ SEQUENCE 315 AA; 35855 MW; 579B590D01874512 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 315;
 Best Local Similarity 83.3%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 117 KIVFFA 122
 RESULT 17
 Q4HSJ7 CAMUP PRELIMINARY; PRT; 362 AA.
 ID Q4HSJ7 CAMUP PRELIMINARY; PRT; 362 AA.
 AC Q4HSJ7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hydrogenase expression/formation protein Hypd.
 GN Name=Hypd; ORFNames=CUP0294;
 OS Campylobacter upsaliensis RM3195.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=306264;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RM3195;
 RA Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Raeko D.A.,
 RA Jacques R.J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
 RA Dodson R.J., Durkin A.S., Madupu R.R., Sullivan S.A., Shetty J.U.,
 RA Ayodeji M.A., Shvartsbeyn A.A., Schatz M.C., Badger J.H., Fraser C.M.,
 RA Nelson K.E.;
 RT "Major structural and novel potential virulence mechanisms from the
 RT genomes of multiple Campylobacter species";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAFJ0100002; FAL53713.1; -; Genomic DNA.
 SQ SEQUENCE 362 AA; 40365 MW; 15B0A8B12D60C8ED CRC64;

Query Match 96.6%; Score 28; DB 2; Length 362;
 Best Local Similarity 83.3%; Pred. No. 3.4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 DB 132 KIIFFA 137

RESULT 18
 Q6D7U3 ERWCT
 ID Q6D7U3 ERWCT PRELIMINARY; PRT; 372 AA.
 AC Q6D7U3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hydrogenase isoenzymes formation protein.
 GN Name=hydp; OrderedLocNames=ECAL232;
 OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Pectobacterium.
 OX NCBI_TaxID=29471;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=SCRI 1043 / ATCC BAA-672;
 RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
 RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
 RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
 RA Ackin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
 RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
 RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
 RA Salmund G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
 RT "Genome sequence of the enterobacterial phytopathogen Erwinia
 RT carotovora subsp. atroseptica and characterization of virulence
 RT factors";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
 RL EMBL; BX950851; CAG74142.1; -; Genomic DNA.
 DR InterPro; IPR002780; Hydp.
 DR Pfam; PF01924; Hydp; 1.
 DR PIRSF; PIRSF005622; Hydrn_mat_hydp; 1.
 DR TIGRFAMs; TIGR00075; hydp; 1.
 KW Complete proteome.
 SQ SEQUENCE 372 AA; 41130 MW; A001A18AC015E620 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 372;
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 DB 139 KIVFFA 144

RESULT 19
 Q7M9N5 WOLSU
 ID Q7M9N5 WOLSU PRELIMINARY; PRT; 373 AA.
 AC Q7M9N5;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE HYDROGENASE PROTEIN.
 GN Name=HYDP; OrderedLocNames=WS0793;
 OS Wolinella succinogenes.
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Wolinella.
 OX NCBI_TaxID=844;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=DSM2 1740;
 RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
 RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
 RA Mandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
 RA Meyer P., Lederer H., Schuster S.C.;
 RT "Complete genome sequence and analysis of Wolinella succinogenes";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
 DR EMBL; BX571659; CAE0906.1; -; Genomic DNA.
 DR InterPro; IPR002780; Hydp.
 DR Pfam; PF01924; Hydp; 1.
 DR PIRSF; PIRSF005622; Hydrn_mat_hydp; 1.
 DR TIGRFAMs; TIGR00075; hydp; 1.
 KW Complete proteome.
 SQ SEQUENCE 373 AA; 41793 MW; 3B7815EDB25790A6 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 373;
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 DB 138 KIVFFA 143

RESULT 20
 Q9V7J0 DROME
 ID Q9V7J0 DROME PRELIMINARY; PRT; 382 AA.
 AC Q9V7J0; Q9CQ81;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE CG8421-PB, isoform B (Aspartyl beta-hydroxylase variant 2).
 GN Name=Asph; ORFNames=CG8421;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriodes; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali K., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser K.D., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426065; PubMed=12537568;
RX CELNIKER S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherz S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celnikier S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celnikier S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celnikier S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RN NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RN [7]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
RA Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
RA O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
RA Friedman P.A.;

RT "Aspartyl beta -hydroxylase (Asph) and an evolutionarily conserved
RT isoform of Asph missing the catalytic domain share exons with
RT junctin.";
RL J. Biol. Chem. 275:39543-39554(2000).
DR EMBL; AE003808; AAF58063.2; -; Genomic_DNA.
DR EMBL; AF289494; AAG40807.1; -; mRNA.
DR Ensembl; CG8421; Drosophila melanogaster.
DR FlyBase; FBgn0034075; Asph.
DR FlyBase; FBgn0034075; CG8421.
SQ SEQUENCE 382 AA; 43287 MW; 60E5C03AEBFC6E8B CRC64;

Query Match 96.6%; Score 28; DB 2; Length 382;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
||:||||
Db 53 KIVFFA 58

RESULT 21

O9KI10_BACCE PRELIMINARY; PRT; 387 AA.
AC O9KI10;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GerN.
GN Name:gerN;
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1396;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC10876;
RX MEDLINE=20576148; PubMed=11133940; DOI=10.1128/JB.183.2.476-482.2001;
RA Thackray P.D., Behravan J., Southworth T.W., Moir A.;
RT "GerN, an antiporter homologue important in germination of *Bacillus*
RT cereus endospores.";
RL J. Bacteriol. 183:476-482(2001).
DR EMBL; AF246294; AAF91326.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; F:cation transporter activity; IEA.
DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K_eff.
DR InterPro; IPR006153; Na_H_porter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932; 2a37; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41093 MW; 40DE45B71B715D01 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
||:||||
Db 184 KIVFFA 189

RESULT 22

O4MT39_BACCE PRELIMINARY; PRT; 387 AA.
AC O4MT39;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Na+/H+ antiporter.
GN ORFNames=BCE_G9241_1647;

OS Bacillus cereus G9241.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=269801;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=G9241;
 RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
 RA Hofmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
 RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
 RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
 RA Ripsone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
 RA Popovic T., Fraser C.M.;
 RT "Identification of anthrax toxin genes in a Bacillus cereus associated
 RT with an illness resembling inhalation anthrax.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAEK01000008; EAL15336.1; -; Genomic DNA.
 SQ SEQUENCE 387 AA; 41122 MW; 15CC136E79B12C38 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 DB 184 KVVFFA 189
 |||||

RESULT 23
 Q63DD4_BACCCZ
 ID Q63DD4_BACCCZ PRELIMINARY; PRT; 387 AA.
 AC Q63DD4
 DT 25-OCT-2004 (TREMELrel. 28, Created)
 DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)
 DE Na+/H+ exchanger family protein.
 GN Name=gerN;
 OS Bacillus cereus (strain ZK).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=288681;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of Bacillus cereus ZK.";
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CP000001; AAV18770.1; -; Genomic DNA.
 DR GO; GO:0016021; AAU18770.1; -; Genomic DNA.
 DR GO; GO:0008324; C:integral to membrane; IEA.
 DR GO; GO:0008324; P:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR004771; K_eff.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGRFAMs; TIGR00932; 2a37; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 41090 MW; DBA5991F6DD63F33 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 DB 184 KVVFFA 189
 |||||

RESULT 24
 Q6HKU6_BACHK PRELIMINARY; PRT; 387 AA.
 ID Q6HKU6;
 AC Q6HKU6;
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Na+/H+ exchanger family protein.
 GN Name=gerN; OrderedLocusNames=BF9727_1493;
 OS Bacillus thuringiensis (subsp. konkukian).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=180856;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=97-27;
 RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
 RA Richardson P., Rubin E., Tice H.;
 RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017355; AAT63168.1; -; Genomic DNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008324; F:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.
 DR GO; GO:0006885; P:regulation of pH; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR004771; K_eff.
 DR InterPro; IPR006153; Na_H_porter.
 DR Pfam; PF00999; Na_H_Exchange; 1.
 DR TIGRFAMs; TIGR00932; 2a37; 1.
 KW Complete proteome; Transmembrane; Transport.
 SQ SEQUENCE 387 AA; 41076 MW; DFECAD90985F951 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 387;
 Best Local Similarity 83.3%; Pred. No. 3.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 DB 184 KVVFFA 189
 |||||

RESULT 25
 Q73AP3_BACCI PRELIMINARY; PRT; 387 AA.
 ID Q73AP3_BACCI PRELIMINARY; PRT; 387 AA.
 AC Q73AP3;
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Germination protein gerN.
 GN OrderedLocusNames=BCE1729;
 OS Bacillus cereus (strain ATCC 10987).
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OX NCBI_TaxID=222523;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
 RA Shores K.A., Fouts D.E., Tourasse N.J., Angiucci S.V., Kolonay J.F.,
 RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
 RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
 RT adaptations and a large plasmid related to Bacillus anthracis pXOI.";
 RL Nucleic Acids Res. 32:977-988(2004).
 DR EMBL; AE017269; AAS40658.1; -; Genomic DNA.
 DR TIGR; BCE1729; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0008324; P:cation transporter activity; IEA.
 DR GO; GO:0015299; F:solute:hydrogen antiporter activity; IEA.
 DR GO; GO:0006812; P:cation transport; IEA.

```
DR GO; GO:0006885; P:regulation of pH; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004771; K.eff.
DR InterPro; IPR006153; Na_Hporter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932_2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 41104 MW; DC7CD48C609FEBA3 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 184 KVVFFA 189

RESULT 26
QB1SK9_BACAN PRELIMINARY; PRT; 387 AA.
ID QB1SK9; Q610U3; Q6KUP8;
AC QB1SK9; Q610U3; Q6KUP8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Germination protein gerN.
GN OrderedLocNames=BAL1639, BAS1521, GBAAL1639;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=225608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oktad O.A., Helgason E., Riltstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson J.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton W.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Ames / isolate 0581;
RX Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Sterne;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017029; AAP35572.1; -; Genomic DNA.
DR EMBL; AE017334; AAT30749.1; -; Genomic DNA.
DR EMBL; AE017225; AAT53839.1; -; Genomic DNA.
DR TIGR; BA1639; -.
DR TIGR; GBAAL1639; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0008324; F: cation transporter activity; IEA.
DR GO; GO:0015299; F: solute:hydrogen antiporter activity; IEA.

DR GO; GO:0006812; P: cation transport; IEA.
DR GO; GO:0006885; P: regulation of pH; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR004771; K.eff.
DR InterPro; IPR006153; Na_Hporter.
DR Pfam; PF00999; Na_H_Exchange; 1.
DR TIGRFAMs; TIGR00932_2a37; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 387 AA; 40932 MW; D59F6A08A283BCA3 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 387;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 184 KVVFFA 189

RESULT 27
Q6L2B4_PICTO PRELIMINARY; PRT; 410 AA.
ID Q6L2B4_PICTO PRELIMINARY; PRT; 410 AA.
AC Q6L2B4_PICTO PRELIMINARY; PRT; 410 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lipopolysaccharide N-acetylglucosaminyltransferase.
GN OrderedLocNames=P00303;
OS Picrophilus torridus.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Picrophilaceae; Picrophilus.
OX NCBI_TaxID=82076;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 9790 / ATCC 700027;
RX PubMed=15184674; DOI=10.1073/pnas.0401356101;
RA Fuetterer O., Angelov A., Liesegang H., Gottschalk G., Schleper C.,
RA Schepers B., Dock C., Antranikian G., Liebl W.;
RT "Genome sequence of Picrophilus torridus and its implications for life
RT around pH 0.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9091-9096(2004).
DR EMBL; AE017261; AAT42888.1; -; Genomic DNA.
DR GO; GO:0016757; F: transferase activity, transferring glycosyl. . .; IEA.
DR GO; GO:0009058; P: biosynthesis; IEA.
DR InterPro; IPR001296; Glyco trans.1.
DR Pfam; PF00534; Glycos transf.1; 1.
KW Complete proteome; Glycosyltransferase; Transferase.
SQ SEQUENCE 410 AA; 48120 MW; C192F0152E66E9B0 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 410;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
   |:||||
Db 235 KIIFFA 240

RESULT 28
Q8C5I3_MOUSE PRELIMINARY; PRT; 410 AA.
ID Q8C5I3_MOUSE PRELIMINARY; PRT; 410 AA.
AC Q8C5I3_MOUSE PRELIMINARY; PRT; 410 AA.
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:6430573D20 product:hypothetical DEAD/DEAH box
DE helicase containing protein, full insert sequence.
GN Name=Ddx58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
```

OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=21085660; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavaletto T.,
 RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=20499374; PubMed=11076861; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=20499374; PubMed=11076861; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hazada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=olfactory brain;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Tananashi F., Takaku-Akai S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL: AK078287; BAC37205.1; -; mRNA.
 DR Ensembl: ENSMUSG0000040296; Mus musculus.
 DR MGI: MGI:2442858; Ddx58.
 DR GO: GO:0005524; P:ATP binding; IEA.
 DR GO: GO:0004386; F:helicase activity; IEA.
 DR GO: GO:0003676; P:nucleic acid binding; IEA.
 DR InterPro: IPR011545; DEAD/DEAH_N.
 DR Pfam: PF00270; DEAD; 1.
 DR SMART: SM00487; DEXDC; 1.
 KW Helicase; Hypothetical protein; Nuclear protein.
 SQ SEQUENCE 410 AA; 46841 MW; ECC9E3D2D2BC5FE0 CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 410;
 Best Local Similarity 83.3%; Pred. No. 3.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 293 KVVFFA 298
 ID Q9PHV5 CAMJE PRELIMINARY; PRT; 442 AA.
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Putative integral membrane protein.
 GN OrderedLocustNames=Cj0560;
 OS Campylobacter jejuni
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
 OC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=197;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=NCCTC 11168;
 RX MEDLINE=20150312; PubMed=10698204; DOI=10.1038/35001088;
 RA Parkhill J., Wren B.W., Mungall K.L., Kelsey J.M., Churcher C.M.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
 RA Jagsels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrell B.G.;
 RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
 reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 DR EMBL: AL139075; CAB75196.1; -; Genomic DNA.
 DR PIR: H81402; H81402.
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0015297; F:antipporter activity; IEA.
 DR GO: GO:0015238; F:drug transporter activity; IEA.
 DR GO: GO:0006855; P:multidrug transport; IEA.
 DR InterPro: IPR002114; Hpr SerP_S.
 DR InterPro: IPR002528; MatE.
 DR Pfam: PF01554; MatE; 1.
 DR TIGRPFam: TIGR00797; matE; 1.
 DR PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 442 AA; 49452 MW; 38EA04E7AB1A8F3E CRC64;
 Query Match 96.6%; Score 28; DB 2; Length 442;
 Best Local Similarity 83.3%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFPA 6
 Db 313 KVVFFA 318

```

RESULT 30
O59243 PYRHO
ID O59243 PYRHO PRELIMINARY; PRT; 447 AA.
AC O59243;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein PH1606.
GN OrderedLocusNames=PH1606;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., HogoYama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:58-76(1998).
DR EMBL; BA000001; BAA30718.1; -; Genomic_DNA.
DR PIR; F71039; F71039.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005355; P:glucose transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000803; Gluc transporter.
DR PRINTS; PR00172; GLUCTRNSPORT.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 447 AA; 51173 MW; 509F45A302D3B059 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 447;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KIVFFA 6
Db 207 KIIFFA 212

RESULT 31
O95593 DROME
ID O95593 DROME PRELIMINARY; PRT; 556 AA.
AC O95593;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE GM05229p.
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., HogoYama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:58-76(1998).
DR EMBL; BA000001; BAA30718.1; -; Genomic_DNA.
DR PIR; F71039; F71039.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005355; P:glucose transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000803; Gluc transporter.
DR PRINTS; PR00172; GLUCTRNSPORT.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 447 AA; 51173 MW; 509F45A302D3B059 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 447;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KIVFFA 6
Db 207 KIIFFA 212

RESULT 32
O9V719 DROME
ID O9V719 DROME PRELIMINARY; PRT; 556 AA.
AC O9V719;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8421-PD, isoform D (CG8421-pe, isoform e).
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova K., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

```

```

Query Match 96.6%; Score 28; DB 2; Length 556;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KIVFFA 6
Db 53 KIIFFA 58

```

```

RESULT 32
O9V719 DROME
ID O9V719 DROME PRELIMINARY; PRT; 556 AA.
AC O9V719;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG8421-PD, isoform D (CG8421-pe, isoform e).
GN Name=Asph; ORFNames=CG8421;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoekins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova K., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasako P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner E., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=OT3;
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

```


RA Weinstock G., Scherer S.E., Myers E.W., Gibbs B.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [3]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RA "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 [4]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [5]
 RN NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RN NUCLEOTIDE SEQUENCE.
 RP FlyBase;
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- INTERACTION:
 CC O46085:EG:63B12.5; NBExp=1; IntAct=EBI-123244, EBI-151469;
 DR EMBL; AE003808; AAF58064.2; -; Genomic_DNA.
 DR IntAct; Q9V719; -;
 DR Ensembl; CG8421; Drosophila melanogaster.
 DR FlyBase; FBgn0034075; Asph.
 DR FlyBase; FBgn0034075; CG8421.
 SQ SEQUENCE 556 AA; 63144 MW; B420980C8D6C357A CRC64;

Query Match 96.6%; Score 28; DB 2; Length 556;
 Best Local Similarity 83.3%; Pred. No. 4.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |||:
 Db 53 KIIFFA 58

RESULT 33
 QSHYEL HUMAN
 ID QSHYEL HUMAN PRELIMINARY; PRT; 703 AA.
 AC QSHYEL;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein DKFZp686N19181 (Fragment).
 GN Name=DKFZp686N19181;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RT TISSUE=Skin endothel;

RG The German cDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX647917; CAI46068.1; -; mRNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004386; F:helicase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR011545; DEAD/DEAF_N.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDc; 1.
 DR SMART; SM00490; HELIcC; 1.
 KW Hypothetical protein.
 FT NON_TER 703
 SQ SEQUENCE 703 AA; 80308 MW; 3CF7500F4F955586 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 703;
 Best Local Similarity 83.3%; Pred. No. 6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 |||:
 Db 247 KIVFFA 252

RESULT 34
 QGAG25 LEIXX
 ID QGAG25 LEIXX PRELIMINARY; PRT; 721 AA.
 AC QGAG25;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE ATP-dependent RNA helicase.
 GN OrderedLocusNames=Lxx07490;
 OS Leifsonia xylis (subsp. xylis).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Micrococineae; Microbacteriaceae; Leifsonia.
 OX NCBI_TaxID=59736;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=CTC807.
 RX PubMed=15305603;
 RA Monteiro-Vitorello C.B., Camargo L.B.A., Van Sluys M.A.,
 RA Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
 RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
 RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
 RA Almeida N.F., Jr., Carrer H., Coutinho L.L., El-Dorri H.A.,
 RA Ferro M.I.T., Gagliardi P.R., Gigliotti E., Goldman M.H.S.,
 RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,
 RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
 RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
 RA Tsai S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Setubal J.C.;
 RT "The genome sequence of the Gram-positive sugarcane pathogen Leifsonia
 RT xylis subsp. xylis.";
 RL Mol. Plant Microbe Interact. 17:827-836(2004).
 DR EMBL; AE016822; AAT88670.1; -; Genomic_DNA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0004386; F:helicase activity; IEA.
 DR InterPro; IPR011545; DEAD/DEAF_N.
 DR InterPro; IPR001650; Helicase_C.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR SMART; SM00487; DEXDc; 1.
 DR SMART; SM00490; HELIcC; 1.
 KW Complete proteome; DNA-binding; Helicase; Hydrolase.
 SQ SEQUENCE 721 AA; 78860 MW; 73F5D2A8435BADE3 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 721;
 Best Local Similarity 83.3%; Pred. No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIVFFA 6
 Db 564 KIVFFA 569
 RESULT 35
 Q9GQ82 DROME PRELIMINARY; PRT; 785 AA.
 ID Q9GQ82 DROME PRELIMINARY; PRT; 785 AA.
 AC Q9GQ82;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Aspartyl beta-hydroxylase variant 1 (CG8421-PA, isoform A).
 GN Name=Asph; ORFNames=CG8421;
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20564328; PubMed=10956665; DOI=10.1074/jbc.M006753200;
 RA Dinchuk J.E., Henderson N.L., Burn T.C., Huber R., Ho S.P., Link J.,
 RA O'Neil K.T., Focht R.J., Scully M.S., Hollis J.M., Hollis G.F.,
 RA Friedman P.A.;
 RT "Aspartyl beta-hydroxylase (Asph) and an evolutionarily conserved
 RT isoform of Asph missing the catalytic domain share exons with
 RT junctin.";
 RL J. Biol. Chem. 275:39543-39554 (2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle B.J.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodge T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22426065; PubMed=12537568;
 RA Celnik S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacle B.J., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
 RT melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirska R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celnik S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 RT a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochownik S.E.,
 RA Smith C.D., Tupy J.B., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celnik S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley Drosophila Genome Project;
 RA Celnik S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacle B.J., Park S., Svirska R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289493; AAG40806.1; -; mRNA.
 DR EMBL; AE003808; AAM70947.1; -; Genomic DNA.
 DR Ensembl; CG8421; Drosophila melanogaster.
 DR FlyBase; FBgn0034075; Asph.
 DR FlyBase; FBgn0034075; CG8421.
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; IEA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0004597; F:peptide-aspartate beta-dioxygenase activity; IEA.
 DR GO; GO:0018193; P:peptidyl-amino acid modification; IEA.
 DR InterPro; IPR007803; Asp Arg Hydrol.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR001440; TPR.
 DR InterPro; IPR011990; TPR-like helical.
 DR Pfam; PF05118; Asp Arg Hydrol; 1.
 DR PROSITE; PS50293; TPR REGION; 1.
 DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
 SQ SEQUENCE 785 AA; 89843 MW; 30A8DFCD6836F7F1 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 785;
 Best Local Similarity 83.3%; Pred. No. 6.6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIVFFA 6

Db 53 KIVFFA 58

RESULT 36

O95786 HUMAN
ID O95786 HUMAN PRELIMINARY; PRT; 925 AA.
AC O95786;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Name=DDX58; Synonyms=RIG-I;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sun Y.W.;
RT "RIG-I, a human homolog gene of RNA helicase, is induced by retinoic
RT acid during the differentiation of acute promyelocytic leukemia
RT cell.";
RL Thesis (1997), Shanghai Institute of Hematology, Rui-Jin Hospital,
RL Shanghai Second Medical University.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Yi-Wu S.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038963; AAD19826.1; -; mRNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR HGNC; HGNC:19102; DDX58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR GO; GO:0001666; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00382; AAA; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR Helicase.
SQ SEQUENCE 925 AA; 106613 MW; 5922B4F3DD0F00D4 CRC64;
KW
QY
Query Match 96.6%; Score 28; DB 2; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 292 KVVFFA 297
QY 1 KIVFFA 6
|:|||||
|:|||||
DB 292 KVVFFA 297

RESULT 37
QSVYTI HUMAN
ID QSVYTI HUMAN PRELIMINARY; PRT; 925 AA.
AC QSVYTI;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE OTTHUMP00000021185.
GN Name=RP11-334P12.2; ORFNames=RP11-334P12.2-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doggett S.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

RA Sehra H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AL353671; CAH71251.1; -; Genomic DNA.
DR EMBL; AL161783; CAH72600.1; -; Genomic DNA.
DR EMBL; AL161783; CAH71251.1; JOINED; Genomic DNA.
DR EMBL; AL353671; CAH72600.1; JOINED; Genomic DNA.
DR Ensembl; ENSG00000107201; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
KW Helicase; Hydrolase; Nuclear protein.
SQ SEQUENCE 925 AA; 106600 MW; BF0D501C395BAE25 CRC64;
Query Match 96.6%; Score 28; DB 2; Length 925;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
|:|||||
|:|||||
DB 292 KVVFFA 297

RESULT 38
Q6Q899 MOUSE
ID Q6Q899 MOUSE PRELIMINARY; PRT; 926 AA.
AC Q6Q899;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE DEAD/H box polypeptide RIG-I.
GN Name=DDX58;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wei J.; Gu J.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY553221; AAS59532.1; -; mRNA.
DR MGI; MGI:2442858; Ddx58.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR006935; Resili.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF04851; Resili; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
SQ SEQUENCE 926 AA; 105877 MW; 632462010107698E CRC64;
Query Match 96.6%; Score 28; DB 2; Length 926;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
|:|||||
|:|||||
DB 293 KVVFFA 298

RESULT 39
Q9GLV6 PIG
ID Q9GLV6 PIG PRELIMINARY; PRT; 940 AA.

```

AC Q9GLV6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RNA helicase.
GN Name=RHIV-1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20261798; PubMed=10799277; DOI=10.1006/mpat.1999.0349;
RA Zhang X., Wang C., Schock L.B., Hawken R.J., Rutherford M.S.;
RT "An RNA helicase, RHIV -1, induced by porcine reproductive and
RT respiratory syndrome virus (PRRSV) is mapped on porcine chromosome
RT 10q13.";
RL Microb. Pathog. 28:267-278(2000).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR EMBL; AF181119; AAC09428.1; -; mRNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR KW Helicase; Hydrolase; Nuclear protein; Repeat.
SQ SEQUENCE 940 AA; 107584 MW; 118CA910B0AF7821 CRC64;

Query Match          96.6%; Score 28; DB 2; Length 940;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 290 KVVFFA 295
:||||
:||||

RESULT 40
NOS2 MOUSE
ID NOS2 MOUSE STANDARD; PRT; 1144 AA.
AC P29477; O70515; O70516;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II)
DE (Inducible NOS) (iNOS) (Macrophage NOS) (MAC-NOS).
GN Name=Nos2; Synonyms=Inos1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92229444; PubMed=1373522;
RA Xie Q.-W., Ding H.-J., Calaycay J., Munford R.A., Swiderek K.M.,
RA Lee T.D., Cho A., Troso T., Nathan C.;
RT "Cloning and characterization of inducible nitric oxide synthase from
RT mouse macrophages.";
RL Science 256:225-228(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92357701; PubMed=1379716;
RA Lowenstein C.J., Glatt C.S., Bredt D.S., Snyder S.H.;
RT "Cloned and expressed macrophage nitric oxide synthase contrasts with
RT the brain enzyme.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:6711-6715(1992).
RN [3]

```

```

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92210618; PubMed=1372907;
RA Lyons C.R., Orloff G.J., Cunningham J.M.;
RT "Molecular cloning and functional expression of an inducible nitric
RT oxide synthase from a murine macrophage cell line.";
RL J. Biol. Chem. 267:6370-6374(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96088781; PubMed=7503239;
RA Kone B.C., Schwoebel J., Turner P., Mohaupt M.G., Cangro C.B.;
RT "Role of NF-kappa B in the regulation of inducible nitric oxide
RT synthase in an M2AL cell line.";
RL Am. J. Physiol. 269:F718-F729(1995).
RN [5]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS ARG-211; LEU-967 AND PHE-968.
RX STRAIN=B10.S/J, BALB/cByJ, DBA/2J, NOD/LtJ, and SJL/J; TISSUE=Spleen;
MEDLINE=93370033; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines Sclay (TCA-3), Sclay2
RT (monocyte chemoattractant protein (MCP)-1), and Sclay2 (MCP-5) are
RT candidates for sae7, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266(1999).
RN [6]
RP EFFECT OF ASPIRIN.
RX TISSUE=Macrophage;
MEDLINE=95372392; PubMed=7544010;
RA Amin A.R., Vyas P., Attur M., Leszczynska-Piziak J., Patel I.R.,
RA Weissmann G., Abramson S.B.;
RT "The mode of action of aspirin-like drugs: effect on inducible nitric
RT oxide synthase.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:7926-7930(1995).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 116-496.
MEDLINE=97477482; PubMed=9334294; DOI=10.1126/science.278.5337.425;
RA Crane B.R., Arvai A.S., Gachhui R., Wu C., Getzoff E.D.,
RA Stuehr D.J., Tainer J.A.;
RT "The structure of nitric oxide synthase oxygenase domain and inhibitor
RT complexes.";
RL Science 278:425-431(1997).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 77-496.
MEDLINE=98182450; PubMed=9516116; DOI=10.1126/science.279.5359.2121;
RA Crane B.R., Arvai A.S., Ghosh D.K., Wu C., Getzoff E.D., Stuehr D.J.,
RA Tainer J.A.;
RT "Structure of nitric oxide synthase oxygenase dimer with pterin and
RT substrate.";
RL Science 279:2121-2126(1998).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
MEDLINE=20031637; PubMed=10562538; DOI=10.1093/emboj/18.22.6260;
RA Ghosh D.K., Crane B.R., Ghosh S., Wolan D., Gachhui R., Crooks C.,
RA Presta A., Tainer J.A., Getzoff E.D., Stuehr D.J.;
RT "Inducible nitric oxide synthase: role of the N-terminal beta-hairpin
RT hook and pterin-binding segment in dimerization and
RT tetrahydrobiopterin interaction.";
RL EMBO J. 18:6260-6270(1999).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-499.
MEDLINE=20031638; PubMed=10562539; DOI=10.1093/emboj/18.22.6271;
RA Crane B.R., Rosenfeld R.J., Arvai A.S., Ghosh D.K., Ghosh S.,
RA Tainer J.A., Stuehr D.J., Getzoff E.D.;
RT "N-terminal domain swapping and metal ion binding in nitric oxide
RT synthase dimerization.";
RL EMBO J. 18:6271-6281(1999).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 77-496.
MEDLINE=20233702; PubMed=10769116; DOI=10.1021/bi992409a;
RA Crane B.R., Arvai A.S., Ghosh S., Getzoff E.D., Stuehr D.J.,
RA Tainer J.A.;
RT "Structures of the N(omega)-hydroxy-L-arginine complex of inducible
RT nitric oxide synthase oxygenase dimer with active and inactive

```

PDB; IM8E; X-ray; A/B=65-498.
PDB; IM8H; X-ray; A/B=65-498.
PDB; IM8I; X-ray; A/B=65-498.
PDB; IM9T; X-ray; A/B=65-498.
PDB; IN2N; X-ray; A/B=77-495.
PDB; INOC; X-ray; A=115-498.
PDB; INOD; X-ray; A/B=77-499.
PDB; INOS; X-ray; @=115-498.
PDB; IQM; X-ray; A/B=65-498.
PDB; IQW4; X-ray; A/B=77-495.
PDB; IOW5; X-ray; A/B=77-495.
PDB; IR35; X-ray; A/B=66-498.
PDB; IVAP; X-ray; A/B=77-495.
PDB; ZBHJ; X-ray; A/B=77-498.
PDB; ZNDQ; X-ray; A/B=77-499.
PDB; ZNOS; X-ray; @=115-498.
PDB; ZNOD; X-ray; A/B=77-499.
DR IntAct; P29477; Mus musculus.
DR Ensembl; ENSMUSG0000020826; Mus musculus.
DR MGI; MGI:97361; N082.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005829; C:cytosol; TAS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; TAS.
DR GO; GO:0020037; F:neme binding; NAS.

Query Match 96.6%; Score 28; DB 1; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIVFFPA 6
 :|||||
 Db 514 KVVFPA 519

RESULT 41
 QSSXT3 MOUSE PRELIMINARY; PRT; 1144 AA.
 AC QSSXT3;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Nitric oxide synthase 2, inducible, macrophage (inducible nitric oxide synthase).
 DE Name=Nos2; ORFNames=RP23-341J22.2-001;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hopkins B.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CD-1;
 RA Coqe P., Levacher B., Rique H., Leopold O., Boutin J.A., Galizzi J.-P.;
 RA "Genomic structure of the murine inducible nitric oxide synthase (i-NOS) gene";
 RT RL
 DR EMBL; AL592185; CAI25275.1; -; Genomic DNA.
 DR EMBL; AF427516; AAL24076.1; -; Genomic DNA.
 SQ SEQUENCE 1144 AA; 130574 MW; 0735BE676113457F CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1144;
 Best Local Similarity 83.3%; Pred. No. 9.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KIVFFPA 6
 :|||||
 Db 514 KVVFPA 519

```

RESULT 42
QBR410 MOUSE
ID QBR410_MOUSE PRELIMINARY; PRT; 1145 AA.
AC QBR410;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Inducible nitric oxide synthase.
GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ICR;
RA Hagiwara K., Endo Y., Xin H., Takahashi M., Huguin, Nukiwa T.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY090567; AAM11887.1; -; mRNA.
DR HSSP; P29477; 1DNV.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0005823; C:cytosol; ISS.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0005516; F:calmodulin binding; ISS.
DR GO; GO:0020037; F:heme binding; ISS.
DR GO; GO:0004517; F:nitric-oxide synthase activity; ISS.
DR GO; GO:0042803; F:protein homodimerization activity; IDA.
DR GO; GO:0042742; P:defense response to bacteria; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0005809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0001542; P:ovulation (sensu Mammalia); IMP.
DR GO; GO:0045585; P:positive regulation of cytotoxic T-cell dif. .; ISS.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006801; P:superoxide metabolism; ISS.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR008254; Flav_nitox_synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130685 MW; DAD5AAPF3680B005 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1145;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 515 KVVFFA 520

RESULT 43
QBP6A0 MOUSE
ID QBP6A0_MOUSE PRELIMINARY; PRT; 1145 AA.
AC QBP6A0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Nos2 protein.

```

```

GN Name=Nos2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062378; AAHG2378.1; -; mRNA.
DR HSSP; P29477; 1JWK.
DR MGI; MGI:97361; Nos2.
DR GO; GO:0030863; C:cortical cytoskeleton; IDA.
DR GO; GO:0048471; C:perinuclear region; IDA.
DR GO; GO:0004517; F:nitric-oxide synthase activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0042803; F:protein homodimerization activity; IDA.
DR GO; GO:0042742; P:defense response to bacteria; IMP.
DR GO; GO:0006809; P:nitric oxide biosynthesis; IDA.
DR GO; GO:0001666; P:response to hypoxia; IDA.
DR GO; GO:0006801; P:superoxide metabolism; IMP.
DR InterPro; IPR003097; FAD binding.
DR InterPro; IPR001094; Flavodoxin_like.
DR InterPro; IPR008254; Flav_nitox_synth.
DR InterPro; IPR001709; FPN_cyt_redctse.
DR InterPro; IPR012144; NOS.
DR InterPro; IPR004030; NO synthase.
DR InterPro; IPR001433; Oxred_FAD/NAD(P).
DR Pfam; PF00667; FAD_binding_1; 1.
DR Pfam; PF00258; Flavodoxin_1; 1.
DR Pfam; PF00175; NAD_binding_1; 1.
DR Pfam; PF02898; NO_synthase; 1.
DR PIRSF; PIRSF000333; NOS; 1.
DR PRINTS; PR00369; FLAVODOXIN.
DR PRINTS; PR00371; FPNCR.
DR PROSITE; PS50902; FLAVODOXIN LIKE; 1.
DR PROSITE; PS60001; NOS; UNKNOWN 1.
SQ SEQUENCE 1145 AA; 130671 MW; C26E09F536923295 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1145;
Best Local Similarity 83.3%; Pred. No. 9.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 515 KVVFFA 520

```

```

RESULT 44
Q68K27 CHLRE PRELIMINARY; PRT; 1384 AA.
AC Q68K27;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Intraflagellar transport particle protein 140.
GN Names=IFT140;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC Chlamydomonadales; Chlamydomonadales; Chlamydomonas.
OX NCBI_TaxID=3055;
RN NUCLEOTIDE SEQUENCE.
RP Walker B.L., Hou Y., Dentler W.L., Witman G.B., Pazour G.J.;
RT "Intraflagellar transport protein IFT140."
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
EMBL; AY686103; AAT95430.1; -; mRNA.
DR GO; GO:0019861; C:flagellum; IEA.
DR InterPro; IPR002885; PPR.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 2.
DR SMART; SM00320; WD40; 5.
DR TIGRFAMs; TIGR00756; PPR; 2.
DR PROSITE; PSS0082; WD_REPEATS_2; 1.
DR PROSITE; PSS0294; WD_REPEATS_REGION; 1.
KW Flagellum.
SQ SEQUENCE 1384 AA; 154603 MW; 5D3E70C8440DABCD CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1384;
Best Local Similarity 83.3%; Pred. NO. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
||:||||
DB 1154 KIIFFA 1159

RESULT 45
Q7QEP0 ANOQA PRELIMINARY; PRT; 1408 AA.
AC Q7QEP0;
DT 01-MAR-2004 (T-EMBLrel. 26, Created)
DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE ENSANGP0000001545 (Fragment).
GN ORFNames=ENSANG0000001308;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
OC Anophelinae; Anophel.
OX NCBI_TaxID=180454;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PEST;
RC The Anopheles gambiae Sequence Committee;
RG The Anopheles gambiae re-annotation.;
RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PEST;
RC The Anopheles gambiae Sequence Committee;
RG The Anopheles gambiae re-annotation.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA01008947; EAA06855.1; -; Genomic_DNA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PSS0294; WD_REPEATS_REGION; 1.

```

```

FT NON_TER 1408 1408
SQ SEQUENCE 1408 AA; 157382 MW; FF63317DAB976DB2 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1408;
Best Local Similarity 83.3%; Pred. NO. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
||:||||
DB 1212 KIIFFA 1217

RESULT 46
Q9VPR0 DROME PRELIMINARY; PRT; 1443 AA.
AC Q9VPR0;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (T-EMBLrel. 26, Last annotation update)
DE CG11838-PA, isoform A.
GN Name=Oseg3; ORFNames=CG11838;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong P.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:12185-12195 (2000).
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

```

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
RT "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomics perspective."
RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochownik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review."
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RG Berkeley Drosophila Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton M., Pacleb J., Park S., Svirkas R., Smith E.,
RA Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE001589; AAF51483.1; -; Genomic_DNA.
DR FlyBase; FBgn0031262; Oeeg3.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR0011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR SMART; SM00320; WD40; 3.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1443 AA; 161316 MW; A8C5997678040888 CRC64;
Query Match 96.6%; Score 28; DB 2; Length 1443;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 1204 KIIFFA 1209
RESULT 47
ID Q5BI64_DROME PRELIMINARY; PRT; 1458 AA.
AC Q5BI64;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE LP14662p.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Berkeley;
RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT021360; AAX33508.1; -; mRNA.
DR InterPro; IPR011990; TPR-like_helical.
DR InterPro; IPR001680; WD40.
DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat.
SQ SEQUENCE 1458 AA; 163133 MW; 2D704C8970E541EC CRC64;
Query Match 96.6%; Score 28; DB 2; Length 1458;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KIVFFA 6
Db 1219 KIIFFA 1224
RESULT 48
ID Q7KTZ4_DROME PRELIMINARY; PRT; 1503 AA.
AC Q7KTZ4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE CG11838-PB, isoform B.
GN Name=Oeeg3; ORFNames=CG11838;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Surtan R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE-22426065; PubMed-12537568;
 RA Celisner S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Swirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
 RT melanogaster euchromatic genome sequence";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE-22426070; PubMed-12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Swirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celisner S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomics perspective";
 RL Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
 [4]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE-22426069; PubMed-12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 [5]
 RP NUCLEOTIDE SEQUENCE.
 RG Berkeley *Drosophila* Genome Project;
 RA Celisner S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
 RA Hoskins R., Stapleton M., Pacleb J., Park S., Swirskas R., Smith E.,
 RA Yu C., Rubin G.;
 RT "Drosophila melanogaster release 4 sequence";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [6]
 RP NUCLEOTIDE SEQUENCE.
 RG FlyBase;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003589; AAS64635.1; -; Genomic_DNA.
 DR InterPro; IPR011990; TPR-like_helical.
 DR InterPro; IPR001680; WD40.
 DR PROSITE; PS00678; WD_REPEATS_1; UNKNOWN 1.
 DR PROSITE; PSS0294; WD_REPEATS_REGION; 1.
 KW Repeat.
 SQ SEQUENCE 1503 AA; 167957 MW; A0DD3F532590486 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1503;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 Db 1264 KIIFFA 1269

RESULT 49
 Q8A6R7 BACTN PRELIMINARY; PRT; 1676 AA.
 AC Q8A6R7; 2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Conserved protein, with weak BamHI domain.
 GN OrderedLocusNames=Brl809;
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX STRAIN=VPI-5482 / ATCC 29148;
 RX MEDLINE-22550858; PubMed-12663928; DOI=10.1126/science.1080029;
 RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
 RA Chiang H.C., Hooper L.V., Gordon J.I.;
 RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis";
 RL Science 299:2074-2076(2003).
 DR EMBL; AE016933; AAO76916.1; -; Genomic_DNA.
 DR InterPro; IPR002048; EF-hand.
 DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 1676 AA; 193673 MW; 28065878C0F6C961 CRC64;

Query Match 96.6%; Score 28; DB 2; Length 1676;
 Best Local Similarity 83.3%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 Db 1656 KIIFFA 1661

RESULT 50

Q9UC33 HUMAN PRELIMINARY; PRT; 33 AA.
 ID Q9UC33; 2000 (TrEMBLrel. 13, Created)
 AC Q9UC33;
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Beta-amyloid peptide (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE-93024877; PubMed-1406936; DOI=10.1038/359325a0;
 RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
 RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
 RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
 RT biological fluids";
 RL Nature 359:325-327(1992).
 DR HSSP; Q16019; 1BA4.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 SQ SEQUENCE 33 AA; 3674 MW; BIDEFE2F4167ABD0 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 33;
 Best Local Similarity 83.3%; Pred. No. 74;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
 ||:||||
 Db 16 KIVFFA 21

RESULT 51
 Q56JG6 GRAGR PRELIMINARY; PRT; 42 AA.
 AC Q56JG6;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)


```

DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Grampus griseus (Risso's dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Grampus.
OX NCBI_TaxID=83653;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926589; AAX81918.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 16 KLVFFA 21

RESULT 52
Q56JJ7 TURTR
ID Q56JJ7_TURTR PRELIMINARY; PRT; 42 AA.
AC Q56JJ7;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Tursiops truncatus (Atlantic bottle-nosed dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;
OC Odontoceti; Delphinidae; Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gallego C., Sarasa M.;
RT "The molecular machinery of Alzheimer's disease in the dolphin.";
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY926588; AAX81917.1; -; mRNA.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 16 KLVFFA 21

RESULT 53
Q7M088 CAVPO
ID Q7M088_CAVPO PRELIMINARY; PRT; 42 AA.
AC Q7M088;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Beta-amyloid protein (Fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]

```

```

RP PROTEIN SEQUENCE.
RX MEDLINE=93290653; PubMed=7685598;
RA Shimohigashi Y., Matsumoto H., Takano Y., Saito R., Iwata T.,
RA Kamiya H., Ohno M.;
RT "Receptor-mediated specific biological activity of a beta-amyloid
RT protein fragment for NK-1 substance p receptors.";
RL Biochem. Biophys. Res. Commun. 193:624-630(1993).
DR FIR; PNO512; PNO512.
DR HSSP; Q16019; 11YT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 42
SQ SEQUENCE 42 AA; 4514 MW; 3AC85563D7858C37 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 42;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 16 KLVFFA 21

RESULT 54
Q8WZ99 HUMAN
ID Q8WZ99_HUMAN PRELIMINARY; PRT; 52 AA.
AC Q8WZ99;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Amyloid protein (Fragment).
GN Name=APP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15201367; DOI=10.1136/jnnp.2003.010611;
RA Wakutani Y., Watanabe K., Adachi Y., Wada-Ise K., Urakami K.,
RA Ninomiya H., Saito T.C., Hashimoto T., Iwatsubo T., Nakashima K.;
RT "Novel amyloid precursor protein gene missense mutation (D678N) in
RT probable familial Alzheimer's disease.";
RL J. Neurol. Neurosurg. Psychiatr. 75:1039-1042(2004).
DR EMBL; AB066441; BAB71958.2; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1
FT NON_TER 52
SQ SEQUENCE 52 AA; 5597 MW; 3P08E9E9EC18011AD CRC64;

Query Match 93.1%; Score 27; DB 2; Length 52;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
DB 16 KLVFFA 21

RESULT 55
A4 URSMA
ID A4_URSMA STANDARD; PRT; 57 AA.
AC Q29149;
DT 01-NOV-1997 (Rel. 35, Created)

```


DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
 DE C-terminal fragment 59]; CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
 DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59) (Fragment).
 DE fragment 57]] (Fragment).
 GN Name=APP;
 OS Ursus maritimus (Polar bear) (Thalartos maritimus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Ursidae;
 OC Ursus
 OC NCBI_TaxID=29073;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; X56128; CAA39593.1; -; mRNA.
 DR FIR; B60045; B60045.
 DR HSSP; P08592; INMJ.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Transmembrane.
 FT CHAIN <1 5 Soluble APP-beta (By similarity).
 FT CHAIN 6 >57 CTF-alpha (By similarity).
 FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
 FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
 FT CHAIN 46 >57 Gamma-CTF(59) (By similarity).
 FT CHAIN 48 >57 Gamma-CTF(57) (By similarity).
 FT TOPO_DOM <1 33 Extracellular (Potential).
 FT TRANSMEM 34 57 Potential.
 FT NON_TER 1 1
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;
 Query Match 93.1%; Score 27; DB 1; Length 57;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 21 KLVFFA 26
 RESULT 56
 ID_A4_CANFA STANDARD; PRT; 58 AA.
 AC Q25280;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
 DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
 DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
 DE fragment 57]] (Fragment).
 GN Name=APP;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: Functional neuronal receptor which couples to
 CC intracellular signaling pathway through the GTP-binding protein
 CC G(O) (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: Belongs to the APP family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; X56125; CAA39590.1; -; mRNA.
 DR HSSP; P08592; INMJ.
 DR Ensembl; ENSCAF00000008557; Canis familiaris.
 DR InterPro; IPR008155; A4_APP.
 DR InterPro; IPR001255; Beta-APP.
 DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00319; A4_EXTRA; PARTIAL.
 DR PROSITE; PS00320; A4_INTRA; PARTIAL.
 KW Amyloid; Transmembrane.
 FT CHAIN <1 6 Soluble APP-beta (By similarity).
 FT CHAIN 7 >58 CTF-alpha (By similarity).
 FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
 FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
 FT CHAIN 47 >58 Gamma-CTF(59) (By similarity).
 FT CHAIN 49 >58 Gamma-CTF(57) (By similarity).
 FT TOPO_DOM <1 34 Extracellular (Potential).
 FT TRANSMEM 35 58 Potential.
 FT NON_TER 1 1
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6285 MW; 8469D48A2E12DFA CRC64;
 Query Match 93.1%; Score 27; DB 1; Length 58;
 Best Local Similarity 83.3%; Pred. No. 1.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 DB 22 KLVFFA 27
 RESULT 57
 ID_A4_RABIT STANDARD; PRT; 58 AA.
 AC Q28748;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DT Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
 DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);

DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal
DE fragment 57)] (Fragment).
GN Name=APP;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X56129; CAA39594.1; -; mRNA.
DR HSSP; P08592; INMJ.
DR InterPro; IPR008155; A4 APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D8EBA82D CRC64;

Query Match 93.1%; Score 27; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|:|:|
Db 21 KLVFFA 26

RESULT 58
A4 SHEEP
ID A4 SHEEP STANDARD; PRT; 58 AA.
AC Q28757;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal

DE fragment 57)] (Fragment).
GN Name=APP;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=92017079; PubMed=1656157; DOI=10.1016/0169-328X(91)90088-F;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis.";
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X56130; CAA39595.1; -; mRNA.
DR HSSP; P08592; INMJ.
DR InterPro; IPR008155; A4 APP.
DR PANTHER; PTHR10083:SF6; Beta-APP; 1.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00319; A4 EXTRA; PARTIAL.
DR PROSITE; PS00320; A4 INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 5 Soluble APP-beta (By similarity).
FT CHAIN 6 >58 CTF-alpha (By similarity).
FT CHAIN 6 47 Beta-amyloid protein 42 (By similarity).
FT CHAIN 6 45 Beta-amyloid protein 40 (By similarity).
FT CHAIN 46 >58 Gamma-CTF(59) (By similarity).
FT CHAIN 48 >58 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 33 Extracellular (Potential).
FT TRANSMEM 34 57 Potential.
FT TOPO_DOM 58 >58 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 58 58
SQ SEQUENCE 58 AA; 6300 MW; F434209D8EBA82D CRC64;

Query Match 93.1%; Score 27; DB 1; Length 58;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
|:|:|:|
Db 21 KLVFFA 26

RESULT 59
A4 BOVIN
ID A4 BOVIN STANDARD; PRT; 59 AA.
AC Q28053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Soluble APP-
DE beta (S-APP-beta); CTF-alpha; Beta-amyloid protein 42 (Beta-APP42);
DE Beta-amyloid protein 40 (Beta-APP40); Gamma-CTF(59) (Gamma-secretase
DE C-terminal fragment 59); Gamma-CTF(57) (Gamma-secretase C-terminal

OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
ON NCBI_TaxID=9913;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RC MEDLINE=92017079; PubMed=156157; DOI=10.1016/0169-328X(91)90088-F;
RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RA "Conservation of the sequence of the Alzheimer's disease amyloid
RT peptide in dog, polar bear and five other mammals by cross-species
RT polymerase chain reaction analysis".
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: Functional neuronal receptor which couples to
CC intracellular signaling pathway through the GTP-binding protein
CC G(O) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the APP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; X56124; CAA39589.1; -; mRNA.
CC EMBL; X56126; CAA39591.1; -; mRNA.
CC HSSP; P08592; 1NMJ.
CC InterPro; IPR008155; A4_APP.
CC InterPro; IPR001255; Beta-APP.
CC PANTHER; PTHR10083:SF6; Beta-APP; 1.
CC Pfam; PF03494; Beta-APP; 1.
CC PRINTS; PR00204; BETAAMYLOID.
CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
CC PROSITE; PS00320; A4_INTRA; PARTIAL.
KW Amyloid; Transmembrane.
FT CHAIN <1 6 Soluble APP-beta (By similarity).
FT CHAIN 7 >59 CTF-alpha (By similarity).
FT CHAIN 7 48 Beta-amyloid protein 42 (By similarity).
FT CHAIN 7 46 Beta-amyloid protein 40 (By similarity).
FT CHAIN 47 >59 Gamma-CTF(59) (By similarity).
FT CHAIN 49 >59 Gamma-CTF(57) (By similarity).
FT TOPO_DOM <1 34 Extracellular (Potential).
FT TRANSMEM 35 58 Potential.
FT TOPO_DOM 59 >59 Cytoplasmic (Potential).
FT NON_TER 1 1
FT NON_TER 59 59
SQ SEQUENCE 59 AA; 6414 MW; F43469D488A2E12D CRC64;

Query Match 93.1%; Score 27; DB 1; Length 59;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
Db 22 KLVFFPA 27

RESULT 60
O35463_CRIGR PRELIMINARY; PRT; 79 AA.
AC O35463;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alzheimer's amyloid beta protein (Fragment).
GN Name=beta APP;
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Cricetulus.
ON NCBI_TaxID=10029;

RN NUCLEOTIDE SEQUENCE.
RP Sambamurti K., Pinnix I., Gandhi S.;
RA Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF030413; AAB86608.1; -; mRNA.
DR HSSP; P08592; 1NMJ.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00204; BETAAMYLOID.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 79;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
Db 36 KLVFFPA 41

RESULT 61
Q8UH58_CHESE PRELIMINARY; PRT; 113 AA.
AC Q8UH58;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Amyloid beta protein (Fragment).
OS Chelydra serpentina serpentina (common snapping turtle).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Testudines; Cryptodira; Testudinoidea; Chelydridae; Chelydra.
ON NCBI_TaxID=134619;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21876906; PubMed=11882478;
RA Trudeau V.L., Chiu S., Kennedy S.W., Brooks R.J.;
RT "Octylphenol (OP) alters the expression of members of the amyloid
RT protein family in the hypothalamus of the snapping turtle, Chelydra
RT serpentina serpentina.";
RL Environ. Health Perspect. 110:269-275(2002).
DR EMBL; AF541917; AAN04908.1; -; mRNA.
DR HSSP; Q16019; 1IYT.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR InterPro; IPR008155; A4_APP.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOIDA4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1 1
SQ SEQUENCE 113 AA; 12750 MW; 72515C930496E053 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 113;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
Db 30 KLVFFPA 35

RESULT 62
Q7UPR1_RHOBA PRELIMINARY; PRT; 137 AA.
AC Q7UPR1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.
 GN OrderedLocusNames=RB6777;
 OS Rhodopirellula baltica.
 OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
 OC Planctomycetaceae; Pirellula.
 OX NCBI_TaxID=117;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=1;
 RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
 RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
 RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
 RA Schlesner H., Amann K., Reinhardt R.;
 RT "Complete genome sequence of the marine planctomycete Pirellula sp.
 RT strain 1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
 DR EMBL; BX294144; CAD75000.1; -; Genomic DNA.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 137 AA; 15530 MW; 5DCC133B06CC5FC0 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 137;
 Best Local Similarity 83.3%; Pred. No. 2.5e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
 |:|
 Db 85 KLVFFA 90

RESULT 63
 QST29 ARATH
 ID Q9ST29 ARATH PRELIMINARY; PRT; 152 AA.
 AC Q9ST29;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Hypothetical protein T20K18.220 (Hypothetical protein AT4g12870).
 GN Name=T20K18.220; Synonyms=AT4g12870;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Bevan M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
 RA Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL049640; CAB41004.1; -; Genomic DNA.
 DR EMBL; AL161535; CAB78329.1; -; Genomic DNA.
 DR PIR; T06645; T06645.
 DR InterPro; IPR004911; GILF.
 DR Pfam; PF03227; GILF; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 152 AA; 17095 MW; ED47CEAE7607B131 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 152;
 Best Local Similarity 83.3%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
 |:|
 Db 85 KLVFFA 90

Oy 1 KIVFFA 6
 |:|
 Db 9 KLVFFA 14

RESULT 64
 Q6AKE9 DESPS
 ID Q6AKE9 DESPS PRELIMINARY; PRT; 203 AA.
 AC Q6AKE9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Related to McbG protein.
 GN OrderedLocusNames=DP2447;
 OS Desulfotalea psychrophila.
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
 OC Desulfobulbaceae; Desulfotalea.
 OX NCBI_TaxID=84980;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LSV54 / DSM 12343;
 RX PubMed=15305914; DOI=10.1111/j.1462-2920.2004.00665.x;
 RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
 RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
 RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
 RA Klenk H.-P.;
 RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
 RT from permanently cold Arctic sediments.";
 RL Environ. Microbiol. 6:887-902(2004).
 DR EMBL; CR522870; CAG37176.1; -; Genomic DNA.
 DR InterPro; IPR001646; Peptide repeat.
 DR Pfam; PF00805; Pentapeptide; 3.
 KW Complete proteome.
 SQ SEQUENCE 203 AA; 23270 MW; 2EA1CD022861292D CRC64;

Query Match 93.1%; Score 27; DB 2; Length 203;
 Best Local Similarity 66.7%; Pred. No. 3.6e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KIVFFA 6
 |:|
 Db 52 KLVFFA 57

RESULT 65
 Q8BPV5 MOUSE
 ID Q8BPV5 MOUSE PRELIMINARY; PRT; 218 AA.
 AC Q8BPV5;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched
 DE library, clone:D430025B14 product:amyloid beta (A4) protein, full
 DE insert sequence. (Fragment).
 GN Name=App;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

DR Pfam. PF03494; Beta-APP; 1.
DR PRINTS; PR00203; AMYLOID4.
DR PRINTS; PR00204; BETAAMYLOID.
DR PROSITE; PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 218 AA; 24118 MW; 95B55AFDAE1D0EF5 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 218;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 135 KLVFFA 140

RESULT 66
Q8VY56 ARATH PRELIMINARY; PRT; 229 AA.
AC Q8VY56;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At4g12870.
GN Name=At4g12870;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Tripp M., Southwick A., Karlin-Neumann G., Nguyen M., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072432; AAL62424.1; -; mRNA.
DR EMBL; AY128863; AAN91263.1; -; mRNA.
DR InterPro; IPR004911; GILT.
DR Pfam; PF03227; GILT.
KW Hypothetical protein.
SQ SEQUENCE 229 AA; 25707 MW; BF3DD2587EAA82D6 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 229;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIVFFA 6
|:||||
Db 9 KLVFFA 14

RESULT 67
Q9SV79 ARATH PRELIMINARY; PRT; 231 AA.
AC Q9SV79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein At4g12900.
GN Name=At4g12900; Synonyms=AT4g12900;

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Bevan M., Robben J., Grymonprez B., Volckaert G., Bancroft I.,
 RA Mewes H.W., Rudd S., Schoof H., Mayer K.F.X.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RA Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes H.W.,
 RA Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RA Robben J., Grymonprez B., Volckaert G., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL079349; CAB53090.1; -; Genomic DNA.
 DR EMBL; AL161535; CAB78332.1; -; Genomic DNA.
 DR F1; H85138; H85138.
 DR InterPro; IPR004911; GILT.
 DR InterPro; IPR000834; Peptidase M14.
 DR Pfam; PF03227; GILT; 1.
 DR PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 231 AA; 26025 MW; 734109A78E942295 CRC64;
 Query Match 93.1%; Score 27; DB 2; Length 231;
 Best Local Similarity 83.3%; Pred. No. 4e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 12 KLVFFA 17
 ID Q9XGY6 SIMCH PRELIMINARY; PRT; 352 AA.
 AC Q9XGY6;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Wax synthase.
 OS Simmondsia chinensis (Jojoba).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Simmondsiaceae; Simmondsia.
 OX NCBI_TaxID=3999;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=2017844; PubMed=10712527; DOI=10.1104/pp.122.3.645;
 RA Lardizabal K.D., Metz J.G., Sakamoto T., Hutton W.C., Pollard M.R.,
 RA Laesner M.W.;
 RT "Purification of a Jojoba embryo wax synthase, cloning of its cDNA and
 RT production of high levels of wax in seeds of transgenic Arabidopsis.";
 RL Plant Physiol. 122:645-655(2000).
 DR EMBL; AF149919; AAD38041.1; -; mRNA.
 DR PIR; T48903; T48903.
 DR InterPro; IPR004299; MBOAT_fam.
 DR Pfam; PF03062; MBOAT; 1.
 SQ SEQUENCE 352 AA; 40156 MW; F91D6BD896003629 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 352;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 135 KLVFFA 140
 ID Q8U460 PYRFU PRELIMINARY; PRT; 357 AA.
 AC Q8U460;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein PF0234.
 GN OrderedLocusNames=PF0234;
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE010148; AAL80358.1; -; Genomic DNA.
 DR InterPro; IPR008553; DUF835.
 DR Pfam; PF05763; DUF835; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 357 AA; 39940 MW; 9EEFE2540CF8D65 CRC64;
 Query Match 93.1%; Score 27; DB 2; Length 357;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KIVFFA 6
 Db 197 KLVFFA 202
 ID Q8UUI8 BRARE PRELIMINARY; PRT; 357 AA.
 AC Q8UUI8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Putative membrane protein (Fragment).
 GN Name=appa;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Whole embryo;
 RX PubMed=11862463; DOI=10.1007/s00427-001-0189-9;
 RA Musa A., Lehrach H., Russo V.B.A.;
 RT "Distinct expression patterns of two zebrafish homologues of the human
 RT APP gene during embryonic development.";
 RL Dev. Genes Evol. 211:563-567(2001).
 DR EMBL; AJ315637; CAC85734.1; -; mRNA.
 DR HSSP; Q16019; 1HZ3.
 DR SMR; Q8UUI8; 62-170.
 DR ZFIN; ZDB-GENE-000616-13; appa.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR InterPro; IPR008155; A4_APP.

DR InterPro: IPR001255; Beta-APP.
 DR Pfam: PF03494; Beta-APP; 1.
 DR PRINTS; PRO0203; AMYLOIDA4.
 DR PROSITE; PRO0204; BETAAMYLOID.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON TER 1
 SQ SEQUENCE 357 AA; 40962 MW; 07D99BEF6C55B2D8 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 357;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |:|||||
 Db 274 KLVFFPA 279

RESULT 71

O8PPL1_XANAC PRELIMINARY; PRT; 366 AA.

AC Q8PPL1; DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Hypothetical protein XAC0675.

GN OrderedLocusNames=XAC0675;

OS Xanthomonas axonopodis (pv. citri).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=92829;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=306 / ATCC 13902 / XV 101;

RX MEDLINE=2022145; PubMed=12024217; DOI=10.1038/417459a;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,

RA Almeida N.P., Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,

RA Camargo L.E.A., Camarotte G., Cannavan F., Cardozo J., Chambergro F.,

RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,

RA El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,

RA Ferro M.I.T., Foghieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katayama A.M., Kishimoto L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Teai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities."

RL Nature 417:459-463(2002).

DR EMBL; AE011696; AAM35564.1; -: Genomic DNA.

SK Complete proteome; Hypothetical protein

SQ SEQUENCE 366 AA; 40845 MW; 6EF65B2BEC89844 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 366;

Best Local Similarity 83.3%; Pred. No. 6e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |:|||||
 Db 340 KLVFFPA 345

RESULT 72

O67225_AQUAE

ID O67225_AQUAE PRELIMINARY; PRT; 380 AA.

AC O67225;

DT 01-AUG-1998 (TrEMBLrel. 07, Created)

DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hydrogenase expression/formation protein HypD.

GN Name=hypD; OrderedLocusNames=AQ_1157;
 OS Aquifex aeolicus
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=VF5;

RX MEDLINE=98196666; PubMed=9537320; DOI=10.1038/32831;

RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,

RA Feldman R.A., Short J.M., Olsen G.J., Swanson R.V.;

RT "The complete genome of the hyperthermophilic bacterium Aquifex

aeolicus";

RL Nature 392:353-358(1998).

DR EMBL; AE000726; AAC07185.1; -: Genomic DNA.

DR PIR; F70399; F70399.

DR InterPro; IPR002780; HypD.

DR Pfam; PF01924; HypD; 1.

DR PIRSF; PIRSF005622; Hydrgn_mat_hypD; 1.

DR TIGRFAMs; TIGR00075; hypD; 1.

KW Complete proteome.

SQ SEQUENCE 380 AA; 42791 MW; 49C0E52BA655A5F5 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 380;

Best Local Similarity 66.7%; Pred. No. 6.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFPA 6
 |:|||||
 Db 141 KVIFFPA 146

RESULT 73

QBPC7 MOUSE

ID QBPC7 MOUSE PRELIMINARY; PRT; 384 AA.

AC QBPC7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DE Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched

DE library, clone:483432109 product:amyloid beta (A4) protein, full

DE insert sequence. (Fragment).

GN Name=App;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning."

RL Meth. Enzymol. 303:19-44(1999).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J; TISSUE=Head;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Harada A.,
 RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kouda M., Koya S.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.
 DR EMBL; AK076506; BAC36369.1; -, mRNA.
 DR HSP; P08592; 1NMJ.
 DR SMR; Q8BPC7; 74-183.
 DR MGI; MGI:88059; App.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 DR GO; GO:0016020; C:membrane; TAS.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0030198; P:extracellular matrix organization and bioge. .; IGI.
 DR InterPro; IPR008155; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA.
 DR PRINTS; PR00204; BETAAMYLOID.
 DR PROSITE; PS00320; A4_INTRA; 1.
 FT NON_TER 1
 SQ SEQUENCE 384 AA; 43990 MW; A81B1AD8AE683173 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 384;
 Best Local Similarity 83.3%; Pred No. 6.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVEFFA 6
 Db 301 KLVFFA 306

RESULT 74

Q4NSU7 THEPA PRELIMINARY; PRT; 391 AA.
 AC Q4NSU7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE Hypothetical protein.
 GN ORFNames=TP02_0195;
 OS Theileria parva.
 OC Eukaryota; Alveolata; Apicomplexa; Piropalmida; Theileridae;
 OC Theileria.
 OX NCBI_TaxID=5875;
 RN [1]
 RC STRAIN=Muguga;
 RP NUCLEOTIDE SEQUENCE.
 RA Gardner W.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
 RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
 RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
 RA Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
 RA Wortman J.R., Haas B., Anguoli S.V., Creasy T.H., Lu C., Suh B.,
 RA Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,
 RA Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
 RA Venter J.C., Fraser C.M., Nene V.;
 RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
 RT lymphocytes";
 RL Science 309:134-137(2005).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Muguga;
 RA Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
 RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
 RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
 RA Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
 RA Haas B., Anguoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
 RA Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
 RA Fraser C.M., Nene V.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBSJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AKG01000002; EAN32476.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 391 AA; 44445 MW; 129227F0ABAF933C CRC64;

Query Match 93.1%; Score 27; DB 2; Length 391;
 Best Local Similarity 83.3%; Pred. No. 6.3e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVEFFA 6
 Db 130 KLVFFA 135

RESULT 75

Q5WPU9 LUTLO PRELIMINARY; PRT; 399 AA.
 AC Q5WPU9;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE 43.2 kDa salivary protein.
 GN ORFNames=LJMI1_Clu9;
 OS Lutzomyia longipalpis (Sand fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Psychodoidea;
 OC Psychodidae; Lutzomyia; Lutzomyia.


```
OX NCBI_TaxID=7200;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Salivary gland;
RX PubMed=15371479; DOI=10.1242/jeb.01185;
RA Valenzuela J.G., Garfield M., Rowton E.D., Pham V.M.;
RT "Identification of the most abundant secreted proteins from the
RT salivary glands of the sand fly Lutzomyia longipalpis, vector of
RT Leishmania chagasi.";
RL J. Exp. Biol. 207:3717-3729(2004).
DR EMBL; AY445935; AAS05318.1; -; mRNA.
DR InterPro: IPR003534; Royaljelly.
DR Pfam: PF03022; MRJP; 1
SQ SEQUENCE 399 AA; 45277 MW; F4E19F115794AAE8 CRC64;

Query Match 93.1%; Score 27; DB 2; Length 399;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIVFFA 6
Db 305 KVIFFA 310
```

Search completed: December 29, 2005, 17:47:27
Job time : 79.1936 secs

THIS PAGE BLANK (USPTO)

; Publication No. US20040172684A1

; GENERAL INFORMATION: David K.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 31699
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C102839_1.pep
US-10-767-701-31699

Query Match 89.7%; Score 26; DB 4; Length 206;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 6 KAVFFS 11

RESULT 73

; Sequence 39451, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39451
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(208)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-39451

Query Match 89.7%; Score 26; DB 5; Length 208;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 37 RAVFFA 42

RESULT 74

; Sequence 61639, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Lianguo
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61639
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Mycobacterium avium
US-10-282-122A-61639

Query Match 89.7%; Score 26; DB 4; Length 210;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 54 RAVFFA 59

RESULT 75

; Sequence 286732, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286732
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_24595C.1.pep
US-10-425-115-286732

Query Match 89.7%; Score 26; DB 4; Length 258;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 ||:||
 Db 212 KAMFFA 217

Search completed: December 29, 2005, 18:49:44
 Job time : 71.2903 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds
(without alignments)
44.518 Million cell updates/sec

Title: US-10-009-122-15
Perfect score: 29
Sequence: 1 KAVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : PIR-80.*

- 1: Pirl.*
- 2: Pirl2.*
- 3: Pirl3.*
- 4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	261	2 D64166	hypothetical prote
2	29	100.0	469	2 T02325	probable selenum-
3	29	100.0	660	1 A28153	gelatinase A (EC 3
4	29	100.0	662	2 S70365	gelatinase A (EC 3
5	29	100.0	662	2 A42496	gelatinase A (EC 3
6	29	100.0	663	1 S34780	gelatinase A (EC 3
7	29	100.0	663	1 S46492	gelatinase A (EC 3
8	29	100.0	1147	1 I53165	nitric-oxide synth
9	29	100.0	1147	1 I56575	nitric-oxide synth
10	29	100.0	1147	1 S38253	nitric-oxide synth
11	29	100.0	1147	1 S47647	nitric-oxide synth
12	29	100.0	1147	2 JC5029	nitric-oxide synth
13	29	100.0	1147	2 JC5028	nitric-oxide synth
14	29	100.0	1147	2 JC5027	nitric-oxide synth
15	29	100.0	1147	2 S65440	nitric-oxide synth
16	28	96.6	169	2 A22630	hypothetical prote
17	28	96.6	283	2 T20734	hypothetical prote
18	26	89.7	58	2 B43358	cysteine-rich prot
19	26	89.7	150	2 S27597	hypothetical prote
20	26	89.7	156	1 P69857	conserved hypotet
21	26	89.7	166	2 D71049	probable L(+)-tart
22	26	89.7	185	2 E70445	C-terminal fumarat
23	26	89.7	192	2 A49648	cysteine-rich prot
24	26	89.7	192	2 S38879	LIM-domain protein
25	26	89.7	229	2 E75252	molybdopterin bios
26	26	89.7	244	2 T16110	hypothetical prote
27	26	89.7	285	2 T01119	hypothetical prote
28	26	89.7	299	1 ZBBE13	33.1K zinc-binding
29	26	89.7	421	2 S40819	probable transport

30	26	89.7	421	2 C86075	probable resistanc
31	26	89.7	421	2 D91228	probable resistanc
32	26	89.7	457	2 AH1799	Grpase homolog lin
33	26	89.7	464	1 VCXFTI	major capsid prote
34	26	89.7	467	1 JQ2215	major capsid prote
35	26	89.7	472	1 VCXFSI	major capsid prote
36	26	89.7	479	2 T50726	hypothetical prote
37	26	89.7	715	2 AB0805	3-hydroxyacyl-CoA
38	26	89.7	1139	2 B54962	sterol regulatory
39	26	89.7	1204	2 S62506	alpha-glucan synth
40	26	89.7	1701	2 T09127	probable erythrocy
41	25	86.2	100	2 AG2447	hypothetical prote
42	25	86.2	120	1 QQSACC	hypothetical prote
43	25	86.2	132	2 I40566	hypothetical prote
44	25	86.2	186	1 WMR219	19K globulin precu
45	25	86.2	186	2 JC4784	alpha-globulin pre
46	25	86.2	191	2 H64441	hypothetical prote
47	25	86.2	202	2 B64668	carbonic anhydrase
48	25	86.2	209	2 AG2405	hypothetical prote
49	25	86.2	210	2 C81216	conserved hypotet
50	25	86.2	210	2 G81793	hypothetical prote
51	25	86.2	212	2 AB3270	threonine efflux p
52	25	86.2	226	2 F69125	conserved hypotet
53	25	86.2	247	2 A71847	carbonic anhydrase
54	25	86.2	260	2 B69983	conserved hypotet
55	25	86.2	263	2 C95942	probable transcrip
56	25	86.2	282	1 A28171	phenylethanolamine
57	25	86.2	285	2 A82458	hypothetical prote
58	25	86.2	298	2 B90435	hypothetical prote
59	25	86.2	302	2 H90717	hypothetical prote
60	25	86.2	308	2 T24732	hypothetical prote
61	25	86.2	321	2 G72347	hypothetical prote
62	25	86.2	323	2 H85567	hypothetical prote
63	25	86.2	326	2 S51509	pectase lyase - As
64	25	86.2	331	2 C72015	glycerol-3-phospha
65	25	86.2	331	2 D86610	glycerol-3-P acylt
66	25	86.2	332	2 E72597	probable alcohol d
67	25	86.2	342	2 AD2306	hypothetical prote
68	25	86.2	347	2 T21067	hypothetical prote
69	25	86.2	352	2 H97272	histidinol-phospha
70	25	86.2	384	2 H64161	hypothetical prote
71	25	86.2	411	2 AF0203	probable membrane
72	25	86.2	420	2 T05877	hypothetical prote
73	25	86.2	442	2 H81402	probable integral
74	25	86.2	462	2 G95233	Cof family protein
75	25	86.2	462	2 AB6717	conserved hypotet
76	25	86.2	463	2 J50376	hypothetical 53.0K
77	25	86.2	468	2 AD0585	probable outer mem
78	25	86.2	468	2 H64802	YbfM protein - Esc
79	25	86.2	472	2 A99098	conserved hypotet
80	25	86.2	483	2 S25606	bleomycin hydrolas
81	25	86.2	499	2 JH0313	potassium channel
82	25	86.2	537	2 T31009	hypothetical prote
83	25	86.2	537	2 AC2467	hypothetical prote
84	25	86.2	560	2 I38065	gene NMB protein -
85	25	86.2	564	2 B81735	conserved hypotet
86	25	86.2	573	2 F89719	protein F09812.1
87	25	86.2	573	2 B96639	protein TIF9.16
88	25	86.2	573	2 B96639	hypothetical prote
89	25	86.2	656	2 S65826	DNA topoisomerase
90	25	86.2	769	2 F81415	hypothetical prote
91	25	86.2	800	2 G84740	hypothetical prote
92	25	86.2	800	2 A84293	helicase [imported
93	25	86.2	1005	2 A64465	hypothetical prote
94	25	86.2	1057	2 T46193	hypothetical prote
95	25	86.2	1144	1 A43271	nitric-oxide synth
96	25	86.2	2526	2 T20531	hypothetical prote
97	25	86.2	2722	2 T20532	hypothetical prote
98	25	86.2	2738	2 B88320	protein F07A11.6
99	25	86.2	33	2 S23094	beta-amyloid prote
100	24	82.8	42	2 PN0512	beta-amyloid prote
101	24	82.8	57	2 A60045	Alzheimer's diseas
102	24	82.8	57	2 D60045	Alzheimer's diseas

103	24	82.8	57	2	E60045	Alzheimer's disease	176	24	82.8	508	1	QJLV6A	photosystem II chl
104	24	82.8	57	2	E60045	Alzheimer's disease	177	24	82.8	508	1	QJLV6A	photosystem II chl
105	24	82.8	57	2	E60045	Alzheimer's disease	178	24	82.8	508	1	QJLV6A	photosystem II chl
106	24	82.8	82	2	PQ0438	Alzheimer's disease	179	24	82.8	508	1	QJLV6A	photosystem II chl
107	24	82.8	96	2	T34068	hypothetical prote	180	24	82.8	508	2	S12132	photosystem II chl
108	24	82.8	111	2	T36555	probable membrane	181	24	82.8	508	2	S04100	photosystem II chl
109	24	82.8	133	2	A13582	hypothetical prote	182	24	82.8	508	2	S01385	photosystem II chl
110	24	82.8	143	2	A70450	hypothetical prote	183	24	82.8	508	2	S14140	photosystem II chl
111	24	82.8	152	2	T06645	hypothetical prote	184	24	82.8	508	2	S33774	photosystem II chl
112	24	82.8	163	2	F86878	hypothetical prote	185	24	82.8	508	2	T07508	photosystem II chl
113	24	82.8	184	2	G90232	hypothetical prote	186	24	82.8	508	2	S12129	photosystem II chl
114	24	82.8	192	2	S77742	probable Mg2+-tran	187	24	82.8	509	2	JA0148	photosystem II chl
115	24	82.8	220	2	A70526	hypothetical prote	188	24	82.8	509	2	AB1824	photosystem II CP4
116	24	82.8	231	2	AD0780	puatative membrane	189	24	82.8	509	2	T11996	photosystem II chl
117	24	82.8	231	2	H85138	hypothetical prote	190	24	82.8	509	2	S78322	photosystem II chl
118	24	82.8	240	2	G70303	cytochrome c - Aqu	191	24	82.8	509	2	T06855	probable amino aci
119	24	82.8	247	2	E86161	hypothetical prote	192	24	82.8	512	2	T36784	YhBX/YhJW/YiJP/Yjd
120	24	82.8	251	2	T15307	hypothetical prote	193	24	82.8	525	2	F81017	probable adp/atp t
121	24	82.8	264	2	D69497	ABC transporter, p	194	24	82.8	528	2	C71561	probable Dioxigena
122	24	82.8	268	2	AH2122	branched-chain ami	195	24	82.8	530	2	G95386	gene 38 proteina -
123	24	82.8	285	1	S38567	phenylethanolamine	196	24	82.8	541	1	W2BE38	ABC transporter in
124	24	82.8	288	2	E81025	H+-transporting tw	197	24	82.8	553	2	T35451	hypothetical prote
125	24	82.8	300	2	T26245	hypothetical prote	198	24	82.8	558	2	T19748	aspartate-tRNA lig
126	24	82.8	304	2	S39892	rnfD protein - Rho	199	24	82.8	615	2	C97723	DNA-directed DNA p
127	24	82.8	307	2	T18990	hypothetical prote	200	24	82.8	619	2	F75199	hypothetical prote
128	24	82.8	309	2	G70213	hypothetical prote	201	24	82.8	640	2	C72351	methyl-accepting c
129	24	82.8	309	2	AD3594	transporter, dme f	202	24	82.8	643	2	E82481	hypothetical prote
130	24	82.8	314	2	G95869	probable suagr ABC	203	24	82.8	674	2	T73229	serine rich pumili
131	24	82.8	316	2	H95389	phage-related prot	204	24	82.8	681	2	T39076	Alzheimer's diseas
132	24	82.8	339	2	G82596	hypothetical prote	205	24	82.8	695	1	A49795	Alzheimer's diseas
133	24	82.8	340	2	E86724	hypothetical prote	206	24	82.8	695	2	A27485	Alzheimer's diseas
134	24	82.8	343	2	A12470	hypothetical prote	207	24	82.8	695	2	S00550	Alzheimer's diseas
135	24	82.8	345	2	F82400	probable hemin ABC	208	24	82.8	708	2	F70131	single-stranded-DN
136	24	82.8	345	2	S72490	N-acetyl-gamma-glu	209	24	82.8	713	2	T37886	probable serine/th
137	24	82.8	347	2	T07588	fructokinase (EC 2	210	24	82.8	747	2	JH0773	Alzheimer's diseas
138	24	82.8	349	2	T26247	hypothetical prote	211	24	82.8	770	1	QRH074	Alzheimer's diseas
139	24	82.8	352	2	T48903	wax synthase limpo	212	24	82.8	781	2	T20699	hypothetical prote
140	24	82.8	355	2	F72279	conserved hypoteth	213	24	82.8	842	2	T04555	hypothetical prote
141	24	82.8	378	2	B89588	protein R09f10.7 l	214	24	82.8	879	2	A47704	endoglucanase I (E
142	24	82.8	379	2	S27502	hypothetical prote	215	24	82.8	969	2	T02842	probable membrane
143	24	82.8	380	2	F70399	hydrogenase expres	216	24	82.8	993	2	S48436	genome polyprotein
144	24	82.8	380	2	T29248	hypothetical prote	217	24	82.8	1016	2	S30236	hypothetical prote
145	24	82.8	384	2	T44870	acyltransferase ho	218	24	82.8	1055	2	T05663	adenylate cyclase
146	24	82.8	388	2	AG2600	hypothetical prote	219	24	82.8	1090	2	A41541	hypothetical prote
147	24	82.8	388	2	H97382	probable transport	220	24	82.8	1121	2	T25715	hypothetical prote
148	24	82.8	389	2	H82825	transport protein	221	24	82.8	1198	2	T20262	hypothetical prote
149	24	82.8	395	2	T15302	hypothetical prote	222	24	82.8	1203	2	C89217	protein CSA6.2 {1
150	24	82.8	407	2	B70962	hypothetical prote	223	24	82.8	1238	2	S63247	probable membrane
151	24	82.8	409	2	A90479	conserved hypoteth	224	24	82.8	1364	2	T51920	probable xanthine
152	24	82.8	414	2	D86556	glutamate symport	225	24	82.8	1506	2	S52957	bimD protein - Eme
153	24	82.8	414	2	G72068	glutamate symport	226	24	82.8	2643	2	T23149	hypothetical prote
154	24	82.8	419	2	F90322	glycosyltransferas	227	23	79.3	52	2	T07338	hypothetical prote
155	24	82.8	423	2	C81271	probable O-acetyl h	228	23	79.3	67	2	C32534	hypothetical prote
156	24	82.8	423	2	AF3466	trehalose/maltose	229	23	79.3	91	2	S21561	hypothetical prote
157	24	82.8	424	2	B81560	probable inner mem	230	23	79.3	91	2	C69361	hypothetical prote
158	24	82.8	428	2	T48008	hypothetical prote	231	23	79.3	119	2	T16347	hypothetical prote
159	24	82.8	429	2	D64499	glycine hydroxymet	232	23	79.3	129	2	T27436	hypothetical prote
160	24	82.8	441	2	G98126	histidine protein	233	23	79.3	131	2	T32405	hypothetical prote
161	24	82.8	441	2	B95261	probable sensor hi	234	23	79.3	141	2	G95996	conserved hypoteth
162	24	82.8	445	2	T35627	probable integral	235	23	79.3	147	1	S75650	hypothetical prote
163	24	82.8	457	2	E70081	purine-cytosine pe	236	23	79.3	160	2	S35649	vegetative-specific
164	24	82.8	463	2	T70219	conserved hypoteth	237	23	79.3	162	2	S76809	hypothetical prote
165	24	82.8	469	2	T40339	ferredoxin-NADP re	238	23	79.3	171	2	T26451	1S1 ribosomal prot
166	24	82.8	477	2	D84306	sodium- and chlori	239	23	79.3	181	2	D90218	conserved hypoteth
167	24	82.8	479	2	T36715	probable cell divi	240	23	79.3	187	2	A95143	hypothetical prote
168	24	82.8	480	2	AD1932	hypothetical prote	241	23	79.3	187	2	G98010	hypothetical prote
169	24	82.8	488	2	A65344	hypothetical prote	242	23	79.3	194	2	T24491	conserved hypoteth
170	24	82.8	492	2	T22119	hypothetical prote	243	23	79.3	195	2	AG2727	glucose-6-P dehydro
171	24	82.8	494	2	B47691	UDP-N-acetylmuram	244	23	79.3	202	2	G86520	succinate dehydrog
172	24	82.8	495	2	AF1130	transcription regu	245	23	79.3	209	2	E84036	hypothetical prote
173	24	82.8	500	2	B83910	hypothetical prote	246	23	79.3	210	2	AH1854	CDPdiacylglycerol -
174	24	82.8	507	2	S06272	photosystem II chl	247	23	79.3	221	2	C69505	NonF-related prote
175	24	82.8	508	1	QUSP6A	photosystem II chl	248	23	79.3	230	2	AC3083	

249 23 79.3 230 2 B98203 nonF-related prote
 250 23 79.3 231 2 AD6154 T6A9.7 protein - A
 251 23 79.3 232 2 AB3612 multidrug resistan
 252 23 79.3 233 2 AD3612 hypothetical prote
 253 23 79.3 234 2 H95396 sec-independent pr
 254 23 79.3 235 2 H82790 hypothetical prote
 255 23 79.3 236 2 F87454 repB protein - Cam
 256 23 79.3 237 2 S49371 hypothetical prote
 257 23 79.3 238 2 T32339 hypothetical prote
 258 23 79.3 239 2 S73385 hypothetical prote
 259 23 79.3 240 2 D72103 glucose-6-p dehydro
 260 23 79.3 241 2 F90372 conserved hypotet
 261 23 79.3 242 2 B97509 hypothetical prote
 262 23 79.3 243 2 A56641 probable membrane
 263 23 79.3 244 2 G89833 teichoic acid tran
 264 23 79.3 245 2 H64054 site-specific DNA-
 265 23 79.3 246 2 C87208 conserved hypotet
 266 23 79.3 247 2 D95168 membrane protein
 267 23 79.3 248 2 T33218 hypothetical prote
 268 23 79.3 249 2 T41674 probable edoplasmi
 269 23 79.3 250 2 PC4287 protein kinase (EC
 270 23 79.3 251 2 AE0963 probable carbohydr
 271 23 79.3 252 2 A88040 protein F47f6.1 [1
 272 23 79.3 253 2 S73736 MG302 homolog A05
 273 23 79.3 254 2 AB2032 hypothetical prote
 274 23 79.3 255 2 B98034 conserved hypotet
 275 23 79.3 256 2 H71729 hypothetical prote
 276 23 79.3 257 2 D82435 D-3-phosphoglycer
 277 23 79.3 258 2 D88109 protein T24E12.6 [1
 278 23 79.3 259 2 B46678 endoglycosidase F3
 279 23 79.3 260 2 S77441 oligopeptide trans
 280 23 79.3 261 2 S77441 cytochrome-c oxida
 281 23 79.3 262 2 T06516 protein farnesyltr
 282 23 79.3 263 2 B95290 hypothetical prote
 283 23 79.3 264 1 MBBS cell fusion protei
 284 23 79.3 265 2 AC1920 ABC phosphate tran
 285 23 79.3 266 2 A95230 conserved hypotet
 286 23 79.3 267 2 D98094 conserved hypotet
 287 23 79.3 268 2 C71281 conserved hypotet
 288 23 79.3 269 2 G72378 glycerol dehydroge
 289 23 79.3 270 1 W2WU18 E2 protein - human
 290 23 79.3 271 2 AB2423 hypothetical prote
 291 23 79.3 272 2 AH2200 two-component hybr
 292 23 79.3 273 2 T32601 hypothetical prote
 293 23 79.3 274 2 A69253 cyanate transport
 294 23 79.3 275 2 B69325 LPS biosynthesis p
 295 23 79.3 276 2 A03223 transposase, IS285
 296 23 79.3 277 2 AB0193 transposase, IS285
 297 23 79.3 278 2 T14710 probable transposa
 298 23 79.3 279 2 AE0267 transposase, IS285
 299 23 79.3 280 2 A10256 transposase, IS285
 300 23 79.3 281 2 AG0264 transposase, IS285

ALIGNMENTS

RESULT 1
 D64166
 C;Species: Haemophilus influenzae
 C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
 C;Accession: D64166
 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
 ; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
 Science 269, 496-512, 1995
 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A;Reference number: A64000; MUID:95350630; PMID:7542800
 A;Accession: D64166
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA

A;Residues: 1-261 <TIGR>
 A;Cross-references: UNIPROT:P45030; UNIPARC:UPI000013BFA0; GB:U2788; GB:L42023; NID:gi1
 A;Note: Best homolog was a hypothetical protein from Escherichia coli
 C;Superfamily: conserved hypothetical protein H1086

Query Match 100.0%; Score 29; DB 2; Length 261;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 Db 205 KAVFFFA 210

RESULT 2
 T02325
 N;Alternate names: hypothetical protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
 C;Accession: T02325; G84755
 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau
 submitted to the EMBL Data Library, July 1998
 A;Description: Arabidopsis thaliana chromosome II BAC F13p17 genomic sequence.
 A;Reference number: Z14657
 A;Accession: T02325
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-469 <ROU>
 A;Cross-references: UNIPROT:Q8S807; UNIPARC:UPI000009FA17; EMBL:AC004481; NID:G3337347;
 A;Experimental source: cultivar Columbia
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: G84755
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-469 <STO>
 A;Cross-references: UNIPARC:UPI000009FA17; GB:AE002093; NID:G6598404; PIDN:AAC26713.2;
 C;Genetics:
 A;Gene: F13p17.21; At2g34370
 A;Map position: 2

Query Match 100.0%; Score 29; DB 2; Length 469;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 Db 213 KAVFFFA 218

RESULT 3
 A28153
 gelatinase A (EC 3.4.24.24) precursor - human
 N;Alternate names: collagenase type IV; matrix metalloproteinase 2 (MMP2); progelatinas
 C;Species: Homo sapiens (man)
 C;Date: 28-Aug-1989 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
 C;Accession: A28153; A34202; A42225; A60187; S13858; S39436; A31480; S44432; A61498; S5
 R;Collier, I.E.; Wilhelm, S.M.; Eisen, A.Z.; Marner, B.L.; Grant, G.A.; Seltzer, J.L.;
 J. Biol. Chem. 263, 6579-6587, 1988
 A;Title: H-ras oncogene-transformed human bronchial epithelial cells (TBS-1) secrete a
 A;Reference number: A28153; MUID:88198218; PMID:2834383
 A;Accession: A28153
 A;Molecule type: mRNA
 A;Residues: 30-660 <COL>
 A;Cross-references: UNIPROT:P08253; UNIPARC:UPI0000172CE7; GB:J03210; NID:gi180670; PIDN
 R;Huhala, P.; Eddy, R.L.; Fan, Y.S.; Byers, M.G.; Shows, T.B.; Tryggvason, K.
 Genomics 6, 554-559, 1990
 A;Title: Completion of the primary structure of the human type IV collagenase preproen-

C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42496
R;Reponen, P.; Sahlgberg, C.; Huhtala, P.; Hurskainen, T.; Thesleff, I.; Tryggvason, K.
J. Biol. Chem. 267, 7856-7862, 1992
A;Title: Molecular cloning of murine 72-kDa type IV collagenase and its expression during
A;Reference number: A42496; MUID:92218452; PMID:1373140
A;Accession: A42496
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <REP>
A;Cross-references: UNIPROT:P33434; UNIPARC:UPI00002777E; GB:M84324; NID:g198465; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:96943, NCBI:P:96945)
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;233-274/Domain: fibronectin type II repeat homology <2F1>
F;291-332/Domain: fibronectin type II repeat homology <2F8>
F;349-390/Domain: fibronectin type II repeat homology <2F9>
F;465-662/Domain: hemopexin repeat homology <PXN>
F;102,403,407,413/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted
F;404/Active site: Glu #status predicted

Query Match 100.0%; Score 29; DB 2; Length 662;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||
Db 533 KAVFFA 538

RESULT 6
S34780
gelatinase A (EC 3.4.24.24) precursor - rat
N;Alternate names: collagenase type IV
C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S34780; S32525
R;Lovett, D.H.
submitted to the EMBL Data Library, June 1993
A;Reference number: S34780
A;Accession: S34780
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <LOV>
A;Cross-references: UNIPROT:P33436; UNIPARC:UPI000012P240; EMBL:X71466; NID:g311750; PID
F;Marti, H.P.; McNeil, L.; Davies, M.; Martin, J.; Lovett, D.H.
Biochem. J. 291, 441-446, 1993
A;Title: Homology cloning of rat 72 kDa type IV collagenase: cytokine and second-messeng
A;Reference number: S32525; MUID:93249363; PMID:7916617
A;Accession: S32525
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'R', 27-662 <VAR>
A;Cross-references: UNIPARC:UPI0000175D90; EMBL:X71466
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;233-274/Domain: fibronectin type II repeat homology <2F1>
F;291-332/Domain: fibronectin type II repeat homology <2F8>
F;349-390/Domain: fibronectin type II repeat homology <2F9>
F;465-662/Domain: hemopexin repeat homology <PXN>
F;102,403,407,413/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;403,407,413/Binding site: zinc, catalytic (His) (active) #status predicted
F;404/Active site: Glu #status predicted

Query Match 100.0%; Score 29; DB 2; Length 662;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||
Db 533 KAVFFA 538

RESULT 7

S46492

gelatinase A (EC 3.4.24.24) precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S46492

R;Aimes, R.T.; French, D.L.; Quigley, J.P.

Biochem. J. 300, 729-736, 1994

A;Title: Cloning of a 72 kDa matrix metalloproteinase (gelatinase) from chicken embryo

A;Reference number: S46492; MUID:94280397; PMID:8010954

A;Accession: S46492

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-663 <AIM>

A;Cross-references: UNIPROT:Q90611; UNIPARC:UPI000012P23E; EMBL:U07775; NID:g504475; PI

A;Note: in the authors' translation 205-Asp is shown after residue 201 and, consequentl

C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homol

C;Keywords: hydrolase; metalloproteinase; zinc; zymogen

F;67-216,391-443/Domain: matrix metalloproteinase homology #status atypical <MMP>

F;230-271/Domain: fibronectin type II repeat homology <2F1>

F;288-329/Domain: fibronectin type II repeat homology <2F8>

F;346-387/Domain: fibronectin type II repeat homology <2F9>

F;466-663/Domain: hemopexin repeat homology <PXN>

F;99,400,404,410/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status

F;400,404,410/Binding site: zinc, catalytic (His) (active) #status predicted

F;401/Active site: Glu #status predicted

Query Match 100.0%; Score 29; DB 1; Length 663;

Best Local Similarity 100.0%; Pred. No. 44;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||||

Db 534 KAVFFA 539

RESULT 8

I53165

nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004

C;Accession: I53165

R;Karlsen, A.E.; Andersen, H.U.; Vissing, H.; Larsen, P.M.; Fey, S.J.; Cuartero, B.G.;

Diabetes 44, 753-758, 1995

A;Title: Cloning and expression of cytokine-inducible nitric oxide synthase cDNA from r

A;Reference number: I53165; MUID:95309542; PMID:7540573

A;Accession: I53165

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1147 <RES>

A;Cross-references: UNIPROT:Q06518; UNIPARC:UPI00001707E9; EMBL:U26686; NID:g886072; PI

C;Genetics:

A;Gene: NOS2

C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduc

C;Keywords: calmodulin binding; chromoprotein; PAD; flavoprotein; FMN; heme; iron; meta

F;536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>

F;538-674/Domain: flavodoxin homology <FLX>

F;137/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1147;

Best Local Similarity 100.0%; Pred. No. 73;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||||

Db 517 KAVFFA 522

RESULT 9

I56575

nitric-oxide synthase (EC 1.14.13.39) [similarity] - rat

S47647
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-Oct-2004
 C:Accession: I56575
 R:Galea, E.; Reis, D.J.; Feinstein, D.L.
 J. Neurosci. Res. 37, 406-414, 1994
 A:Title: Cloning and expression of inducible nitric oxide synthase from rat astrocytes.
 A:Reference number: I56575; MUID:94231594; PMID:7513765
 A:Accession: I56575
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1147 <RES>
 A:Cross-references: UNIPROT:Q06518; UNIPARC:UPI00001707BD; EMBL:U03699; NID:G430718; PID
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
 F:536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F:538-674/Domain: flavodoxin homology <FLX>
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1147;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 517 KAVFFA 522

RESULT 10
 S38253
 nitric-oxide synthase (EC 1.14.13.39) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
 C:Accession: S38253; JN0457
 R:Adachi, H.; Iida, S.; Oguchi, S.; Ohshima, H.; Suzuki, K.; Kawasaki, H.;
 Eur. J. Biochem. 217, 37-43, 1993
 A:Title: Molecular cloning of a cDNA encoding an inducible calmodulin-dependent nitric-o
 A:Reference number: S38253; MUID:94039059; PMID:7693462
 A:Accession: S38253
 A:Molecule type: mRNA
 A:Residues: 1-1147 <ADA>
 A:Cross-references: UNIPROT:Q06518; UNIPARC:UPI0000170A6C; GB:D12520; NID:G391858; PIDN:
 A:Experimental source: liver
 R:Wood, E.R.; Berger Jr., H.; Sherman, P.A.; Lapetina, E.G.
 Biochem. Biophys. Res. Commun. 191, 767-774, 1993
 A:Title: Hepatocytes and macrophages express an identical cytokine inducible nitric oxid
 A:Reference number: JN0457; MUID:93221515; PMID:7682072
 A:Accession: JN0457
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-41, 'SS', 44-103, 105-190, 'Q', 192-213, 'R', 215-247, 'T', 249-263, 'I', 265-373, 'H
 'S', 896-1000, 'IG', 1003-1015, 'RR', 1018-1026, 'EQ', 1029-1147 <WOO>
 A:Cross-references: UNIPARC:UPI000017223C; PIDN:AAB26037.1
 A:Experimental source: liver
 C:Genetics:
 A:Gene: NOS
 C:Function:
 A:Description: catalyzes the oxidation of an L-arginine guanidino nitrogen and of NADPH
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
 F:536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F:538-674/Domain: flavodoxin homology <FLX>
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1147;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 517 KAVFFA 522

RESULT 11

S47647
 nitric-oxide synthase (EC 1.14.13.39) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-Oct-2004
 C:Accession: S47647; JCI1472
 R:Geng, Y.; Almqvist, M.; Hansson, G.K.
 Biochim. Biophys. Acta 1218, 421-424, 1994
 A:Title: cDNA cloning and expression of inducible nitric oxide synthase from rat vascula
 A:Reference number: S47647; MUID:94325351; PMID:7519448
 A:Accession: S47647
 A:Molecule type: mRNA
 A:Residues: 1-1147 <GEN>
 A:Cross-references: UNIPROT:Q06518; UNIPARC:UPI0000170BE9; EMBL:X76881; NID:G439283; PID
 R:Nunokawa, Y.; Iehida, N.; Tanaka, S.
 Biochem. Biophys. Res. Commun. 191, 89-94, 1993
 A:Title: Cloning of inducible nitric oxide synthase in rat vascular smooth muscle cells.
 A:Reference number: JCI1472; MUID:93191721; PMID:7680561
 A:Accession: JCI1472
 A:Molecule type: DNA
 A:Residues: 1-71, 'Y', 73-347, 'PV', 350-678, 'VP', 681-720, 'L', 722-739, 'L', 741-843, 'G', 845-10
 A:Cross-references: UNIPARC:UPI0000170BA7; DDBJ:D14051; NID:G286260; PIDN:BAA03138.1; PI
 A:Experimental source: vascular smooth muscle
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
 F:536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F:538-674/Domain: flavodoxin homology <FLX>
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 1; Length 1147;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 517 KAVFFA 522

RESULT 12
 JC5029
 nitric-oxide synthase (EC 1.14.13.39) U - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
 C:Accession: JC5029
 R:Ishutsumshita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, I
 Biol. Pharm. Bull. 19, 1374-1376, 1996
 A:Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and
 A:Reference number: JC5027; MUID:97070590; PMID:8913516
 A:Accession: JC5029
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1147 <TSU>
 A:Cross-references: UNIPROT:Q9R0M4; UNIPARC:UPI0000017526E
 A:Experimental source: uterus
 C:Comment: This protein synthesizes nitric oxide from L-arginine.
 C:Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
 C:Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; meta
 F:536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
 F:538-674/Domain: flavodoxin homology <FLX>
 F:197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 2; Length 1147;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 517 KAVFFA 522

RESULT 13
 JC5028
 nitric-oxide synthase (EC 1.14.13.39) L - rat
 C:Species: Rattus norvegicus (Norway rat)

C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5028
R;Tautsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M
Biol. Pharm. Bull. 19, 1374-1376, 1996
A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u
A;Reference number: JC5027; MUID:97070590; PMID:8913516
A;Accession: JC5028
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1147 <TSU>
A;Cross-references: UNIPROT:Q9R0W4; UNIPARC:UPI0000017526D
A;Experimental source: lung
C;Comment: This protein synthesizes nitric oxide from L-arginine.
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
F;536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;538-674/Domain: flavodoxin homology <FLX>
F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
|||
DB 517 KAVFFFA 522

RESULT 14
JC5027
nitric-oxide synthase (RC 1.14.13.39) K - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1997 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: JC5027
R;Tautsumishita, Y.; Kawai, Y.; Takahara, H.; Onda, T.; Miyoshi, J.; Futaki, S.; Niwa, M
Biol. Pharm. Bull. 19, 1374-1376, 1996
A;Title: Sequence analysis of inducible nitric oxide synthase in rat kidney, lung, and u
A;Reference number: JC5027; MUID:97070590; PMID:8913516
A;Accession: JC5027
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1147 <TSU>
A;Cross-references: UNIPROT:Q06518; UNIPARC:UPI0000170A6D; DBJ:D83661; NID:g1209382; PI
A;Experimental source: kidney
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; metal
F;191-199/Domain: heme-binding #status predicted <HMB>
F;536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;538-674/Domain: flavodoxin homology <FLX>
F;620-647/Domain: FMN binding #status predicted <FMN>
F;764-775/Domain: FAD binding #status predicted <FAD>
F;975-993/Domain: NADPH binding #status predicted <NDP>
F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
|||
DB 517 KAVFFFA 522

RESULT 15
S65440
nitric-oxide synthase (RC 1.14.13.39) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S65440
R;Iwashina, M.; Hirata, Y.; Inai, T.; Sato, K.; Marumo, F.
Eur. J. Biochem. 237, 668-673, 1996
A;Title: Molecular cloning of endothelial, inducible nitric oxide synthase gene from rat
A;Reference number: S65440; MUID:96235231; PMID:8647111

A;Accession: S65440
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1147 <IWA>
C;Cross-references: UNIPROT:Q9R0W4; UNIPARC:UPI0000017526F
C;Superfamily: nitric-oxide synthase; flavodoxin homology; NADPH-ferrihemoprotein reduct
C;Keywords: calmodulin binding; chromoprotein; FAD; flavoprotein; FMN; heme; iron; meta
F;506-535/Region: calmodulin binding
F;536-1124/Domain: NADPH-ferrihemoprotein reductase homology <FEH>
F;538-674/Domain: flavodoxin homology <FLX>
F;599-618/Region: biopterin binding
F;620-647/Region: FMN binding #status predicted
F;764-775/Region: FAD binding #status predicted
F;901-910/Region: FAD binding #status predicted
F;975-993/Region: NADPH binding #status predicted
F;1074-1087/Region: NADPH binding #status predicted
F;197/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 100.0%; Score 29; DB 2; Length 1147;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
|||
DB 517 KAVFFFA 522

RESULT 16
AF2630
hypothetical protein Atu0441 [imported] - Agrobacterium tumefaciens (strain C58, Dupont
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2630
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erge, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2630
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <KUR>
A;Cross-references: UNIPROT:Q8UI59; UNIPARC:UPI00000D17ED; GB:AE008688; PIDN:AAL41460.1
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0441
A;Map position: circular chromosome

Query Match 96.6%; Score 28; DB 2; Length 169;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
|||
DB 114 KAIFFA 119

RESULT 17
T20734
hypothetical protein M79.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20734; T23833
R;Harris, B.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z19316
A;Accession: T20734
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-283 <WIL>

A;Cross-references: UNIPROT:Q19334; UNIPARC:UPI000007F46F; EMBL:Z50857; PIDN:CAA90720.1;
A;Experimental source: clone F1A1
R:Mortimore, B.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z19805
A;Accession: T23833
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-283 <W12>
A;Cross-references: UNIPARC:UPI000007F46F; EMBL:Z50806; PIDN:CAA90692.1; GSPDB:GN000028;
A;Experimental source: clone M79
C;Genetics:
A;Gene: CBSP:M79.2
A;Map position: X
A;Intron: 42/3; 71/2; 108/3; 126/3; 167/2; 196/3
C;Superfamily: Caenorhabditis elegans hypothetical protein M79.2
Query Match 96.6%; Score 28; DB 2; Length 283;
Best Local Similarity 83.3%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
||:||||
Db 157 KAIFFA 162
RESULT 18
B44358
cysteine-rich protein hCRP homolog - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: B44358
R;Sadler, I.; Crawford, A.W.; Michelsen, J.W.; Beckerle, M.C.
J. Cell Biol. 119, 1573-1587, 1992
A;Title: Zyxin and cCRP: two interactive LIM domain proteins associated with the cytoske
A;Reference number: A44358; MUID:93107157; PMID:1469049
A;Accession: B44358
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-58 <SAD>
A;Cross-references: UNIPROT:P32965; UNIPARC:UPI00001799A8
A;Note: sequence extracted from NCBI backbone (NCBIP:121176)
C;Superfamily: cysteine and glycine-rich protein; LIM metal-binding repeat homology
F;9-58/Domain: LIM metal-binding repeat homology (fragment) <LIM>
Query Match 89.7%; Score 26; DB 2; Length 58;
Best Local Similarity 83.3%; Pred. No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
||:||||
Db 14 KAVYFA 19
RESULT 19
S27597
hypothetical protein - Nostoc sp.
C;Species: Nostoc sp.
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S27597
R;Walton, D.K.; Gendel, S.M.; Atherly, A.G.
submitted to the EMBL Data Library, February 1992
A;Reference number: S27596
A;Accession: S27597
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-150 <WAL>
A;Cross-references: UNIPROT:Q51314; UNIPARC:UPI00000B0C14; EMBL:M81381; NID:g150381; PID

QY 1 KAVFFA 6
||:||||
Db 36 KALFFA 41
RESULT 20
F69857
conserved hypothetical protein ykna - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C;Accession: F69857
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Asevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Hoisappel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowaka, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: F69857
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-156 <KUN>
A;Cross-references: UNIPROT:O34598; UNIPARC:UPI00000602B4; GB:Z99110; GB:AL009126; NID:g
C;Genetics:
A;Experimental source: strain 168
C;Gene: ykna
C;Superfamily: deaminase
Query Match 89.7%; Score 26; DB 1; Length 156;
Best Local Similarity 83.3%; Pred. No. 61;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
||:||||
Db 96 KAVYFA 101
RESULT 21
D71049
probable L(+)-tartarate dehydratase - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Oct-2004
C;Accession: D71049
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71049
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-166 <KAW>
A;Cross-references: UNIPROT:O59317; UNIPARC:UPI00000668B7; GB:AF000006; NID:g3236133; P
A;Experimental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Gene: PH1684
C;Superfamily: iron-dependent tartrate dehydratase beta chain
F;14-165/Domain: iron-dependent tartrate dehydratase beta chain homology <TTDB>
Query Match 89.7%; Score 26; DB 2; Length 166;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||:|
 Db 107 KAVYFA 112

RESULT 22

E70445

C-terminal fumarate hydratase, class I - Aquifex aeolicus

C/Species: Aquifex aeolicus

C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C/Accession: E70445

R/Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ory, V.

A/Title: Nature 392, 353-358, 1998

A/Reference number: A70300; MUID:98196666; PMID:9537320

A/Accession: E70445

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-185 <AQF>

A/Cross-references: UNIPROT:O67590; UNIPARC:UPI00000566AD; GB:AE000750; NID:G2983999; PMID:9537320

A/Experimental source: strain VF5

C/Genetics:

A/Gene: funx

C/Superfamily: iron-dependent tartrate dehydratase beta chain; iron-dependent tartrate dehydratase beta chain homology <TTDB>

F/13-175/Domain: iron-dependent tartrate dehydratase beta chain homology <TTDB>

Query Match 89.7%; Score 26; DB 2; Length 185;

Best Local Similarity 83.3%; Pred. No. 71;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||:|

Db 117 KAVYFA 122

RESULT 23

A49648

cysteine-rich protein - chicken

N/Alternate names: zyxin-binding protein

C/Species: Gallus gallus (chicken)

C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 05-Oct-2004

C/Accession: A49648; S34179

R/Crawford, A.W.; Pino, J.D.; Beckerle, M.C.

J. Cell Biol. 124, 117-127, 1994

A/Title: Biochemical and molecular characterization of the chicken cysteine-rich protein

A/Reference number: A49648; MUID:94124603; PMID:8294495

A/Accession: A49648

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-192 <CRA>

A/Cross-references: UNIPROT:P32965; UNIPARC:UPI00001711EC; EMBL:X73831; NID:G313286; PMID:8294495

C/Superfamily: cysteine and glycine-rich protein; LIM metal-binding repeat homology

F/10-61/Domain: LIM metal-binding repeat homology <LIM1>

F/118-169/Domain: LIM metal-binding repeat homology <LIM2>

Query Match 89.7%; Score 26; DB 2; Length 192;

Best Local Similarity 83.3%; Pred. No. 73;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||:|

Db 15 KAVYFA 20

RESULT 24

S38879

LIM-domain protein CRP1 - Japanese quail

C/Species: Coturnix coturnix japonica (Japanese quail)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Oct-2004

C/Accession: S38879

R/Weiskirchen, R.; Beckerle, M.C.; Biester, K.

submitted to the EMBL Data Library, November 1993

A/Description: The CRP family of LIM-domain proteins: identification of two different

A/Reference number: S38879

A/Accession: S38879

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-192 <WEI>

A/Cross-references: UNIPROT:P32965; UNIPARC:UPI00001711EC; EMBL:Z28333; NID:G429159; PMID:8294495

C/Superfamily: cysteine and glycine-rich protein; LIM metal-binding repeat homology

F/10-61/Domain: LIM metal-binding repeat homology <LIM1>

F/118-169/Domain: LIM metal-binding repeat homology <LIM2>

Query Match 89.7%; Score 26; DB 2; Length 192;

Best Local Similarity 83.3%; Pred. No. 73;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||:|

Db 15 KAVYFA 20

RESULT 25

E75252

molybdopterin biosynthesis protein D/E DR2607 [similarity] - Deinococcus radiodurans

N/Alternate names: moaD-moaE fusion protein; molybdopterin-converting factor

C/Species: Deinococcus radiodurans

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004

C/Accession: E75252

R/White, O.; Eisen, J.A.; Heideberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.

Science 286, 1571-1577, 1999

A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A/Reference number: A75250; MUID:20036896; PMID:10567266

A/Accession: E75252

A/Molecule type: DNA

A/Residues: 1-229 <WHI>

A/Cross-references: UNIPROT:Q9RR88; UNIPARC:UPI0000033FEF; GB:AE002090; GB:AE000513; NID:G2983999

A/Experimental source: strain R1

C/Genetics:

A/Gene: DR2607

A/Map position: 1

C/Superfamily: Molybdopterin biosynthesis protein D/E

C/Keywords: molybdopterin biosynthesis

Query Match 89.7%; Score 26; DB 2; Length 229;

Best Local Similarity 83.3%; Pred. No. 86;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||:|

Db 4 KAVYFA 9

RESULT 26

T16110

hypothetical protein F20D12.5 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C/Accession: T16110

R/Wu, X.

submitted to the EMBL Data Library, November 1995

A/Description: The sequence of C. elegans cosmid F20D12.

A/Reference number: Z18462

A/Accession: T16110

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-244 <WUX>

A/Cross-references: UNIPARC:UPI000017B915; EMBL:U40933; NID:G1072142; PID:G1072144; PMID:8294495

C/Genetics:

A/Gene: CESP:F20D12.5

A/Introns: 14/1; 47/3; 84/3; 118/1; 203/3

Fri Dec 30 10:25:19 2005

```

Query Match      89.7%; Score 26; DB 2; Length 244;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
      |||||
Db      9 KAVFFA 14

RESULT 27
T01119
Hypothetical protein At2g32880 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T21L14.18
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01119; F84738
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, December 1997
A:Description: Arabidopsis thaliana chromosome II BAC T21L14 genomic sequence.
A:Reference number: Z14209
A:Accession: T01119
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-285 <R0U>
A:Cross-references: UNIPROT:Q48777; UNIPARC:UPI000099E1EC; EMBL:AC003033; NID:g2702261;
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: F84738
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-285 <STO>
A:Cross-references: UNIPARC:UPI000099E1EC; GB:AE002093; NID:g2702282; PIDN:AAB91985.1; C
C:Genetics:
A:Gene: T21L14.18; At2g32880
A:Map position: 2; 105/1; 206/2
A:Introns: 11/1; 54/2;
C:Superfamily: Arabidopsis thaliana hypothetical protein A_TW018A10.12

Query Match      89.7%; Score 26; DB 2; Length 285;
Best Local Similarity 83.3%; Pred. No. 11e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
      |||||
Db     137 KAVFFA 142

RESULT 28
ZBBE13
33.1K zinc-binding protein - ictalurid herpesvirus 1 (strain auburn 1)
C:Species: ictalurid herpesvirus 1
A:Note: host ictalurid punctatus (channel catfish)
C:Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: D36787
R:Davidson, A.J.
submitted to GenBank, January 1992
A:Description: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A36804
A:Accession: D36787
A:Molecule type: DNA
A:Residues: 1-299 <DAV>
A:Cross-references: UNIPROT:Q00165; UNIPARC:UPI00001384D1; GB:M75136; NID:g331209; PIDN:
R:Davidson, A.J.
Virology 186, 9-14, 1992
A:Title: Channel catfish virus: a new type of herpesvirus.
A:Reference number: A39447; MUID:92087490; PMID:1727613
A:Contents: annotation
A:Note: neither amino acid nor nucleotide sequence is given

```

```

C:Genetics:
A:Gene: 12
C:Superfamily: ictalurid herpesvirus 33.1K zinc binding protein
C:Keywords: zinc finger

Query Match      89.7%; Score 26; DB 1; Length 299;
Best Local Similarity 83.3%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
      |||||
Db      39 RAVFFA 44

RESULT 29
S40819
Probable transport protein yihN - Escherichia coli (strain K-12)
N:Alternate names: hypothetical protein o421
C:Species: Escherichia coli
C:Date: 19-May-1994 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S40819; E65192
R:Plunkett III, G.; Burland, V.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 21, 3391-3398, 1993
A:Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region from 8
A:Reference number: S40802; MUID:93347969; PMID:8346018
A:Accession: S40819
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-421 <PLU>
A:Cross-references: UNIPROT:P32135; UNIPARC:UPI000003EB31; EMBL:L19201; NID:g304961; PID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: E65192
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-421 <BLAT>
A:Cross-references: UNIPARC:UPI000003EB31; GB:AE0000463; GB:U00096; NID:g2367320; PIDN:A
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yihN
C:Superfamily: Escherichia coli probable transport protein yqce
C:Keywords: transmembrane protein; transport protein

Query Match      89.7%; Score 26; DB 2; Length 421;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
      |||||
Db     332 RAVFFA 337

RESULT 30
C86075
probable resistance protein (transport) yihN [imported] - Escherichia coli (strain O157
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: C86075
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: C86075
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-421 <STO>
A:Cross-references: UNIPROT:Q8X8F3; UNIPARC:UPI000000D75F3; GB:AE005174; NID:g12518756;
A:Experimental source: strain O157:H7, substrain EDL933

```

C;Genetics:
A;Gene: yibN
C;Superfamily: Escherichia coli probable transport protein yqcE

Query Match 89.7%; Score 26; DB 2; Length 421;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPFA 6
:|||||

Db 332 KAVPFA 337

RESULT 31

D91228
Probable resistance protein [imported] - Escherichia coli (strain O157:H7, substrain RIM

C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: D91228
R;Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gaekara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: D91228

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-421 <HAY>

A;Cross-references: UNIPROT:Q8X8F3; UNIPARC:UPI00000D75F3; GB:BA000007; PIDN:BA38219.1;

A;Experimental source: strain O157:H7, substrain RIMD 050952

C;Genetics:

A;Gene: EC64796

C;Superfamily: Escherichia coli probable transport protein yqcE

Query Match 89.7%; Score 26; DB 2; Length 421;
Best Local Similarity 83.3%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPFA 6
:|||||

Db 332 KAVPFA 337

RESULT 32

AH1799
GTPase homolog lin2943 [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AH1799
R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AH1799

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-457 <GLA>

A;Cross-references: UNIPROT:Q926U7; UNIPARC:UPI000013744F; GB:AL592022; PIDN:CAC98168.1;

A;Experimental source: strain Clip11262
C;Genetics:

A;Gene: lin2943

C;Superfamily: thiophen / furan oxidation protein; translation elongation factor Tu homolog

Query Match 89.7%; Score 26; DB 2; Length 457;
Best Local Similarity 83.3%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPFA 6
:|||||

Db 374 KALFFA 379

RESULT 33

VCXFTI

major capsid protein - Tipula iridescent virus (type 1)
C;Species: Tipula iridescent virus

A;Note: host Tipula paludosa (European crane fly)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C;Accession: A33558

R;Tajbakhsh, S.; Lee, P.B.; Watson, D.C.; Seligy, V.L.

J. Virol. 64, 125-136, 1990

A;Title: Molecular cloning, characterization, and expression of the Tipula iridescent v

A;Reference number: A33558; MUID:90080113; PMID:2293661

A;Accession: A33558

A;Molecule type: DNA

A;Residues: 1-464 <PAJ>

A;Cross-references: UNIPROT:PI8162; UNIPARC:UPI0000127D5B; EMBL:M33542; NID:G331317; PI

C;Superfamily: Tipula iridescent virus major capsid protein

C;Keywords: capsid protein

Query Match 89.7%; Score 26; DB 1; Length 464;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPFA 6
:|||||

Db 302 KALFFA 307

RESULT 34

JQ2215

major capsid protein - Chilo iridescent virus

C;Species: Chilo iridescent virus

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: JQ2215

R;Stohwasser, R.; Raab, K.; Schnitzler, P.; Janssen, W.; Darai, G.

J. Gen. Virol. 74, 873-879, 1993

A;Title: Identification of the gene encoding the major capsid protein of insect iridesc

A;Reference number: JQ2215; MUID:93260401; PMID:8492091

A;Accession: JQ2215

A;Molecule type: DNA

A;Residues: 1-467 <STO>

A;Cross-references: UNIPROT:Q05815; UNIPARC:UPI00001749ED; GB:M99395; NID:G292992; PIDN

A;Note: the authors translated codon GTT for residue 231 as Tyr, codon TAT for residue

C;Superfamily: Tipula iridescent virus major capsid protein

C;Keywords: capsid protein

Query Match 89.7%; Score 26; DB 1; Length 467;

Best Local Similarity 83.3%; Pred. No. 1.7e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPFA 6
:|||||

Db 306 KALFFA 311

RESULT 35

VCXFSI

major capsid protein - Simulium iridescent virus (type 22)

C;Species: Simulium iridescent virus

A;Note: host Simulium spp. (blackfly)

C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C;Accession: B37075

A;Molecule type: DNA

A;Residues: 1-472 <CAM>

A;Cross-references: UNIPROT:P22166; UNIPARC:UPI0000127D5D; EMBL:M32799; NID:G331321; PI

A;Accession: B37075

A;Molecule type: DNA

A;Residues: 1-472 <CAM>

A;Cross-references: UNIPROT:P22166; UNIPARC:UPI0000127D5D; EMBL:M32799; NID:G331321; PI

A;Accession: B37075

A;Molecule type: DNA

A;Residues: 1-472 <CAM>

A;Cross-references: UNIPROT:P22166; UNIPARC:UPI0000127D5D; EMBL:M32799; NID:G331321; PI

A;Accession: B37075

A;Molecule type: protein
A;Residues: 72-81;89-116 <CA2>
A;Cross-references: UNIPARC:UPI00001749EB; UNIPARC:UPI00001749EC
C;Species: Rhodobacter sphaeroides
C;Superfamily: Tipula iridescent virus major capsid protein
C;Keywords: capsid protein

Query Match 89.7%; Score 26; DB 1; Length 472;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||:|
DB 302 KALFFA 307

RESULT 36
T50726
hypothetical protein 479 [imported] - Rhodobacter sphaeroides
C;Species: Rhodobacter sphaeroides
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50726
R;Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A;Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2
A;Reference number: Z25222; MUID:20115911; PMID:10648776
A;Accession: T50726
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-479 <CHO>
A;Cross-references: UNIPROT:Q9RFP8; UNIPARC:UPI00000B2P99; EMBL:AF195122; PIDN:AAF24270.
A;Experimental source: strain 2.4.1

Query Match 89.7%; Score 26; DB 2; Length 479;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||:|
DB 349 KAMFFA 354

RESULT 37
AB0805
3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) - Salmonella enterica subsp. enterica sero
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0805
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moutle, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0805
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-715 <PAR>
A;Cross-references: UNIPARC:UPI0000059B21; GB:AL513382; PIDN:CAD07620.1; PID:g16503611;
C;Genetics:
C;Keywords: oxidoreductase

Query Match 89.7%; Score 26; DB 2; Length 715;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||:|
DB 286 RAVFFA 291

RESULT 38
B54962
sterol regulatory element binding protein 2 precursor - Chinese hamster
C;Species: Cricetus griseus (Chinese hamster)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: B54962
R;Yang, J.; Sato, R.; Goldstein, J.L.; Brown, M.S.
Genes Dev. 8, 1910-1919, 1994
A;Title: Sterol-resistant transcription in CHO cells caused by gene rearrangement that t
A;Reference number: A54962; MUID:95047343; PMID:7958866
A;Accession: B54962
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1139 <YAN>
A;Cross-references: UNIPROT:Q60429; UNIPARC:UPI0000178926; GB:U12330
A;Note: 493 Ser was also found
C;Superfamily: sterol regulatory element binding protein
C;Keywords: DNA binding; membrane protein

Query Match 89.7%; Score 26; DB 2; Length 1139;
Best Local Similarity 83.3%; Pred. No. 3.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||:|
DB 916 KAVFFA 921

RESULT 39
S62506
alpha-glucan synthase (EC 2.4.1.-) mok11 - fission yeast (Schizosaccharomyces pombe) (fr
N;Alternate names: morphological/kinase-inhibitor supersensitive protein mok11
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: T38290; T43430; S62506
R;Niblett, D.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z21783
A;Accession: T38290
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1204 <NT2>
A;Cross-references: UNIPROT:Q09854; UNIPARC:UPI000016208E; EMBL:Z64354; NID:g10393338; P
R;Katayama, S.; Toda, T.
submitted to the EMBL Data Library, October 1998
A;Description: Fission yeast alpha-glucan synthase Mok1 localizes closely with actin an
A;Reference number: Z22509
A;Accession: T43430
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1204 <KAT>
A;Cross-references: UNIPARC:UPI000016208E; EMBL:AB018380; PIDN:BAA76557.1
A;Experimental source: strain h- 972
C;Genetics:
A;Gene: mok11
A;Map position: 1R
C;Function:
A;Description: involved in cell morphogenesis interdependently of the actin cytoskeleton
C;Keywords: glycosyltransferase; hexosyltransferase; transmembrane protein

Query Match 89.7%; Score 26; DB 2; Length 1204;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||:|
DB 120 KAVFFA 125

RESULT 40
T09127
probable erythrocyte-binding protein MAEBL - Plasmodium yoelii

C;Species: Plasmodium yoelii
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T09127
 R;Kapke, S.H.I.; Noe, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
 Proc. Natl. Acad. Sci. U.S.A. 95, 1230-1235, 1998
 A;Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
 A;Reference number: 216577; MUID:98115903; PMID:9448314
 A;Accession: T09127
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1701 <KAP>
 A;Cross-references: UNIPROT:O61164; UNIPARC:UPI000007D433; EMBL:AF031886; NID:G2947227;
 A;Introns: 62/1; 1648/1; 1674/2; 1697/1
 A;Gene: mabbl
 C;Keywords: alternative splicing; cell binding; erythrocyte invasion

Query Match 89.7%; Score 26; DB 2; Length 1701;
 Best Local Similarity 83.3%; Pred. No. 5.5e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 1648 KAVYFA 1653

RESULT 41

AG2447
 hypothetical protein alr5135 [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C;Accession: AG2447
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
 DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AG2447
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-100 <KUR>
 A;Cross-references: UNIPROT:Q8YM06; UNIPARC:UPI00000CED8A; GB:BA000019; PIDN:BA076834.1;
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: alr5135

Query Match 86.2%; Score 25; DB 2; Length 100;
 Best Local Similarity 100.0%; Pred. No. 70;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
 |||||
 DB 37 KAVFF 41

RESULT 42

Q05ACC
 hypothetical protein C-120 - Staphylococcus aureus plasmid pC194
 C;Species: Staphylococcus aureus
 C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
 C;Accession: A04490
 R;Horinouchi, S.; Weisblum, B.
 J. Bacteriol. 150, 815-825, 1982
 A;Title: Nucleotide sequence and functional map of pC194, a plasmid that specifies inducible beta-lactamase
 A;Reference number: A91791; MUID:82167188; PMID:6950931
 A;Accession: A04490
 A;Molecule type: DNA
 A;Residues: 1-120 <HOR>
 A;Cross-references: UNIPROT:P03861; UNIPARC:UPI000013BD18
 C;Genetics:
 A;Genome: plasmid

C;Superfamily: Staphylococcus aureus plasmid pC194 hypothetical 14.6K protein
 Query Match 86.2%; Score 25; DB 1; Length 120;
 Best Local Similarity 83.3%; Pred. No. 83;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 62 KATFFA 67

RESULT 43

I40566
 hypothetical protein 5.60 - Bacillus subtilis plasmid pTA1060
 C;Species: Bacillus subtilis
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
 C;Accession: I40566
 R;Meijer, W.J.; Venema, G.; Bron, S.
 Nucleic Acids Res. 23, 612-619, 1995
 A;Title: Characterization of single strand origins of cryptic rolling-circle plasmids
 A;Reference number: I40549; MUID:95206941; PMID:7899081
 A;Accession: I40566
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-132 <RES>
 A;Cross-references: UNIPROT:Q45455; UNIPARC:UPI00000B6E18; EMBL:U32380; NID:GI049123; P
 A;Experimental source: plasmid pTA1060
 C;Genetics:
 A;Genome: plasmid

Query Match 86.2%; Score 25; DB 2; Length 132;
 Best Local Similarity 83.3%; Pred. No. 90;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 94 KGVFFA 99

RESULT 44

WMR219
 19K globulin precursor - rice
 N;Alternate names: alpha-globulin
 C;Species: Oryza sativa (rice)
 C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2004
 C;Accession: S20024; S25735; PNO497
 R;Shorrosh, B.S.; Wen, L.; Zen, K.C.; Huang, J.K.; Pan, J.S.; Hermodson, M.A.; Tanaka, K.
 Plant Mol. Biol. 18, 151-154, 1992
 A;Title: A novel cereal storage protein: molecular genetics of the 19 kDa globulin of rice
 A;Reference number: S20024; MUID:92119226; PMID:1731968
 A;Accession: S20024
 A;Molecule type: mRNA
 A;Residues: 1-186 <SHO>
 A;Cross-references: UNIPROT:P29835; UNIPARC:UPI000012B4D1; EMBL:X63990; NID:G20158; PID
 A;Accession: S25735
 A;Molecule type: protein
 A;Residues: 66-74;108-133;171-186 <SH2>
 A;Cross-references: UNIPARC:UPI0000173296; UNIPARC:UPI0000173297; UNIPARC:UPI0000173298
 R;Kishan, H.B.; Pueppke, S.G.
 Biochem. Biophys. Res. Commun. 193, 460-466, 1993
 A;Title: Nucleotide sequence of an abundant rice seed globulin: homology with the high molecular weight seed storage protein
 A;Reference number: PNO497; MUID:93277591; PMID:8503935
 A;Accession: PNO497
 A;Molecule type: mRNA
 A;Residues: 6-186 <KRI>
 A;Cross-references: UNIPARC:UPI0000173299; GB:L12252
 A;Experimental source: seed
 C;Superfamily: Alpha amylase inhibitor
 C;Keywords: storage protein
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-186/Product: 19K globulin #status predicted <MAT>

Query Match 86.2%; Score 25; DB 1; Length 186;
 Best Local Similarity 83.3%; Pred. No. 90;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 94 KGVFFA 99

Best Local Similarity 83.3%; Pred. No. 1.2e+02; Mismatches 5; Conservative 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| ||||
DB 4 KVVFFA 9

RESULT 45
JC4784
alpha-globulin precursor - rice
C:Species: Oryza sativa (rice)
C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 31-Dec-2004
R;Accession: JC4784
R;Nakase, M.; Hotta, H.; Adachi, T.; Aoki, N.; Nakamura, R.; Masumura, T.; Tanaka, K.; M
Gene 170, 223-226, 1996
A>Title: Cloning of the rice seed alpha-globulin-encoding gene: Sequence similarity of t
A;Reference number: JC4784; MUID:96235139; PMID:8666249
A;Accession: JC4784
A;Molecule type: DNA
A;Residues: 1-186 <NAK>
A;Cross-references: UNIPROT:P93414; UNIPARC:UPI00000A4C3C; DDBJ:D50643; NID:g840704; PID
A;Experimental source: seed
C;Genetics:
A;Gene: Glb
C;Superfamily: Alpha amylase inhibitor
C;Keywords: globulin; seed
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-186/Product: alpha-globulin #status predicted <MAT>

Query Match 86.2%; Score 25; DB 2; Length 186;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
| ||||
DB 4 KVVFFA 9

RESULT 46
H64441
hypothetical protein MJ1137 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: H64441
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; M
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: H64441
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-191 <BUL>
A;Cross-references: UNIPROT:Q58537; UNIPARC:UPI0000065085; GB:U67556; GB:L77117; NID:g15
C;Genetics:
A;Map position: REV1078609-1078034
A;Start codon: TTG

Query Match 86.2%; Score 25; DB 2; Length 191;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
| ||||
DB 89 KAVFF 93

RESULT 47
B64668

A:Molecule type: DNA
A:Residues: 1-210 <TET>
A:Cross-references: UNIPROT:Q9K184; UNIPARC:UPI000000C4451; GB:AE002385; GB:AE002098; NID
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0283

Query Match 86.2%; Score 25; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||
Db 116 KAVFF 120

RESULT 50

G81793

hypothetical protein NMA2204 [imported] - Neisseria meningitidis (strain Z2491 serogroup
C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: G81793

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A:Reference number: A81775; MUID:2022556; PMID:10761919

A:Accession: G81793

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-210 <PAR>

A:Cross-references: UNIPROT:Q9JSP2; UNIPARC:UPI000000C4D6C; GB:AL162758; GB:AL157959; NID

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: NMA2204

Query Match 86.2%; Score 25; DB 2; Length 210;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

|||
Db 116 KAVFF 120

RESULT 51

AB3270

threonine efflux protein [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C;Accession: AB3270

R;DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujex, C.; Los, T.; Ivanova,
; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A:Reference number: AD3252; PMID:1175668

A:Accession: AB3270

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-212 <KUR>

A:Cross-references: UNIPROT:Q9L6H7; UNIPARC:UPI0000057B7C; GB:AE008917; PIDN:ANL51325.1;

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI0143

A:Map position: I

Query Match

Best Local Similarity 86.2%; Score 25; DB 2; Length 212;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

|||
Db 131 KAVFF 135

RESULT 52

F69125

conserved hypothetical protein MTH209 - Methanobacterium thermoautotrophicum (strain De
C;Species: Methanobacterium thermoautotrophicum

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: F69125

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniele, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func

A:Reference number: A69000; MUID:98037514; PMID:9371463

A:Accession: F69125

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-226 <MTH>

A:Cross-references: UNIPROT:Q26311; UNIPARC:UPI0000066675; GB:AE000808; GB:AE000666; NID

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH209

C;Superfamily: hypothetical protein MJ1437

Query Match

Best Local Similarity 86.2%; Score 25; DB 2; Length 226;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

|||
Db 3 KAVFF 7

RESULT 53

A71847

carbonic anhydrase - Helicobacter pylori (strain J99)

C;Species: Helicobacter pylori

A:Variety: strain J99

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Accession: A71847

R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.

; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric pat

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: A71847

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-247 <ARN>

A:Cross-references: UNIPROT:Q9ZK30; UNIPARC:UPI000000D36F4; GB:AE001539; GB:AE001439; NID

A:Experimental source: strain J99

C:Genetics:

A:Gene: jhp112

C;Superfamily: carbonate dehydratase; carbonic anhydrase homology

Query Match

Best Local Similarity 86.2%; Score 25; DB 2; Length 247;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

|||
Db 78 KAVFF 82

RESULT 54

B69983

conserved hypothetical protein ysaA - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: B69983

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Brrington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galled
A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: B69983
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-260 <N>
A:Cross-references: UNIPROT:P94512; UNIPARC:UPI00000608A7; GB:Z99118; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: ysaA
C:Superfamily: hypothetical protein MJ1437

Query Match 86.2%; Score 25; DB 2; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0

QY 1 KAVFF 5
|||
2 KAVFF 6

Db

RESULT 55

C95942
Probable transcription regulator, deoR family protein [imported] - *Sinorhizobium meliloti*
C:Species: *Sinorhizobium meliloti*
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C:Accession: C95942
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
A:Reference number: A95842; MUID:21396508; PMID:11481431
A:Accession: C95942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-263 <KUR>
A:Cross-references: UNIPROT:Q92VA5; UNIPARC:UPI00000CB676; GB:AL591985; PIDN:CAC49203.1;
A:Experimental source: strain 1021, megaplasmid pSymb
R:Galibert, F.; Finan, T.M.; Long, S.R.; Fuhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.P.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
C:Genetics:
A:Gene: deoR; SM21299
A:Genome: plasmid
C:Superfamily: deo operon repressor

Query Match 86.2%; Score 25; DB 2; Length 263;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 6
|||
218 KAVFF 223

Db

RESULT 56

A28171
phenylethanolamine N-methyltransferase (BC 2.1.1.28) - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A28171; S10894; A28210
R:Kaneda, N.; Ichinose, H.; Kobayashi, K.; Oka, K.; Kishi, F.; Nakazawa, A.; Kurosawa, Y
J. Biol. Chem. 263, 7672-7677, 1988
A:Title: Molecular cloning of cDNA and chromosomal assignment of the gene for human phen
A:Reference number: A28171; MUID:88227966; PMID:3372503
A:Accession: A28171
A:Molecule type: mRNA
A:Residues: 1-282 <KAN>
A:Cross-references: UNIPROT:P11086; UNIPARC:UPI0000111BE4; GB:J03727; NID:gl90141; PIDN:
R:Sasaoka, T.; Kaneda, N.; Kurosawa, Y.; Fujita, K.; Nagatsu, T.
Neurochem. Int. 15, 555-565, 1989
A:Title: Structure of human phenylethanolamine N-methyltransferase gene: existence of tw
A:Reference number: S10894
A:Accession: S10894
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <SAS>
A:Cross-references: UNIPARC:UPI0000111BE4; EMBL:X52730; NID:g35560; PIDN:CAA36944.1; PID
R:Baetge, E.E.; Behringer, R.R.; Messing, A.; Brinster, R.L.; Palmiter, R.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 3648-3652, 1988
A:Title: Transgenic mice express the human phenylethanolamine N-methyltransferase gene i
A:Reference number: A28210; MUID:88217959; PMID:2835776
A:Accession: A28210
A:Molecule type: mRNA
A:Residues: 1-168, 'AQ', 171-282 <BAE>
A:Cross-references: UNIPARC:UPI000016AED9; GB:J03280; NID:gl90143; PIDN:AAA60131.1; PID:
C:Genetics:
A:Gene: GDB:PNMT; PENT
A:Cross-references: GDB:120271; OMIM:171190
A:Map position: 1pter-17qter
A:Introns: 68/1; 137/2
C:Superfamily: phenylethanolamine N-methyltransferase
C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 86.2%; Score 25; DB 1; Length 282;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 6
|||
270 KGVFF 275

Db

RESULT 57

A82458
hypothetical protein VCA0458 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: A82458
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: A82458
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-285 <HEI>
A:Cross-references: UNIPROT:Q9KMB5; UNIPARC:UPI00000C352C; GB:AE004378; GB:AE003853; NTI
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0458
A:Map position: 2

Query Match 86.2%; Score 25; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5

```

Db          217 KAVFF 221
|||||
RESULT 58
B90435
hypothetical protein dppC-3 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: B90435
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arrett, R.A.; Ragan, M.A.; Jensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: B90435
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <KUR>
A;Cross-references: UNIPROT:Q97VK7; UNIPARC:UPI00000647C9; GB:AE006641; NID:gl3815922; F
C;Genetics:
C;Superfamily: oligopeptide permease protein oppB
Query Match      86.2%; Score 25; DB 2; Length 298;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      1 KAVFFA 6
      |||||
Db      156 KATFFA 161
|||||
RESULT 59
H90717
hypothetical protein ECs0712 [imported] - Escherichia coli (strain O157:H7, substrain R1
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90717
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gaawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90717
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-302 <HAY>
A;Cross-references: UNIPROT:Q8X9H6; UNIPARC:UPI00001653CA; GB:BA0000007; PIDN:BA834135.1;
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs0712
Query Match      86.2%; Score 25; DB 2; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 KAVFF 5
      |||||
Db      189 KAVFF 193
|||||
RESULT 60
T24732
hypothetical protein T09B9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24732
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24732

```

```

A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-308 <WIL>
A;Cross-references: UNIPROT:Q10049; UNIPARC:UPI000013C01F; EMBL:Z47070; PIDN:CAA87343.1
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: CBSP:T09B9.3
A;Map position: X
A;Introns: 33/3; 65/3; 96/3; 149/2; 182/3; 220/2; 242/2
Query Match      86.2%; Score 25; DB 2; Length 308;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 KAVFF 5
      |||||
Db      66 KAVFF 70
|||||
RESULT 61
G72347
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72347
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke-
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se-
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72347
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-321 <ARN>
A;Cross-references: UNIPROT:Q9WZ88; UNIPARC:UPI00000C13B4; GB:AE001740; GB:AE000512; NT1
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0682
Query Match      86.2%; Score 25; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 KAVFF 5
      |||||
Db      179 KAVFF 183
|||||
RESULT 62
H85567
hypothetical protein ybfM [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85567
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe-
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousia, K.; Apodaca
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H85567
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-323 <STO>
A;Cross-references: UNIPROT:Q8X9H6; UNIPARC:UPI00000D0807; GB:AE005174; NID:gl2513583;
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ybfM
Query Match      86.2%; Score 25; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Fr1 Dec 30 10:25:19 2005

QY 1 KAVFF 5
DB 210 KAVFF 214

RESULT 63

pectate lyase - Aspergillus sp.
C:Species: Aspergillus sp.
C:Date: 15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change 17-Mar-2000
C:Accession: S51509
R:Ho, M.C.; Whitehead, M.P.; Cleveland, T.E.; Dean, R.A.
Curr. Genet. 27, 142-149, 1995
A:Title: Sequence analysis of the Aspergillus nidulans pectate lyase gene and evidence for a novel pectate lyase gene
A:Reference number: S51509; MUID:95308536; PMID:7788717
A:Accession: S51509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-326 <HOM>
A:Cross-references: UNIPARC:UPI00001760B4
C:Superfamily: pectate lyase

Query Match 86.2%; Score 25; DB 2; Length 326;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 264 RAFFA 269

RESULT 64

C72015

glycerol-3-phosphate acyltransferase, probable CP0902 [imported] - Chlamydomophila pneumoniae

Alternate names: glycerol-3-p acyltransferase
C:Species: Chlamydomophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: C72015; E81525
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; J.
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: C72015
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <ARN>
A:Cross-references: UNIPROT:Q9Z6V0; UNIPARC:UPI00000D411C; GB:AE001675; GB:AE001363; NID:1
A:Experimental source: strain CWD029
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: AB1500; MUID:20150255; PMID:10684935
A:Accession: E81525
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <REA>
A:Cross-references: UNIPARC:UPI00000D411C; GB:AE002249; GB:AE002161; NID:g7189811; PIDN
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: plsB; CP0902
C:Superfamily: glycerol-3-phosphate O-acyltransferase

Query Match 86.2%; Score 25; DB 2; Length 331;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 278 RAFFA 283

RESULT 65

A;Residues: 1-342 <KUR>
A;Cross-references: UNIPROT:Q8YQ33; UNIPARC:UPI00000CE9A4; GB:BA000019; PIDN:BA875702.1;
A;Experimental source: strain PCC 7120
C;Genetics:
C;Superfamily: photosystem II chlorophyll a-binding protein psbc

Query Match 86.2%; Score 25; DB 2; Length 342;
Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVVFF 5
|||
Db 157 KAVVFF 161

RESULT 68

T21067
hypothetical protein F17C8.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21067
R;Sulston, J.

submitted to the EMBL Data Library, August 1994
A;Reference number: Z19367

A;Accession: T21067
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 1-347 <WIL>

A;Cross-references: UNIPROT:Q19525; UNIPARC:UPI0000083195; EMBL:Z35719; NID:G528945; PID
A;Experimental source: clone F17C8

C;Genetics:

A;Gene: CRSP.F17C8.5

A;Map position: 3

A;Introns: 29/1; 128/3; 182/2; 279/3; 325/1

Query Match 86.2%; Score 25; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVVFA 6
|||
Db 111 KAIFFS 116

RESULT 69

H97272
histidinol-phosphate aminotransferase [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97272

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: H97272

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-352 <KUR>

A;Cross-references: UNIPROT:Q57ES6; UNIPARC:UPI000012C887; GB:AE001437; PIDN:AAK80971.1;
A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:

A;Gene: CAC3031

C;Superfamily: histidinol phosphate aminotransferase

Query Match 86.2%; Score 25; DB 2; Length 352;
Best Local Similarity 83.3%; Pred. No. 2.2e+02; Indels 1; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVVFA 6
|||
Db 102 KTVFFA 107

RESULT 70

H64161

hypothetical protein HI0934 - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae

C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004

C;Accession: H64161

R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, S.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, G.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800

A;Accession: H64161

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-384 <TIGR>

A;Cross-references: UNIPROT:P44942; UNIPARC:UPI00001304FC; GB:U32775; GB:I42023; NID:G1

Query Match 86.2%; Score 25; DB 2; Length 384;
Best Local Similarity 83.3%; Pred. No. 2.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVVFA 6
|||
Db 17 KTVFFA 22

RESULT 71

AF0203

probable membrane protein YPO1668 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AF0203

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tittball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AF0203

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-411 <KUR>

A;Cross-references: UNIPROT:Q8ZF99; UNIPARC:UPI00000DC7ED; GB:AL590842; PIDN:CAC90490.1;
C;Genetics:

A;Gene: YPO1668

C;Superfamily: Escherichia coli probable transport protein yqce

Query Match 86.2%; Score 25; DB 2; Length 411;
Best Local Similarity 66.7%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVVFA 6
|||
Db 328 RAIFPA 333

RESULT 72

T05877

hypothetical protein T29A15.210 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T05877

R;Sevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; H.
submitted to the Protein Sequence Database, March 1999

A;Reference number: Z15455

A;Accession: T05877

A;Molecule type: DNA

A;Residues: 1-420 <BEV>

A;Cross-references: UNIPROT:Q9T094; UNIPARC:UPI00000A61C0; EMBL:AL035602

A;Experimental source: cultivar Columbia; BAC clone T29A15		Db	4 KAVFF 8
C;Genetics:		RESULT 75	
A;Map position: 4		A86717	
A;Introns: 51/1; 99/2; 155/3; 246/1; 334/3; 378/3		conserved hypothetical protein yheD [imported] - Lactococcus lactis subsp. lactis (strain	
A;Note: T29A15.210		C;Species: Lactococcus lactis subsp. lactis	
C;Superfamily: Arabidopsis thaliana hypothetical protein F2K15.170		C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004	
Query Match		C;Accession: A86717	
Best Local Similarity 100.0%; Score 25; DB 2; Length 420;		R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehrlich	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		Genome Res. 11, 731-753, 2001	
Qy 1 KAVFF 5		A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp	
Db 169 KAVFF 173		A;Reference number: A86625; MUID:21235186; PMID:11337471	
RESULT 73		A;Accession: A86717	
H81402		A;Status: preliminary	
probable integral membrane protein Cj0560 [imported] - Campylobacter jejuni (strain NCTC		A;Molecule type: DNA	
C;Species: Campylobacter jejuni		A;Residues: 1-462 <STO>	
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004		A;Cross-references: UNIPROT:Q9CHJ4; UNIPARC:UPI000000C68CE; GB:AE005176; PID:gl2723652; PJ	
C;Accession: H81402		A;Experimental source: strain IL1403	
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling		C;Genetics:	
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell		A;Gene: yheD	
Nature 403, 665-668, 2000		Query Match	
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp		Best Local Similarity 86.2%; Score 25; DB 2; Length 462;	
A;Reference number: A81250; MUID:20150912; PMID:10688204		Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
A;Accession: H81402		Qy 1 KAVFF 5	
A;Status: preliminary		Db 4 KAVFF 8	
A;Molecule type: DNA		Search completed: December 29, 2005, 17:49:19	
A;Residues: 1-442 <PAR>		Job time : 13.9677 secs	
A;Cross-references: UNIPROT:Q9PHV5; UNIPARC:UPI000000C217E; GB:AL139075; GB:AL111168; NID			
A;Experimental source: serotype O2, strain NCTC 11168			
C;Genetics:			
A;Gene: Cj0560			
Query Match			
Best Local Similarity 86.2%; Score 25; DB 2; Length 442;			
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
Qy 1 KAVFF 6			
Db 313 KVVFF 318			
RESULT 74			
G95233			
Cof family protein [imported] - Streptococcus pneumoniae (strain TIGR4)			
C;Species: Streptococcus pneumoniae			
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004			
C;Accession: G95233			
R;Fetzelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid			
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,			
nson, T.; Hickey, E.K.; Holt, I.E.			
Science 293, 498-506, 2001			
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,			
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.			
A;Reference number: A95000; MUID:21357209; PMID:11463916			
A;Accession: G95233			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-462 <KUR>			
A;Cross-references: UNIPROT:Q9TNM3; UNIPARC:UPI000000C9CFF; GB:AE005672; PIDN:AAK76064.1;			
A;Experimental source: strain TIGR4			
C;Genetics:			
A;Gene: SP1997			
Query Match			
Best Local Similarity 86.2%; Score 25; DB 2; Length 462;			
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy 1 KAVFF 5			
Db 11111111			

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 , Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-15

Perfect score: 29

Sequence: 1 KAVFPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA New.*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pap:*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pap:*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap:*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pap:*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pap:*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap:*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pap:*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	660	7	US-11-186-284-125
2	29	100.0	708	6	US-10-821-234-917
3	25	86.2	210	6	US-10-467-657-6318
4	25	86.2	560	6	US-10-623-155-225
5	25	86.2	563	6	US-10-821-234-1067
6	24	82.8	19	6	US-10-923-605-5
7	24	82.8	19	6	US-10-934-818-5
8	24	82.8	40	7	US-11-016-706-36
9	24	82.8	40	7	US-11-098-774-12
10	24	82.8	42	6	US-10-923-605-1
11	24	82.8	42	6	US-10-934-818-1
12	24	82.8	42	7	US-11-016-706-37
13	24	82.8	43	6	US-10-934-818-6
14	24	82.8	43	6	US-10-250-581-1
15	24	82.8	43	6	US-10-250-581-1
16	24	82.8	288	6	US-10-467-657-1272
17	24	82.8	423	6	US-10-525-710-44
18	24	82.8	489	6	US-10-467-657-7846
19	24	82.8	770	6	US-10-982-545-15
20	24	82.8	770	6	US-10-789-273-38
21	23	79.3	9	6	US-10-982-891-44
22	23	79.3	114	6	US-10-467-657-5012
23	23	79.3	283	7	US-11-082-389-252
24	23	79.3	283	7	US-11-082-389-254
25	23	79.3	310	6	US-10-454-437-328
26	23	79.3	411	6	US-10-793-626-2080
27	23	79.3	557	6	US-10-467-657-5540
28	23	79.3	974	6	US-10-995-561-895
29	23	79.3	997	6	US-10-995-561-896
30	22	75.9	190	6	US-10-467-657-3436
31	22	75.9	211	6	US-10-821-234-1372
32	22	75.9	216	6	US-10-467-657-5376
33	22	75.9	269	7	US-11-179-977-11
34	22	75.9	335	7	US-11-092-353-2
35	22	75.9	341	6	US-10-131-826A-256
36	22	75.9	341	6	US-11-099-691-6
37	22	75.9	397	6	US-10-467-657-2684
38	22	75.9	478	7	US-11-092-353-4
39	22	75.9	550	6	US-10-467-657-234
40	22	75.9	550	6	US-10-467-657-924
41	22	75.9	645	6	US-10-510-386-32
42	22	75.9	989	6	US-10-821-234-975
43	22	75.9	1070	7	US-11/062
44	22	75.9	1095	7	US-11/062
45	22	75.9	1169	7	US-11-077-550-20
46	21	72.4	28	6	US-10-250-581-14
47	21	72.4	28	6	US-10-250-581-17
48	21	72.4	28	6	US-10-250-581-17
49	21	72.4	28	6	US-10-250-581-17
50	21	72.4	40	6	US-10-250-581-15
51	21	72.4	40	6	US-10-250-581-15
52	21	72.4	40	6	US-10-250-581-15
53	21	72.4	40	6	US-10-250-581-16
54	21	72.4	42	6	US-10-250-581-19
55	21	72.4	42	6	US-10-250-581-16
56	21	72.4	42	6	US-10-250-581-19
57	21	72.4	42	6	US-10-250-581-19
58	21	72.4	54	6	US-10-467-657-4978
59	21	72.4	71	7	US-11-123-896-344
60	21	72.4	73	7	US-11-123-896-335
61	21	72.4	105	6	US-10-467-657-9209
62	21	72.4	105	6	US-11-000-463-759
63	21	72.4	115	6	US-10-793-626-1554
64	21	72.4	127	6	US-10-467-657-3152
65	21	72.4	134	6	US-10-467-657-6860
66	21	72.4	153	6	US-10-467-657-4112
67	21	72.4	162	6	US-10-467-657-9046
68	21	72.4	167	6	US-10-467-657-5306
69	21	72.4	189	6	US-10-467-657-6854
70	21	72.4	189	6	US-10-467-657-7856
71	21	72.4	191	6	US-10-467-657-818
72	21	72.4	213	6	US-10-981-873-40
73	21	72.4	227	6	US-10-980-388-86
74	21	72.4	230	6	US-10-510-386-198
75	21	72.4	244	6	US-10-454-437-238
76	21	72.4	244	6	US-10-454-437-240
77	21	72.4	264	6	US-10-873-528-70
78	21	72.4	299	6	US-10-467-657-4424
79	21	72.4	355	6	US-10-467-657-7996
80	21	72.4	358	6	US-10-467-657-7030
81	21	72.4	366	6	US-10-467-657-7024
82	21	72.4	372	6	US-10-467-657-7964
83	21	72.4	406	6	US-10-467-657-590
84	21	72.4	418	6	US-10-467-657-7420
85	21	72.4	422	6	US-10-467-657-5788
86	21	72.4	422	6	US-10-525-710-40
87	21	72.4	429	6	US-10-858-730-79
88	21	72.4	439	6	US-10-793-626-2408
89	21	72.4	481	6	US-10-995-561-959
90	21	72.4	481	6	US-10-793-626-3132
91	21	72.4	495	6	US-10-613-744-5
92	21	72.4	500	7	US-10-957-569-18
93	21	72.4	550	7	US-11-055-822-866
94	21	72.4	613	6	US-10-467-657-5796
95	21	72.4	616	6	US-10-613-744-4
96	21	72.4	716	6	US-10-131-826A-512
97	21	72.4	716	7	US-11-147-047-52
98	21	72.4	801	6	US-10-467-657-6470

99	21	72.4	897	6	US-10-821-234-1523	Sequence 1523, Ap	172	20	69.0	338	6	US-10-467-657-6798	Sequence 6798, Ap
100	21	72.4	898	7	US-11-099-691-7	Sequence 7, Appli	173	20	69.0	347	6	US-10-467-657-2014	Sequence 2014, Ap
101	21	72.4	1141	6	US-10-995-561-1009	Sequence 1009, Ap	174	20	69.0	355	7	US-10-454-437-102	Sequence 102, App
102	21	72.4	1141	6	US-10-995-561-1010	Sequence 1010, Ap	175	20	69.0	355	7	US-11-088-686-4	Sequence 4, Appli
103	20	69.0	5	7	US-11-098-674-1	Sequence 1, Appli	176	20	69.0	356	7	US-11-075-185-16	Sequence 16, Appl
104	20	69.0	9	7	US-11-032-498-28	Sequence 28, Appl	177	20	69.0	357	6	US-10-467-657-2500	Sequence 2500, Ap
105	20	69.0	28	6	US-10-250-581-2	Sequence 2, Appli	178	20	69.0	357	6	US-10-467-657-6648	Sequence 6648, Ap
106	20	69.0	38	6	US-10-250-581-2	Sequence 2, Appli	179	20	69.0	363	6	US-10-995-561-602	Sequence 602, App
107	20	69.0	38	6	US-10-467-657-2058	Sequence 2058, Ap	180	20	69.0	365	6	US-10-624-932-24	Sequence 24, Appl
108	20	69.0	40	6	US-10-250-581-3	Sequence 3, Appli	181	20	69.0	376	6	US-10-995-561-844	Sequence 844, App
109	20	69.0	40	6	US-10-250-581-3	Sequence 3, Appli	182	20	69.0	376	6	US-10-995-561-848	Sequence 848, App
110	20	69.0	42	6	US-10-250-581-4	Sequence 4, Appli	183	20	69.0	380	6	US-10-624-932-20	Sequence 20, Appl
111	20	69.0	42	6	US-10-250-581-4	Sequence 4, Appli	184	20	69.0	380	6	US-10-624-932-22	Sequence 22, Appl
112	20	69.0	47	6	US-10-467-657-5436	Sequence 5436, Ap	185	20	69.0	380	6	US-10-995-561-846	Sequence 846, App
113	20	69.0	48	6	US-10-467-657-4322	Sequence 1050, Ap	186	20	69.0	380	7	US-11-108-528-28	Sequence 28, Appl
114	20	69.0	56	6	US-10-467-657-1050	Sequence 1050, Ap	187	20	69.0	387	6	US-10-467-657-5522	Sequence 5522, Ap
115	20	69.0	75	6	US-10-467-657-1496	Sequence 1496, Ap	188	20	69.0	390	6	US-10-995-561-847	Sequence 847, App
116	20	69.0	92	6	US-10-467-657-2378	Sequence 2378, Ap	189	20	69.0	395	6	US-10-467-657-1950	Sequence 1950, Ap
117	20	69.0	95	6	US-10-467-657-8785	Sequence 8785, Ap	190	20	69.0	396	6	US-10-510-386-238	Sequence 238, App
118	20	69.0	100	7	US-11-123-896-137	Sequence 137, App	191	20	69.0	399	6	US-10-510-386-30	Sequence 30, Appl
119	20	69.0	104	6	US-10-821-234-1227	Sequence 1237, App	192	20	69.0	400	6	US-10-793-626-1056	Sequence 1056, Ap
120	20	69.0	107	6	US-10-793-626-1586	Sequence 1586, Ap	193	20	69.0	401	7	US-11-055-822-336	Sequence 336, App
121	20	69.0	126	6	US-10-793-626-2766	Sequence 2766, Ap	194	20	69.0	402	6	US-10-467-657-9070	Sequence 9070, Ap
122	20	69.0	127	7	US-11-106-796-10	Sequence 10, Appl	195	20	69.0	402	7	US-11-000-463-449	Sequence 449, App
123	20	69.0	129	6	US-10-501-039-8	Sequence 8, Appli	196	20	69.0	413	6	US-10-467-657-1858	Sequence 1858, Ap
124	20	69.0	131	6	US-10-467-657-9073	Sequence 9073, Ap	197	20	69.0	426	6	US-10-467-657-2120	Sequence 2120, Ap
125	20	69.0	133	6	US-10-467-657-9195	Sequence 9195, Ap	198	20	69.0	428	7	US-11-000-463-448	Sequence 448, App
126	20	69.0	137	6	US-10-793-626-5330	Sequence 5330, App	199	20	69.0	436	6	US-10-467-657-7694	Sequence 7694, Ap
127	20	69.0	137	6	US-10-467-657-6584	Sequence 6584, Ap	200	20	69.0	444	6	US-10-467-657-362	Sequence 362, App
128	20	69.0	155	6	US-10-467-657-2420	Sequence 2420, Ap	201	20	69.0	450	6	US-10-467-657-7094	Sequence 7094, Ap
129	20	69.0	156	6	US-10-793-626-2452	Sequence 2452, Ap	202	20	69.0	450	6	US-10-467-657-8028	Sequence 8028, Ap
130	20	69.0	168	7	US-11-000-463-824	Sequence 824, App	203	20	69.0	451	6	US-10-467-657-7104	Sequence 7104, Ap
131	20	69.0	175	6	US-10-467-657-7504	Sequence 7504, Ap	204	20	69.0	453	7	US-11-082-389-198	Sequence 198, App
132	20	69.0	183	6	US-10-467-657-6906	Sequence 6906, Ap	205	20	69.0	456	6	US-10-467-657-4150	Sequence 4150, Ap
133	20	69.0	196	6	US-10-793-626-630	Sequence 630, App	206	20	69.0	472	6	US-10-467-657-2268	Sequence 2268, Ap
134	20	69.0	196	6	US-10-967-527A-26	Sequence 26, Appl	207	20	69.0	485	6	US-10-821-234-934	Sequence 934, App
135	20	69.0	201	6	US-10-467-657-458	Sequence 458, App	208	20	69.0	485	6	US-10-204-029-7	Sequence 7, Appli
136	20	69.0	202	7	US-11-082-389-364	Sequence 364, App	209	20	69.0	490	7	US-11-074-176-316	Sequence 316, App
137	20	69.0	207	6	US-10-467-657-1816	Sequence 1816, Ap	210	20	69.0	494	6	US-10-467-657-4376	Sequence 4376, Ap
138	20	69.0	211	6	US-10-467-657-6932	Sequence 6932, Ap	211	20	69.0	495	7	US-11-074-176-60	Sequence 60, Appl
139	20	69.0	215	6	US-10-131-826A-4	Sequence 4, Appli	212	20	69.0	507	6	US-10-467-657-1612	Sequence 1612, Ap
140	20	69.0	220	6	US-10-467-657-3154	Sequence 3154, Ap	213	20	69.0	513	6	US-10-467-657-5464	Sequence 5464, Ap
141	20	69.0	227	6	US-10-467-657-1514	Sequence 1514, Ap	214	20	69.0	514	7	US-11-186-284-228	Sequence 228, App
142	20	69.0	228	6	US-10-793-626-1862	Sequence 1862, Ap	215	20	69.0	523	6	US-10-131-826A-246	Sequence 246, App
143	20	69.0	228	6	US-10-467-657-568	Sequence 568, App	216	20	69.0	524	6	US-10-689-742-13	Sequence 13, Appl
144	20	69.0	228	6	US-10-467-657-4838	Sequence 4838, Ap	217	20	69.0	525	7	US-11-082-389-350	Sequence 350, App
145	20	69.0	229	6	US-10-467-657-4838	Sequence 4838, Ap	218	20	69.0	528	6	US-10-793-626-1930	Sequence 1930, Ap
146	20	69.0	233	6	US-10-131-826A-110	Sequence 410, App	219	20	69.0	540	6	US-10-858-730-293	Sequence 293, App
147	20	69.0	239	6	US-10-821-234-1322	Sequence 1322, Ap	220	20	69.0	554	7	US-11-000-463-240	Sequence 240, App
148	20	69.0	240	6	US-10-980-388-78	Sequence 78, Appl	221	20	69.0	555	6	US-10-454-437-100	Sequence 100, App
149	20	69.0	242	6	US-10-467-657-6276	Sequence 6276, Ap	222	20	69.0	558	6	US-10-467-657-4258	Sequence 4258, Ap
150	20	69.0	254	7	US-10-821-234-1073	Sequence 1073, Ap	223	20	69.0	560	7	US-11-080-991-62	Sequence 62, Appl
151	20	69.0	255	7	US-11-185-111-36	Sequence 27, Appl	224	20	69.0	572	6	US-10-467-657-1022	Sequence 1022, Ap
152	20	69.0	257	7	US-11-102-883-22	Sequence 36, Appl	225	20	69.0	578	6	US-10-858-730-103	Sequence 103, App
153	20	69.0	269	6	US-11-102-240-94	Sequence 94, Appl	226	20	69.0	582	7	US-11-090-439-58	Sequence 58, Appl
154	20	69.0	272	6	US-10-467-657-330	Sequence 330, App	227	20	69.0	592	6	US-10-467-962B-95	Sequence 95, Appl
155	20	69.0	288	6	US-10-873-528-2520	Sequence 2520, Ap	228	20	69.0	592	6	US-10-524-647-112	Sequence 112, App
156	20	69.0	291	6	US-10-873-528-18	Sequence 18, Appl	229	20	69.0	599	6	US-10-467-657-3972	Sequence 3972, Ap
157	20	69.0	291	7	US-10-432-483-12	Sequence 12, Appl	230	20	69.0	614	7	US-11-126-841A-2	Sequence 2, Appli
158	20	69.0	292	7	US-11-102-883-22	Sequence 22, Appl	231	20	69.0	614	7	US-11-126-841A-13	Sequence 13, Appl
159	20	69.0	294	6	US-10-467-657-7686	Sequence 7686, Ap	232	20	69.0	626	6	US-10-467-657-1196	Sequence 1196, Ap
160	20	69.0	311	6	US-10-793-626-2450	Sequence 2450, Ap	233	20	69.0	677	6	US-10-131-826A-230	Sequence 230, App
161	20	69.0	316	7	US-10-467-657-2334	Sequence 2334, Ap	234	20	69.0	693	6	US-10-467-657-6176	Sequence 6176, Ap
162	20	69.0	316	7	US-11-082-389-62	Sequence 62, Appl	235	20	69.0	721	6	US-10-467-962B-49	Sequence 49, Appl
163	20	69.0	318	6	US-10-131-826A-374	Sequence 374, App	236	20	69.0	724	7	US-11-184-380-4	Sequence 4, Appli
164	20	69.0	321	6	US-10-467-657-2504	Sequence 2504, Ap	237	20	69.0	741	6	US-10-467-657-6266	Sequence 6266, Ap
165	20	69.0	324	6	US-10-467-657-7692	Sequence 7692, Ap	238	20	69.0	835	7	US-11-186-283-2	Sequence 2, Appli
166	20	69.0	325	6	US-10-467-657-8440	Sequence 8440, Ap	239	20	69.0	852	7	US-11-186-283-8	Sequence 8, Appli
167	20	69.0	326	6	US-10-467-657-8440	Sequence 8440, Ap	240	20	69.0	858	6	US-10-467-657-5004	Sequence 5004, Ap
168	20	69.0	330	6	US-10-454-437-142	Sequence 142, App	241	20	69.0	907	7	US-11-103-957-82	Sequence 6, Appl
169	20	69.0	333	7	US-10-510-386-82	Sequence 82, Appl	242	20	69.0	916	6	US-10-467-657-4242	Sequence 4242, Ap
170	20	69.0	335	6	US-11-082-389-202	Sequence 202, App	243	20	69.0	964	7	US-11-103-957-13	Sequence 13, Appl
171	20	69.0	338	6	US-10-467-657-3818	Sequence 3818, Ap	244	20	69.0				
					Sequence 136, App								

245	20	69.0	1027	6	US-10-793-626-3106	Sequence 3106, Ap
246	20	69.0	1076	6	US-10-467-657-5708	Sequence 5708, Ap
247	20	69.0	1144	6	US-10-467-962B-89	Sequence 89, Appl
248	20	69.0	1259	6	US-10-467-657-5510	Sequence 5510, Ap
249	20	69.0	1274	6	US-10-454-437-360	Sequence 360, App
250	20	69.0	1362	7	US-11-043-693-33	Sequence 33, Appl
251	20	69.0	1363	7	US-11-043-693-32	Sequence 32, Appl
252	20	69.0	1368	7	US-11-043-693-34	Sequence 34, Appl
253	20	69.0	1531	7	US-11-103-957-15	Sequence 15, Appl
254	20	69.0	2004	6	US-10-467-657-84	Sequence 84, Appl
255	20	69.0	2004	6	US-10-467-657-6322	Sequence 6322, Ap
256	20	69.0	3433	6	US-10-714-781A-67	Sequence 67, Appl
257	20	69.0	3623	6	US-10-995-561-593	Sequence 593, App
258	20	69.0	4128	6	US-10-770-726-77	Sequence 77, Appl
259	19	65.5	28	6	US-10-250-581-5	Sequence 5, Appl
260	19	65.5	28	6	US-10-250-581-8	Sequence 8, Appl
261	19	65.5	28	6	US-10-250-581-11	Sequence 11, Appl
262	19	65.5	28	6	US-10-250-581-5	Sequence 5, Appl
263	19	65.5	28	6	US-10-250-581-8	Sequence 8, Appl
264	19	65.5	28	6	US-10-250-581-11	Sequence 11, Appl
265	19	65.5	39	6	US-10-467-657-2174	Sequence 2174, Ap
266	19	65.5	40	6	US-10-250-581-6	Sequence 6, Appl
267	19	65.5	40	6	US-10-250-581-9	Sequence 9, Appl
268	19	65.5	40	6	US-10-250-581-12	Sequence 12, Appl
269	19	65.5	40	6	US-10-250-581-6	Sequence 6, Appl
270	19	65.5	40	6	US-10-250-581-9	Sequence 9, Appl
271	19	65.5	40	6	US-10-250-581-12	Sequence 12, Appl
272	19	65.5	42	6	US-10-250-581-7	Sequence 7, Appl
273	19	65.5	42	6	US-10-250-581-10	Sequence 10, Appl
274	19	65.5	42	6	US-10-250-581-13	Sequence 13, Appl
275	19	65.5	42	6	US-10-250-581-7	Sequence 7, Appl
276	19	65.5	42	6	US-10-250-581-10	Sequence 10, Appl
277	19	65.5	42	6	US-10-250-581-13	Sequence 13, Appl
278	19	65.5	50	6	US-10-250-581-13	Sequence 13, Appl
279	19	65.5	52	6	US-10-467-657-7892	Sequence 7892, Ap
280	19	65.5	52	6	US-10-467-657-3656	Sequence 3656, Ap
281	19	65.5	83	7	US-11-055-822-238	Sequence 238, App
282	19	65.5	95	7	US-11-055-822-632	Sequence 632, App
283	19	65.5	95	7	US-11-055-822-1102	Sequence 1102, Ap
284	19	65.5	96	6	US-10-467-657-3380	Sequence 3380, Ap
285	19	65.5	97	6	US-10-650-326B-2	Sequence 2, Appl
286	19	65.5	97	6	US-10-995-561-900	Sequence 900, App
287	19	65.5	98	6	US-10-467-657-3490	Sequence 3490, Ap
288	19	65.5	102	6	US-10-667-295-43	Sequence 43, Appl
289	19	65.5	107	6	US-10-793-626-2592	Sequence 2592, Ap
290	19	65.5	107	6	US-10-467-657-1018	Sequence 1018, Ap
291	19	65.5	113	7	US-11-073-605-10	Sequence 10, Appl
292	19	65.5	124	6	US-10-467-657-8348	Sequence 8348, Ap
293	19	65.5	128	6	US-10-793-626-1208	Sequence 1208, Ap
294	19	65.5	138	6	US-10-467-657-2052	Sequence 2052, Ap
295	19	65.5	141	6	US-10-667-295-42	Sequence 42, Appl
296	19	65.5	141	6	US-10-467-657-5544	Sequence 5544, Ap
297	19	65.5	150	7	US-11-109-156-32	Sequence 32, Appl
298	19	65.5	153	6	US-10-467-657-7674	Sequence 7674, Ap
299	19	65.5	153	6	US-10-467-657-8432	Sequence 8432, Ap
300	19	65.5	157			

ALIGNMENTS

RESULT 1

US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.

```

; APPLICANT: BURGART, LAWRENCE J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FAST-SEQ FOR WINDOWS VERSION 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-284-125

Query Match      100.0%; Score 29; DB 7; Length 660;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      531 KAVFFA 536
      |||||

RESULT 2
US-10-821-234-917
; Sequence 917, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SEQ ID NO 917
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-917

Query Match      100.0%; Score 29; DB 6; Length 708;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      579 KAVFFA 584
      |||||

RESULT 3
US-10-467-657-6318
; Sequence 6318, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

```

```
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 6318
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-6318

Query Match      86.2%; Score 25; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 116 KAVFF 120

RESULT 4
US-10-623-155-225
; Sequence 225, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-225

Query Match      86.2%; Score 25; DB 6; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 537 KAVFF 541

RESULT 5
US-10-821-234-1067
; Sequence 1067, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1067

; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence

US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence

US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; NAME/KEY: MOD RES
; LOCATION: (1)-
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match      82.8%; Score 24; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 6.3;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 6
Db 4 KLVFF 9

RESULT 7
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: Inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match      82.8%; Score 24; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 6.3;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 4 KLVFFA 9

RESULT 8
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match      82.8%; Score 24; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 16 KLVFFA 21

RESULT 9
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elimova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; TITLE OF INVENTION: Identification and Use
; FILE REFERENCE: FTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match      82.8%; Score 24; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 16 KLVFFA 21

RESULT 10
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match      82.8%; Score 24; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 16 KLVFFA 21

RESULT 11
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1
```

```
Query Match      82.8%; Score 24; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVEFFA 6
Db      16 KLVFFA 21

RESULT 12
US-11-016-706-37
; Sequence 37, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match      82.8%; Score 24; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVEFFA 6
Db      16 KLVFFA 21

RESULT 13
US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match      82.8%; Score 24; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVEFFA 6
Db      16 KLVFFA 21

RESULT 14
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      82.8%; Score 24; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVEFFA 6
Db      16 KLVFFA 21

RESULT 15
US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match      82.8%; Score 24; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVEFFA 6
Db      16 KLVFFA 21

RESULT 16
US-10-467-657-1272
; Sequence 1272, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
```

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1272
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1272

Query Match 82.8%; Score 24; DB 6; Length 288;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
|||
Db 44 AVFFA 48

RESULT 17
US-10-525-710-44
; Sequence 44, Application US/10525710
; Publication No. US20050260721A1
; GENERAL INFORMATION:
; APPLICANT: Kroger, Burkhard
; APPLICANT: Zelder, Oskar
; APPLICANT: Kolprogge, Corinna
; APPLICANT: Schroder, Hartwig
; APPLICANT: Hafner, Stefan
; TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
; TITLE OF INVENTION: Sulphur (met)
; FILE REFERENCE: 13111-00006-US
; CURRENT APPLICATION NUMBER: US/10/525,710
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: PCT/EP 2003/009453
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: DE 102 39 082.7
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
US-10-525-710-44

Query Match 82.8%; Score 24; DB 6; Length 423;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|||
Db 146 KAIFF 150

RESULT 18
US-10-467-657-7846
; Sequence 7846, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8

; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7846
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7846

Query Match 82.8%; Score 24; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
|||
Db 28 AVFFA 32

RESULT 19
US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Alun
; APPLICANT: McGuire, James
; APPLICANT: Simonsen, Anja Hviid
; APPLICANT: Blennow, Kaj
; APPLICANT: Podust, Vladimir
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease
; FILE REFERENCE: 016866-011550US
; CURRENT APPLICATION NUMBER: US/10/982,545
; CURRENT FILING DATE: 2004-11-06
; PRIOR APPLICATION NUMBER: US 60/518,360
; PRIOR FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/526,753
; PRIOR FILING DATE: 2003-12-02
; PRIOR APPLICATION NUMBER: US 60/546,423
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/547,250
; PRIOR FILING DATE: 2004-02-23
; PRIOR APPLICATION NUMBER: US 60/558,896
; PRIOR FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: US 60/572,617
; PRIOR FILING DATE: 2004-05-18
; PRIOR APPLICATION NUMBER: US 60/586,503
; PRIOR FILING DATE: 2004-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease
; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),
; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,
; OTHER INFORMATION: Alzheimer's disease amyloid protein
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(17)
; OTHER INFORMATION: signal peptide
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(40)
; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-N1), A-beta 1-40
; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (18)..(687)
; OTHER INFORMATION: soluble APP-alpha
; FEATURE:
; NAME/KEY: PEPTIDE

```
; LOCATION: (18)..(671)
; OTHER INFORMATION: soluble APP-beta
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(770)
; OTHER INFORMATION: C99
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(713)
; OTHER INFORMATION: beta-amyloid protein 42
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (672)..(711)
; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid
; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(770)
; OTHER INFORMATION: C83
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(713)
; OTHER INFORMATION: P3(42)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (688)..(711)
; OTHER INFORMATION: P3(40)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (712)..(770)
; OTHER INFORMATION: gamma-CTF(59)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (714)..(770)
; OTHER INFORMATION: gamma-CTF(57)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (721)..(770)
; OTHER INFORMATION: gamma-CTF(50)
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (740)..(770)
; OTHER INFORMATION: C31
; US-10-982-545-15

Query Match      82.8%; Score 24; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 687 KLVFFA 692

RESULT 20
US-10-789-273-38
; Sequence 38, Application US/10789273
; Publication No. US20050249725A1
; GENERAL INFORMATION:
; APPLICANT: Basi, Gurig
; APPLICANT: Saldanha, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002CP
; CURRENT APPLICATION NUMBER: US/10/789,273
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US/10/388,389
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/010,942
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
```

```
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-789-273-38

Query Match      82.8%; Score 24; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 687 KLVFFA 692

RESULT 21
US-10-982-891-44
; Sequence 44, Application US/10982891
; Publication No. US20050244844A1
; GENERAL INFORMATION:
; APPLICANT: GARCIA, ALPHONSE
; APPLICANT: CAYLA, XAVIER
; APPLICANT: REBOLLO, ANGELITA
; TITLE OF INVENTION: METHODS OF SCREENING OF PPI-INTERACTING POLYPEPTIDES OR PROTEINS,
; TITLE OF INVENTION: PEPTIDES INHIBITING PP1c BINDING TO Bcl-2 PROTEINS, BCL-XL AND
; TITLE OF INVENTION: BCL-W, AND USES THEREOF
; FILE REFERENCE: 260990USOCONT
; CURRENT APPLICATION NUMBER: US/10/982,891
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: PCT/EP03/05453
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: EP 02291170
; PRIOR FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: MAMMALIAN
; US-10-982-891-44

Query Match      79.3%; Score 23; DB 6; Length 9;
Best Local Similarity 83.3%; Pred. No. 4.4e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 3 KAVMFA 8

RESULT 22
US-10-467-657-5012
; Sequence 5012, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5012
; LENGTH: 114
; TYPE: PRT
```



```

; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5012

Query Match          79.3%; Score 23; DB 6; Length 114;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 34 RAVFFS 39

RESULT 23
US-11-082-389-252
; Sequence 252, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: TRANSPORT
; FILE REFERENCE: BGI-131CPCN
; CURRENT APPLICATION NUMBER: US 11/082,389
; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 252
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-254

Query Match          79.3%; Score 23; DB 7; Length 283;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
DB 264 AIFFA 268

RESULT 25
US-10-454-437-328
; Sequence 328, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9

; ORGANISM: Corynebacterium glutamicum
US-11-082-389-252

Query Match          79.3%; Score 23; DB 7; Length 283;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
DB 264 AIFFA 268

RESULT 24
US-11-082-389-254
; Sequence 254, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig

```

```
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 328
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-328

Query Match          79.3%; Score 23; DB 6; Length 310;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
   |:|
Db 63 AIFFA 67

RESULT 26
US-10-793-626-2080
; Sequence 2080, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2080
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2080

Query Match          79.3%; Score 23; DB 6; Length 411;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
   |:|
Db 304 AIFFA 308

RESULT 27
US-10-467-657-5540
; Sequence 5540, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
```

```
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5540
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5540

Query Match          79.3%; Score 23; DB 6; Length 557;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   |:|
Db 166 KAVNFA 171

RESULT 28
US-10-995-561-895
; Sequence 895, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 895
; LENGTH: 974
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-895

Query Match          79.3%; Score 23; DB 6; Length 974;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   |:|
Db 497 KAVLFA 502

RESULT 29
US-10-995-561-896
; Sequence 896, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 896
; LENGTH: 997
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-896

Query Match          79.3%; Score 23; DB 6; Length 997;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
   |:|
Db 520 KAVLFA 525
```

RESULT 30
 US-10-467-657-3436
 ; Sequence 3436, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 3436
 ; LENGTH: 190
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-3436

Query Match 75.9%; Score 22; DB 6; Length 190;
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 | | | |
 DB 46 KTVVFA 51

RESULT 31
 US-10-821-234-1372
 ; Sequence 1372, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; APPLICANT: Stache-Crain, Birgit
 ; APPLICANT: Andarmani, Susan
 ; APPLICANT: Tang, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821,234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462,047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_seq_genes Version 1.0
 ; SEQ ID NO 1372
 ; LENGTH: 211
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-1372

Query Match 75.9%; Score 22; DB 6; Length 211;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 | | | |
 DB 33 KTVVFA 38

RESULT 32
 US-10-467-657-5976
 ; Sequence 5976, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SpA
 ; APPLICANT: FONTANA Maria Rita

; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 5976
 ; LENGTH: 216
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-5976

Query Match 75.9%; Score 22; DB 6; Length 216;
 Best Local Similarity 80.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
 | | | |
 DB 8 KSVFF 12

RESULT 33
 US-11-179-977-11
 ; Sequence 11, Application US/11179977
 ; Publication No. US20050249789A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genencor International, Inc.
 ; TITLE OF INVENTION: Alpha/Beta Hydrolase-Fold Enzymes
 ; FILE REFERENCE: GCS11-PCT
 ; CURRENT APPLICATION NUMBER: US/11/179,977
 ; CURRENT FILING DATE: 2005-07-12
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 11
 ; LENGTH: 269
 ; TYPE: PRT
 ; ORGANISM: Bacillus
 US-11-179-977-11

Query Match 75.9%; Score 22; DB 7; Length 269;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 | | | |
 DB 193 KAAFFS 198

RESULT 34
 US-11-092-353-2
 ; Sequence 2, Application US/11092353
 ; Publication No. US20050272653A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Knopf, John
 ; APPLICANT: Seehra, Jaabir
 ; TITLE OF INVENTION: BMP-3 PROPEPTIDES AND RELATED METHODS
 ; FILE REFERENCE: PHPH-P01-002
 ; CURRENT APPLICATION NUMBER: US/11/092,353
 ; CURRENT FILING DATE: 2005-03-28
 ; PRIOR APPLICATION NUMBER: US 60/557,100
 ; PRIOR FILING DATE: 2004-03-26
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 335
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-092-353-2

Query Match 75.9%; Score 22; DB 7; Length 335;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPF 5
|||:
Db 79 KAVPF 83

RESULT 35
US-10-131-826A-256
; Sequence 256, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P333081C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 256
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-256

Query Match 75.9%; Score 22; DB 6; Length 341;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPF 5
|||:
Db 102 KALPF 106

RESULT 36
US-11-099-691-6
; Sequence 6, Application US/11099691
; Publication No. US20050260644A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: BANDMAN, Olga
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: YANG, Junning
; TITLE OF INVENTION: CELL SIGNALING PROTEINS
; FILE REFERENCE: PF-0521 PCT
; CURRENT APPLICATION NUMBER: US/11/099,691
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/09/700,444
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 60/085,343
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,010
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte Clone 2472655
US-11-099-691-6

Query Match 75.9%; Score 22; DB 7; Length 341;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVPF 5
|||:
Db 102 KALPF 106

RESULT 37
US-10-467-657-2684
; Sequence 2684, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103434.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2684
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2684

Query Match 75.9%; Score 22; DB 6; Length 397;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY      1 KAVFFA 6
Db      309 KADFFA 314

RESULT 38
US-11-092-353-4
; Sequence 4, Application US/11092353
; Publication No. US20050272653A1
; GENERAL INFORMATION:
; APPLICANT: Knopf, John
; APPLICANT: Seehra, Jabir
; TITLE OF INVENTION: BMP-3 PROPEPTIDES AND RELATED METHODS
; FILE REFERENCE: PHPH-P01-002
; CURRENT APPLICATION NUMBER: US/11/092,353
; PRIOR FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: US 60/557,100
; PRIOR FILING DATE: 2004-03-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-092-353-4

Query Match      75.9%; Score 22; DB 7; Length 478;
Best Local Similarity 80.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      112 KAVYF 116

RESULT 39
US-10-467-657-234
; Sequence 234, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 234
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-234

Query Match      75.9%; Score 22; DB 6; Length 550;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      176 RAVFF 180

RESULT 40
US-10-467-657-924
; Sequence 924, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 924
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-924

Query Match      75.9%; Score 22; DB 6; Length 550;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFF 5
Db      176 RAVFF 180

RESULT 41
US-10-510-386-32
; Sequence 32, Application US/10510386
; Publication No. US2005024922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-32

Query Match      75.9%; Score 22; DB 6; Length 645;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      123 KGLFFA 128

RESULT 42
US-10-821-234-975
; Sequence 975, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
```

```
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 975
; LENGTH: 989
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-975
```

```
Query Match          75.9%; Score 22; DB 6; Length 989;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KAVFFA 6
Db 312 ESVRFA 317
```

```
RESULT 43
US/11/062
; Sequence 4, Application US/11062471A
; Publication No. US20050255093A1
; GENERAL INFORMATION:
; APPLICANT: SHONE, Clifford Charles
; APPLICANT: SUTTON, John Mark
; APPLICANT: HALLIS, Bassam
; APPLICANT: SILMAN, Nigel
; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
; FILE REFERENCE: 1581.0800001
; CURRENT APPLICATION NUMBER: US/11/062,471A
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 09/831,050
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PCT/GB99/03699
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: GB 9824282.9
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Construct comprising Mn-SOD from B. stearothermophilus, a linker.
US/11/062,471A-4
```

```
Query Match          75.9%; Score 22; DB 7; Length 1070;
Best Local Similarity 80.0%; Pred. No. 9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KAVFF 5
Db 762 KSVFF 766
```

```
RESULT 44
US/11/062
; Sequence 7, Application US/11062471A
; Publication No. US20050255093A1
; GENERAL INFORMATION:
; APPLICANT: SHONE, Clifford Charles
; APPLICANT: SUTTON, John Mark
; APPLICANT: HALLIS, Bassam
; APPLICANT: SILMAN, Nigel
; TITLE OF INVENTION: Delivery of Superoxide Dismutase to Neuronal Cells
; FILE REFERENCE: 1581.0800001
; CURRENT APPLICATION NUMBER: US/11/062,471A
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 09/831,050
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: PCT/GB99/03699
; PRIOR FILING DATE: 1999-11-05
```

```
; PRIOR APPLICATION NUMBER: GB 9824282.9
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Construct comprising a mitochondrial leader sequence from Human M.
US/11/062,471A-7
```

```
Query Match          75.9%; Score 22; DB 7; Length 1095;
Best Local Similarity 80.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KAVFF 5
Db 787 KSVFF 791
```

```
RESULT 45
US-11-077-550-20
; Sequence 20, Application US/11077550
; Publication No. US20050244435A1
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford Charles
; APPLICANT: Quinn, Conrad Padraig
; APPLICANT: Foster, Keith Alan
; APPLICANT: Chaddock, John
; APPLICANT: Marks, Philip
; APPLICANT: Sutton, J. Mark
; APPLICANT: Stancombe, Patrick
; APPLICANT: Wayne, Jonathan
; TITLE OF INVENTION: Recombinant Toxin Fragments
; FILE REFERENCE: 1581.0130004
; CURRENT APPLICATION NUMBER: US/11/077,550
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 10/241,596
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: 09/255,829
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: PCT/GB97/02273
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 08/782,893
; PRIOR FILING DATE: 1996-12-27
; PRIOR APPLICATION NUMBER: GB9625996.5
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: GB9617671.4
; PRIOR FILING DATE: 1996-08-23
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1169
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-11-077-550-20
```

```
Query Match          75.9%; Score 22; DB 7; Length 1169;
Best Local Similarity 80.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 KAVFF 5
Db 983 KSVFF 987
```

```
RESULT 46
US-10-250-581-14
; Sequence 14, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
```

; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 14
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-14

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFP 5
| | | |
DB 16 KXVFP 20

RESULT 47
US-10-250-581-17
; Sequence 17, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-17

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFP 5
| | | |
DB 16 KXVFP 20

RESULT 48
US-10-250-581-14
; Sequence 14, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....

; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 14
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-14

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFP 5
| | | |
DB 16 KXVFP 20

RESULT 49
US-10-250-581-17
; Sequence 17, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 17
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-17

Query Match 72.4%; Score 21; DB 6; Length 28;
Best Local Similarity 80.0%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFP 5
| | | |
DB 16 KXVFP 20

RESULT 50
US-10-250-581-15
; Sequence 15, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069

; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-15

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|
Db 16 KXVFF 20

RESULT 51

US-10-250-581-18
; Sequence 18, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 18
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-18

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|
Db 16 KXVFF 20

RESULT 52

US-10-250-581-15
; Sequence 15, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581

; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 15
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-15

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|
Db 16 KXVFF 20

RESULT 53

US-10-250-581-18
; Sequence 18, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 18
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-18

Query Match 72.4%; Score 21; DB 6; Length 40;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFF 5
|
Db 16 KXVFF 20

RESULT 54

US-10-250-581-16
; Sequence 16, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 16
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-16

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 55
US-10-250-581-19
; Sequence 19, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 19
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-19

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 56
US-10-250-581-16
; Sequence 16, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 16
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Orn
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-16

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 57
US-10-250-581-19
; Sequence 19, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 19
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)
; OTHER INFORMATION: Xaa=Dab
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(21)
; OTHER INFORMATION: The side chains of the amino acids at positions 17 and 21 are
; OTHER INFORMATION: linked together through an intramolecular bridge.
US-10-250-581-19

Query Match 72.4%; Score 21; DB 6; Length 42;
Best Local Similarity 80.0%; Pred. No. 63;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|
|
|
|
Db 16 KXVFF 20

RESULT 58
US-10-467-657-4978
; Sequence 4978, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:

```

; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4978
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4978

Query Match          72.4%; Score 21; DB 6; Length 54;
Best Local Similarity 80.0%; Pred. No. 81;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AVFFA 6
      :|||
Db      41 SVFFA 45

RESULT 59
US-11-123-896-344
; Sequence 344, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James
; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Tulipa gesneriana
US-11-123-896-344

Query Match          72.4%; Score 21; DB 7; Length 71;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFF 5
      :|||
Db      3 RAIFF 7

RESULT 60
US-11-123-896-335
; Sequence 335, Application US/11123896
; Publication No. US20050273881A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro Acevedo, Pedro A.
; APPLICANT: Harvell, Leslie
; APPLICANT: Cahoon, Rebecca
; APPLICANT: McCutchen, Billy Fred
; APPLICANT: Lu, Albert
; APPLICANT: Herrmann, Rafael
; APPLICANT: Wong, James

; TITLE OF INVENTION: Defensin Polynucleotides and Methods of
; FILE REFERENCE: 35718/246703
; CURRENT APPLICATION NUMBER: US/11/123,896
; CURRENT FILING DATE: 2005-05-06
; PRIOR APPLICATION NUMBER: 60/300,152
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Tulipa gesneriana
US-11-123-896-335

Query Match          72.4%; Score 21; DB 7; Length 71;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFF 5
      :|||
Db      3 RAIFF 7

RESULT 61
US-10-467-657-9209
; Sequence 9209, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9209
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9209

Query Match          72.4%; Score 21; DB 6; Length 105;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
      :|||
Db      3 QTVFFA 8

RESULT 62
US-11-000-463-759
; Sequence 759, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping

```

; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIPACN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 759
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-759

Query Match 72.4%; Score 21; DB 7; Length 105;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
Db 68 AVFFA 72

RESULT 63
US-10-793-626-1554
; Sequence 1554; Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1554
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1554

Query Match 72.4%; Score 21; DB 6; Length 115;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
Db 23 SVFFA 27

RESULT 64
US-10-467-657-3152
; Sequence 3152; Application US/10467657
; Publication No. US20050260581A1

; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3152
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3152

Query Match 72.4%; Score 21; DB 6; Length 127;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
Db 52 ALFFA 56

RESULT 65
US-10-467-657-6860
; Sequence 6860; Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6860
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6860

Query Match 72.4%; Score 21; DB 6; Length 134;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 AVFFA 6
Db 78 ALFFA 82

RESULT 66
US-10-467-657-4112
; Sequence 4112; Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

```
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4112
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4112

Query Match          72.4%; Score 21; DB 6; Length 153;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AVFFA 6
Db      111 AVYFA 115

RESULT 67
US-10-467-657-9046
; Sequence 9046, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 9046
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9046

Query Match          72.4%; Score 21; DB 6; Length 162;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      87 RAYFFA 92

RESULT 68
US-10-467-657-5306
; Sequence 5306, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5306
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5306

Query Match          72.4%; Score 21; DB 6; Length 167;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      159 KAVAF 164

RESULT 69
US-10-467-657-6854
; Sequence 6854, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6854
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6854

Query Match          72.4%; Score 21; DB 6; Length 189;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 AVFFA 6
Db      87 ALFFA 91

RESULT 70
US-10-467-657-7856
; Sequence 7856, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7856
; LENGTH: 189
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7856

Query Match          72.4%; Score 21; DB 6; Length 189;
```

Best Local Similarity 80.0%; Pred. No. 2.8e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1;

QY 2 AVFFA 6
|:|:|
Db 87 ALFFA 91

RESULT 71

US-10-467-657-818
; Sequence 818, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 818
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-818

Query Match 72.4%; Score 21; DB 6; Length 191;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|:|:|
Db 122 QAVFF 126

RESULT 72

US-10-981-873-40
; Sequence 40, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: US\$ THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-981-873-40

Query Match 72.4%; Score 21; DB 6; Length 213;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KAVFF 5
|:|:|
Db 203 KAAFF 207

RESULT 73

US-10-980-388-86
; Sequence 86, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Huff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-86

Query Match 72.4%; Score 21; DB 6; Length 227;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
|:|:|
Db 81 KSIFP 85

RESULT 74

US-10-510-386-198
; Sequence 198, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3

```
; SEQ ID NO 198
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-198

Query Match      72.4%; Score 21; DB 6; Length 230;
Best Local Similarity 80.0%; Pred. NO. 3.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFF 5
      ||||
Db      94 KAAPP 98

RESULT 75
US-10-454-437-238
; Sequence 238, Application US/10454437
; Publication No. US20050277115A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE REFERENCE: BGI-128CPCN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 238
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-238

Query Match      72.4%; Score 21; DB 6; Length 244;
Best Local Similarity 83.3%; Pred. NO. 3.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
      |||||
Db      20 KAVFSA 25

Search completed: December 29, 2005, 18:50:20
Job time : 4.29032 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-15

Perfect score: 29

Sequence: 1 KAVPPA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA Main:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp:**

2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:**

3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp:**

4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp:**

5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp:**

6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pcp:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	3	US-09-867-847-16
2	29	100.0	6	3	US-09-867-847-24
3	29	100.0	6	3	US-09-915-092-6
4	29	100.0	6	3	US-09-915-092-14
5	29	100.0	6	3	US-09-747-408-7
6	29	100.0	6	3	US-09-747-408-15
7	29	100.0	6	5	US-10-728-028-6
8	29	100.0	6	5	US-10-728-028-14
9	29	100.0	6	5	US-10-825-958-14
10	29	100.0	6	5	US-10-825-958-22
11	29	100.0	37	4	US-10-641-924-6
12	29	100.0	37	4	US-10-642-255-6
13	29	100.0	74	4	US-10-115-223-19
14	29	100.0	74	4	US-10-115-223-25
15	29	100.0	74	4	US-10-402-212-19
16	29	100.0	74	4	US-10-402-212-25
17	29	100.0	108	4	US-10-115-223-20
18	29	100.0	108	4	US-10-115-223-26
19	29	100.0	108	4	US-10-402-212-20
20	29	100.0	108	4	US-10-402-212-26
21	29	100.0	193	4	US-10-115-223-18
22	29	100.0	193	4	US-10-115-223-24
23	29	100.0	193	4	US-10-402-212-18
24	29	100.0	193	4	US-10-402-212-24
25	29	100.0	222	4	US-10-115-223-17
26	29	100.0	222	4	US-10-402-212-17
27	29	100.0	228	4	US-10-115-223-23

28	29	100.0	228	4	US-10-402-212-23	Sequence 23, Appl
29	29	100.0	261	5	US-10-795-159-697	Sequence 697, App
30	29	100.0	429	4	US-10-115-223-45	Sequence 45, Appl
31	29	100.0	429	4	US-10-402-212-45	Sequence 45, Appl
32	29	100.0	468	5	US-10-450-763-54360	Sequence 54360, A
33	29	100.0	660	3	US-09-391-104-19	Sequence 19, Appl
34	29	100.0	660	3	US-09-801-196-35	Sequence 35, Appl
35	29	100.0	660	3	US-09-918-715-208	Sequence 208, App
36	29	100.0	660	4	US-10-219-329-14	Sequence 14, Appl
37	29	100.0	660	4	US-10-301-822-125	Sequence 125, App
38	29	100.0	660	4	US-10-153-185-14	Sequence 14, Appl
39	29	100.0	660	4	US-10-219-561-14	Sequence 14, Appl
40	29	100.0	660	4	US-10-131-985-25	Sequence 25, Appl
41	29	100.0	660	4	US-10-447-315-3	Sequence 3, Appl
42	29	100.0	660	4	US-10-032-376A-14	Sequence 14, Appl
43	29	100.0	660	4	US-10-335-207-14	Sequence 14, Appl
44	29	100.0	660	4	US-10-480-621-1	Sequence 1, Appl
45	29	100.0	660	4	US-10-474-794-208	Sequence 208, App
46	29	100.0	660	5	US-10-601-059-14	Sequence 14, Appl
47	29	100.0	660	5	US-10-872-198-131	Sequence 131, App
48	29	100.0	660	5	US-10-901-417-25	Sequence 25, Appl
49	29	100.0	660	5	US-10-979-159-208	Sequence 208, App
50	29	100.0	660	5	US-10-287-436A-489	Sequence 489, App
51	29	100.0	660	5	US-10-287-436A-1185	Sequence 1185, Ap
52	29	100.0	660	6	US-11-021-951-131	Sequence 131, App
53	29	100.0	660	6	US-11-031-488-14	Sequence 14, Appl
54	29	100.0	663	4	US-10-115-223-30	Sequence 30, Appl
55	29	100.0	663	4	US-10-402-212-30	Sequence 30, Appl
56	29	100.0	718	4	US-10-369-493-4873	Sequence 4873, Ap
57	29	100.0	737	4	US-10-369-493-7633	Sequence 7633, Ap
58	29	100.0	770	4	US-10-437-963-138526	Sequence 138526, A
59	29	100.0	1330	5	US-10-450-763-54358	Sequence 54358, A
60	28	96.6	383	4	US-10-369-493-4941	Sequence 4941, Ap
61	28	96.6	383	4	US-10-369-493-7639	Sequence 7639, Ap
62	26	89.7	49	4	US-10-424-599-150066	Sequence 150066, A
63	26	89.7	61	4	US-10-424-599-150066	Sequence 150066, A
64	26	89.7	65	5	US-10-926-683-1595	Sequence 1595, Ap
65	26	89.7	89	4	US-10-425-115-35391	Sequence 35391, A
66	26	89.7	103	4	US-10-424-599-210814	Sequence 210814, A
67	26	89.7	108	4	US-10-437-963-114838	Sequence 114838, A
68	26	89.7	124	4	US-10-424-599-182643	Sequence 182643, A
69	26	89.7	131	4	US-10-767-701-41102	Sequence 41102, A
70	26	89.7	138	5	US-10-450-763-39449	Sequence 39449, A
71	26	89.7	172	4	US-10-437-963-172959	Sequence 172959, A
72	26	89.7	206	4	US-10-767-701-31699	Sequence 31699, A
73	26	89.7	208	5	US-10-450-763-39451	Sequence 39451, A
74	26	89.7	210	4	US-10-282-122A-61639	Sequence 61639, A
75	26	89.7	258	4	US-10-425-115-286732	Sequence 286732, A
76	26	89.7	270	4	US-10-437-963-176878	Sequence 176878, A
77	26	89.7	308	4	US-10-425-115-332957	Sequence 332957, A
78	26	89.7	314	4	US-10-425-115-286735	Sequence 286735, A
79	26	89.7	320	4	US-10-425-114-43310	Sequence 43310, A
80	26	89.7	320	4	US-10-425-114-64659	Sequence 64659, A
81	26	89.7	323	4	US-10-437-963-117099	Sequence 117099, A
82	26	89.7	334	3	US-09-933-767-348	Sequence 348, App
83	26	89.7	334	4	US-10-004-860-348	Sequence 348, App
84	26	89.7	334	4	US-10-023-282-348	Sequence 348, App
85	26	89.7	421	3	US-09-741-669-400	Sequence 400, App
86	26	89.7	421	4	US-10-282-122A-42751	Sequence 42751, A
87	26	89.7	441	5	US-10-821-273-34	Sequence 34, Appl
88	26	89.7	556	5	US-10-820-474A-119	Sequence 119, App
89	26	89.7	715	4	US-10-282-122A-75547	Sequence 75547, A
90	26	89.7	859	4	US-10-437-963-201533	Sequence 201533, A
91	26	89.7	1042	4	US-10-282-122A-61918	Sequence 61918, A
92	26	89.7	1166	4	US-10-437-963-128203	Sequence 128203, A
93	26	89.7	1172	5	US-10-450-763-36972	Sequence 36972, A
94	26	89.7	1749	4	US-10-437-963-142580	Sequence 142580, A
95	25	86.2	5	3	US-09-850-061A-40	Sequence 40, Appl
96	25	86.2	5	4	US-10-721-774-40	Sequence 40, Appl
97	25	86.2	6	3	US-09-867-847-18	Sequence 18, Appl
98	25	86.2	6	3	US-09-867-847-26	Sequence 26, Appl
99	25	86.2	6	3	US-09-915-092-8	Sequence 8, Appl
100	25	86.2	6	3	US-09-915-092-16	Sequence 16, Appl

101	25	86.2	6	3	US-09-747-408-9	Sequence 9, Appli	174	25	86.2	256	5	US-10-732-923-20752	Sequence 20752, A
102	25	86.2	6	3	US-09-747-408-17	Sequence 17, Appli	175	25	86.2	268	4	US-10-369-493-20071	Sequence 20071, A
103	25	86.2	6	5	US-10-728-028-8	Sequence 8, Appli	176	25	86.2	268	4	US-10-425-115-308997	Sequence 308997, A
104	25	86.2	6	5	US-10-728-028-16	Sequence 16, Appli	177	25	86.2	282	3	US-09-845-713A-2	Sequence 2, Appli
105	25	86.2	6	5	US-10-825-958-16	Sequence 16, Appli	178	25	86.2	282	4	US-10-435-696-35	Sequence 35, Appli
106	25	86.2	6	5	US-10-825-958-24	Sequence 24, Appli	179	25	86.2	289	4	US-10-425-115-215163	Sequence 215163, A
107	25	86.2	22	4	US-10-425-115-347015	Sequence 347015, A	180	25	86.2	297	4	US-10-425-114-73046	Sequence 73046, A
108	25	86.2	25	3	US-09-764-877-1260	Sequence 1260, Ap	181	25	86.2	303	5	US-10-491-0067A-5	Sequence 5, Appli
109	25	86.2	25	4	US-10-424-515-1260	Sequence 1260, Ap	182	25	86.2	314	3	US-09-908-0067A-16	Sequence 16, Appli
110	25	86.2	34	5	US-10-499-352A-444	Sequence 444, App	183	25	86.2	317	4	US-10-425-115-225676	Sequence 225676, A
111	25	86.2	37	4	US-10-641-924-7	Sequence 7, Appli	184	25	86.2	322	3	US-09-816-028A-48	Sequence 48, Appli
112	25	86.2	37	4	US-10-642-255-7	Sequence 7, Appli	185	25	86.2	322	3	US-09-886-035-253	Sequence 253, App
113	25	86.2	39	4	US-10-424-599-220682	Sequence 220682, A	186	25	86.2	322	3	US-09-804-291-253	Sequence 253, App
114	25	86.2	55	4	US-10-424-599-171652	Sequence 171652, A	187	25	86.2	322	4	US-10-017-161-156	Sequence 156, App
115	25	86.2	60	4	US-10-437-963-173619	Sequence 173619, A	188	25	86.2	322	4	US-10-303-161-48	Sequence 48, Appli
116	25	86.2	62	4	US-10-424-599-197144	Sequence 197144, A	189	25	86.2	322	4	US-10-303-118-48	Sequence 48, Appli
117	25	86.2	62	4	US-10-424-599-212719	Sequence 212719, A	190	25	86.2	322	4	US-10-303-128-48	Sequence 48, Appli
118	25	86.2	63	4	US-10-424-599-217238	Sequence 217238, A	191	25	86.2	322	4	US-10-303-134-48	Sequence 48, Appli
119	25	86.2	65	4	US-10-029-386-28659	Sequence 28659, A	192	25	86.2	322	4	US-10-303-162-48	Sequence 48, Appli
120	25	86.2	66	4	US-10-425-115-367811	Sequence 367811, A	193	25	86.2	322	4	US-10-387-629-76	Sequence 76, Appli
121	25	86.2	69	4	US-10-424-599-201270	Sequence 201270, A	194	25	86.2	322	4	US-10-292-798-134	Sequence 134, App
122	25	86.2	70	4	US-10-425-115-292851	Sequence 292851, A	195	25	86.2	322	4	US-10-343-650A-582	Sequence 582, App
123	25	86.2	71	4	US-10-424-599-170927	Sequence 170927, A	196	25	86.2	322	4	US-10-473-518-2	Sequence 2, Appli
124	25	86.2	75	4	US-10-425-115-239056	Sequence 239056, A	197	25	86.2	322	4	US-10-820-536-48	Sequence 48, Appli
125	25	86.2	80	4	US-10-243-552-570	Sequence 570, App	198	25	86.2	322	4	US-10-845-408-48	Sequence 48, Appli
126	25	86.2	80	4	US-10-437-963-111335	Sequence 111335, A	199	25	86.2	322	4	US-10-845-412-48	Sequence 48, Appli
127	25	86.2	81	4	US-10-425-115-229931	Sequence 229931, A	200	25	86.2	322	5	US-10-846-219-48	Sequence 48, Appli
128	25	86.2	84	4	US-10-424-599-245453	Sequence 245453, A	201	25	86.2	322	5	US-10-821-604-48	Sequence 48, Appli
129	25	86.2	87	4	US-10-437-963-133986	Sequence 133986, A	202	25	86.2	322	5	US-10-847-983-48	Sequence 48, Appli
130	25	86.2	89	4	US-10-425-115-302836	Sequence 302836, A	203	25	86.2	322	5	US-10-821-507-48	Sequence 48, Appli
131	25	86.2	90	4	US-10-424-599-147666	Sequence 147666, A	204	25	86.2	322	5	US-10-850-873-48	Sequence 48, Appli
132	25	86.2	90	4	US-10-425-115-236215	Sequence 236215, A	205	25	86.2	322	5	US-10-850-125-48	Sequence 48, Appli
133	25	86.2	95	4	US-10-437-963-197590	Sequence 197590, A	206	25	86.2	322	5	US-10-830-825-48	Sequence 48, Appli
134	25	86.2	98	4	US-10-425-115-364147	Sequence 364147, A	207	25	86.2	322	5	US-10-962-334-48	Sequence 48, Appli
135	25	86.2	99	4	US-10-437-963-150181	Sequence 150181, A	208	25	86.2	322	5	US-10-830-397-48	Sequence 48, Appli
136	25	86.2	109	4	US-10-437-963-105773	Sequence 105773, A	209	25	86.2	322	5	US-10-962-235-48	Sequence 48, Appli
137	25	86.2	109	4	US-10-425-115-226514	Sequence 226514, A	210	25	86.2	322	5	US-10-961-882-48	Sequence 48, Appli
138	25	86.2	117	3	US-09-864-761-37128	Sequence 37128, A	211	25	86.2	322	5	US-10-819-316-253	Sequence 253, App
139	25	86.2	127	4	US-10-425-115-362628	Sequence 362628, A	212	25	86.2	322	5	US-10-819-316-531	Sequence 531, App
140	25	86.2	127	4	US-10-767-701-47243	Sequence 47243, A	213	25	86.2	327	4	US-10-437-963-109308	Sequence 109308, A
141	25	86.2	128	4	US-10-425-115-192450	Sequence 192450, A	214	25	86.2	332	4	US-10-274-694-2	Sequence 2, Appli
142	25	86.2	129	4	US-10-424-599-278483	Sequence 278483, A	215	25	86.2	332	4	US-10-369-493-11167	Sequence 11167, A
143	25	86.2	130	4	US-10-424-599-170319	Sequence 170319, A	216	25	86.2	332	4	US-10-369-493-22884	Sequence 22884, A
144	25	86.2	132	4	US-10-029-386-28941	Sequence 28941, A	217	25	86.2	332	5	US-10-332-448-2	Sequence 2, Appli
145	25	86.2	133	4	US-10-424-599-270652	Sequence 270652, A	218	25	86.2	347	3	US-09-939-484-6	Sequence 6, Appli
146	25	86.2	133	4	US-10-425-115-305393	Sequence 305393, A	219	25	86.2	347	3	US-09-939-483-6	Sequence 6, Appli
147	25	86.2	135	4	US-10-437-963-141578	Sequence 141578, A	220	25	86.2	354	6	US-11-037-143-6189	Sequence 6189, Ap
148	25	86.2	140	4	US-10-424-599-151465	Sequence 151465, A	221	25	86.2	356	4	US-10-424-599-278238	Sequence 278238, A
149	25	86.2	150	4	US-10-335-977-6540	Sequence 6540, Ap	222	25	86.2	366	4	US-10-437-963-167534	Sequence 167534, A
150	25	86.2	155	4	US-10-424-599-200083	Sequence 200083, A	223	25	86.2	373	4	US-10-369-493-7986	Sequence 7986, Ap
151	25	86.2	171	4	US-10-424-599-229782	Sequence 229782, A	224	25	86.2	380	4	US-10-369-493-11163	Sequence 11163, A
152	25	86.2	175	4	US-10-437-963-123124	Sequence 123124, A	225	25	86.2	382	4	US-10-369-493-11163	Sequence 77801, A
153	25	86.2	180	4	US-10-424-599-252237	Sequence 252237, A	226	25	86.2	411	4	US-10-282-122A-77801	Sequence 68770, A
154	25	86.2	186	5	US-10-481-032A-214	Sequence 214, App	227	25	86.2	415	4	US-10-282-122A-68770	Sequence 68770, A
155	25	86.2	186	5	US-10-481-032A-218	Sequence 218, App	228	25	86.2	416	6	US-10-055-475-14	Sequence 14, Appli
156	25	86.2	188	4	US-10-437-963-172476	Sequence 172476, A	229	25	86.2	430	4	US-11-042-922-14	Sequence 14, Appli
157	25	86.2	190	4	US-10-437-963-137998	Sequence 137998, A	230	25	86.2	430	4	US-10-058-636-2	Sequence 2, Appli
158	25	86.2	198	4	US-10-437-963-172452	Sequence 172452, A	231	25	86.2	430	4	US-10-799-016-2	Sequence 2, Appli
159	25	86.2	201	4	US-10-425-114-67850	Sequence 67850, A	232	25	86.2	454	3	US-09-939-811-12	Sequence 12, Appli
160	25	86.2	202	5	US-10-732-923-19034	Sequence 19034, A	233	25	86.2	472	5	US-10-472-328-4158	Sequence 4158, Ap
161	25	86.2	209	4	US-10-424-599-280085	Sequence 280085, A	234	25	86.2	473	5	US-10-617-320-3273	Sequence 3273, Ap
162	25	86.2	210	4	US-10-282-122A-65447	Sequence 65447, A	235	25	86.2	481	6	US-11-037-143-3162	Sequence 3162, Ap
163	25	86.2	210	4	US-10-282-122A-66099	Sequence 66099, A	236	25	86.2	507	4	US-10-223-070-9	Sequence 9, Appli
164	25	86.2	224	4	US-10-424-599-246461	Sequence 246461, A	237	25	86.2	514	6	US-10-055-475-13	Sequence 13, Appli
165	25	86.2	224	4	US-10-424-599-257424	Sequence 257424, A	238	25	86.2	514	6	US-11-042-922-13	Sequence 13, Appli
166	25	86.2	246	6	US-11-097-143-2748	Sequence 2748, Ap	239	25	86.2	530	3	US-09-804-014A-28	Sequence 28, Appli
167	25	86.2	247	4	US-10-335-977-6541	Sequence 6541, Ap	240	25	86.2	532	3	US-09-939-811-6	Sequence 6, Appli
168	25	86.2	247	4	US-10-335-977-6542	Sequence 6542, Ap	241	25	86.2	532	3	US-09-875-321-13	Sequence 13, Appli
169	25	86.2	247	5	US-10-732-923-19035	Sequence 19035, A	242	25	86.2	532	3	US-09-804-014A-31	Sequence 31, Appli
170	25	86.2	249	4	US-10-369-493-10584	Sequence 10584, A	243	25	86.2	532	4	US-10-162-012-13	Sequence 13, Appli
171	25	86.2	254	4	US-10-369-493-18714	Sequence 18714, A	244	25	86.2	532	4	US-10-254-010-2	Sequence 2, Appli
172	25	86.2	255	5	US-10-732-923-20940	Sequence 20940, A	245	25	86.2	532	5	US-10-162-102-13	Sequence 13, Appli
173	25	86.2	255	6	US-11-097-143-29655	Sequence 29655, A	246	25	86.2	539	4	US-10-916-061-13	Sequence 13, Appli
												US-10-282-122A-48163	Sequence 48163, A

247 25 86.2 4 US-10-282-122A-49134 Sequence 49134, A
248 25 86.2 4 US-10-282-122A-50632 Sequence 50632, A
249 25 86.2 3 US-09-735-705-225 Sequence 225, App
250 25 86.2 3 US-09-850-716A-225 Sequence 225, App
251 25 86.2 3 US-09-897-778-225 Sequence 225, App
252 25 86.2 3 US-09-943-075A-6 Sequence 6, Appl
253 25 86.2 3 US-09-738-626-5465 Sequence 5465, Ap
254 25 86.2 3 US-10-039-272-2 Sequence 2, Appl
255 25 86.2 4 US-10-007-700-225 Sequence 225, App
256 25 86.2 4 US-10-117-982-225 Sequence 225, App
257 25 86.2 4 US-10-463-106-2 Sequence 2, Appl
258 25 86.2 4 US-10-295-027-1258 Sequence 1258, Ap
259 25 86.2 4 US-10-313-986-225 Sequence 225, App
260 25 86.2 4 US-10-309-290-152 Sequence 152, App
261 25 86.2 4 US-10-408-765A-466 Sequence 466, App
262 25 86.2 5 US-10-775-972-225 Sequence 225, App
263 25 86.2 5 US-10-723-860-1128 Sequence 1128, Ap
264 25 86.2 5 US-10-922-124-225 Sequence 225, App
265 25 86.2 5 US-10-978-758-6 Sequence 6, Appl
266 25 86.2 5 US-10-631-467-821 Sequence 821, App
267 25 86.2 5 US-10-450-763-39378 Sequence 39378, A
268 25 86.2 4 US-10-282-122A-50907 Sequence 50907, A
269 25 86.2 4 US-10-227-884-42 Sequence 42, Appl
270 25 86.2 4 US-10-230-163-42 Sequence 42, Appl
271 25 86.2 4 US-10-230-338-42 Sequence 42, Appl
272 25 86.2 4 US-10-218-631-42 Sequence 42, Appl
273 25 86.2 4 US-10-230-414-42 Sequence 42, Appl
274 25 86.2 4 US-10-232-224-42 Sequence 42, Appl
275 25 86.2 4 US-10-216-159A-42 Sequence 42, Appl
276 25 86.2 4 US-10-218-849-42 Sequence 42, Appl
277 25 86.2 4 US-10-227-873-42 Sequence 42, Appl
278 25 86.2 4 US-10-227-883-42 Sequence 42, Appl
279 25 86.2 4 US-10-219-076-42 Sequence 42, Appl
280 25 86.2 4 US-10-230-434-42 Sequence 42, Appl
281 25 86.2 4 US-10-219-003-42 Sequence 42, Appl
282 25 86.2 4 US-10-219-075-42 Sequence 42, Appl
283 25 86.2 4 US-10-219-464-42 Sequence 42, Appl
284 25 86.2 4 US-10-219-466-42 Sequence 42, Appl
285 25 86.2 4 US-10-219-479-42 Sequence 42, Appl
286 25 86.2 4 US-10-219-481-42 Sequence 42, Appl
287 25 86.2 4 US-10-230-260-42 Sequence 42, Appl
288 25 86.2 4 US-10-232-231-42 Sequence 42, Appl
289 25 86.2 4 US-10-232-233-42 Sequence 42, Appl
290 25 86.2 4 US-10-216-165-42 Sequence 42, Appl
291 25 86.2 4 US-10-218-956-42 Sequence 42, Appl
292 25 86.2 4 US-10-219-468-42 Sequence 42, Appl
293 25 86.2 4 US-10-219-478-42 Sequence 42, Appl
294 25 86.2 4 US-10-219-536-42 Sequence 42, Appl
295 25 86.2 4 US-10-233-205-42 Sequence 42, Appl
296 25 86.2 4 US-10-219-072-42 Sequence 42, Appl
297 25 86.2 4 US-10-219-470-42 Sequence 42, Appl
298 25 86.2 4 US-10-219-474-42 Sequence 42, Appl
299 25 86.2 4 US-10-219-524-42 Sequence 42, Appl
300 25 86.2 4 US-10-219-528-42 Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-09-867-847-16
; Sequence 16, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

US-09-867-847-24
; Sequence 24, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

US-09-867-847-594
; Sequence 594, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

US-09-867-847-847
; Sequence 847, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

US-09-867-847-16
; Sequence 16, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

US-09-867-847-24
; Sequence 24, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

US-09-867-847-594
; Sequence 594, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

US-09-867-847-847
; Sequence 847, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xiangqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

```
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-747-408-7

Query Match          100.0%;   Score 29;   DB 3;   Length 6;
Best Local Similarity 100.0%;   Pred. No. 1.7e+06;
Matches 6;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;
```

RESULT 6
US-09-747-408-15
; Sequence 15, Application US/09747408
; Publication No. US2003003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine

```

; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/0747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-15

Query Match          100.0%; Score 29; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFFA 6
   |||||
Db 1 KAVFFFA 6

```

US-10-728-028--6
 ; Sequence 6, Application US/10728028
 ; Publication No. US20050048000A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GERVAIS, Francine
 ; APPLICANT: KONG, Xiangi
 ; APPLICANT: CHALIFOUR, Robert
 ; APPLICANT: MICHAELT, David

```

, TITLE OF INVENTION:  USES THEREOF
, FILE REFERENCE:  NBI-139CP
, CURRENT APPLICATION NUMBER:  US/10/728,028
, CURRENT FILING DATE:  2003-12-03
, PRIOR APPLICATION NUMBER:  60/443291
, PRIOR FILING DATE:  2003-01-29
, PRIOR APPLICATION NUMBER:  09/915092
, PRIOR FILING DATE:  2001-07-24
, PRIOR APPLICATION NUMBER:  60/220808
, PRIOR FILING DATE:  2000-07-25
, NUMBER OF SEQ ID NOS:  28
, SOFTWARE:  Fast-SEQ for Windows Version 4.0
, SEQ ID NO 6
, LENGTH:  6
, TYPE:  PRT
, ORGANISM:  Artificial Sequence

```

```
;
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-6

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 8
US-10-728-028-14
; Sequence 14, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNEAULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-14

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 9
US-10-825-958-14
; Sequence 14, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-825-958-14

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 10
US-10-825-958-22
; Sequence 22, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-22

Query Match      100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      1 KAVFFA 6

RESULT 11
US-10-641-924-6
; Sequence 6, Application US/10641924
; Publication No. US20040096881A1
; GENERAL INFORMATION:
; APPLICANT: Blasko, Eric
; APPLICANT: Kausner, Katalin
; APPLICANT: Parkinson, John
; TITLE OF INVENTION: enOS Mutants Useful for Gene Therapy
; FILE REFERENCE: 53035AUSM1
; CURRENT APPLICATION NUMBER: US/10/641,924
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,638
; PRIOR FILING DATE: 2002-08-16
```

```
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-641-924-6

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      18 KAVFFA 23

RESULT 12
US-10-642-255-6
; Sequence 6, Application US/10642255
; Publication No. US20040120930A1
; GENERAL INFORMATION:
; APPLICANT: Dole, William P.
; APPLICANT: Kausser, Katalin
; APPLICANT: Qian, Hu Sheng
; APPLICANT: Rubany1, Gabor
; TITLE OF INVENTION: Gene Therapy for Critical Limb Ischemia with Wild Type or Mutant
; FILE REFERENCE: 52339AUSM1
; CURRENT APPLICATION NUMBER: US/10/642,255
; CURRENT FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 60/403,637
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-642-255-6

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      18 KAVFFA 23

RESULT 13
US-10-115-223-19
; Sequence 19, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19

Query Match      100.0%; Score 29; DB 4; Length 37;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      18 KAVFFA 23

RESULT 14
US-10-115-223-25
; Sequence 25, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-25

Query Match      100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      64 KAVFFA 69

RESULT 15
US-10-402-212-19
; Sequence 19, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
```

; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-19

Query Match 100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 16

US-10-402-212-25
; Sequence 25, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-25

Query Match 100.0%; Score 29; DB 4; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 17

US-10-115-223-20
; Sequence 20, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773

; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-20

Query Match 100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 18

US-10-115-223-26
; Sequence 26, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-26

Query Match 100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 19

US-10-402-212-20
; Sequence 20, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223

```
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-20

Query Match          100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 20
US-10-402-212-26
; Sequence 26, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-26

Query Match          100.0%; Score 29; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 21
US-10-115-223-18
; Sequence 18, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-24

Query Match          100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 23
US-10-402-212-18
; Sequence 18, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-24

Query Match          100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 23
US-10-402-212-18
; Sequence 18, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
```

; APPLICANT: Chereesh, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-18

Query Match 100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 64 KAVFFA 69

RESULT 24
US-10-402-212-24
; Sequence 24, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Chereesh, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-24

Query Match 100.0%; Score 29; DB 4; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 64 KAVFFA 69

RESULT 25
US-10-115-223-17
; Sequence 17, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Chereesh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-17

Query Match 100.0%; Score 29; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 93 KAVFFA 98

RESULT 26
US-10-402-212-17
; Sequence 17, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Chereesh, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-402-212-17

Query Match 100.0%; Score 29; DB 4; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
| | | | |
Db 93 KAVFFA 98

RESULT 27

US-10-115-223-23
; Sequence 23, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-23

Query Match 100.0%; Score 29; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
| | | | |
Db 99 KAVFFA 104

RESULT 28

US-10-402-212-23
; Sequence 23, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheresch, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-23

Query Match 100.0%; Score 29; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
| | | | |
Db 99 KAVFFA 104

RESULT 29

US-10-795-159-697
; Sequence 697, Application US/10795159
; Publication No. US20050221439A1
; GENERAL INFORMATION:
; APPLICANT: BAKALETZ et al.
; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
; FILE REFERENCE: 28335/38815A
; CURRENT APPLICATION NUMBER: US/10/795,159
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/453,134
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 771
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 697
; LENGTH: 261
; TYPE: PRT
; ORGANISM: H. influenzae
US-10-795-159-697

Query Match 100.0%; Score 29; DB 5; Length 261;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
| | | | |
Db 205 KAVFFA 210

RESULT 30

US-10-115-223-45
; Sequence 45, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-223-45

Query Match 100.0%; Score 29; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
| | | | |
Db 300 KAVFFA 305

OTHER INFORMATION: Fibronectin type II domain identified by Pfam, accession name
OTHER INFORMATION: fn2, E-value=4.4e-55, Pfam score of 147.1

RESULT 31

US-10-402-212-45
Sequence 45, Application US/10402212
Publication No. US20040063790A1
GENERAL INFORMATION:

APPLICANT: Brooks, Peter C.
APPLICANT: Cheresch, David A.
APPLICANT: Silletti, Steven A.
APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS

FILE REFERENCE: TSRI-419.3
CURRENT APPLICATION NUMBER: US/10/402,212
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: 10/115,223
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 09/194,468
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: PCT/US97/09158
PRIOR FILING DATE: 1997-05-30
PRIOR APPLICATION NUMBER: 60/018,773
PRIOR FILING DATE: 1996-05-31
PRIOR APPLICATION NUMBER: 60/015,869
PRIOR FILING DATE: 1996-05-31
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 45

LENGTH: 429

TYPE: PRT

ORGANISM: Homo sapiens

US-10-402-212-45

Query Match 100.0%; Score 29; DB 4; Length 429;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

DB 300 KAVFFA 305

RESULT 32

US-10-450-763-54360
Sequence 54360, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:

APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom

SEQ ID NO 54360

LENGTH: 468

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (221)..(258)

OTHER INFORMATION: Type II fibronectin collagen-binding domain proteins domain

OTHER INFORMATION: identified by eMATRIX, accession number BL00023, p-value=4.682e-3

OTHER INFORMATION: raw score of 24.31

FEATURE:

NAME/KEY: DOMAIN

LOCATION: (167)..(264)

FEATURES:

NAME/KEY: misc_feature
LOCATION: (1)..(468)
OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-54360

Query Match 100.0%; Score 29; DB 5; Length 468;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

DB 361 KAVFFA 366

RESULT 33

US-09-391-104-19
Sequence 19, Application US/09391104
Publication No. US20020031817A1
GENERAL INFORMATION:

APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
FILE REFERENCE: 6073.US.P1
CURRENT APPLICATION NUMBER: US/09/391,104
CURRENT FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/814,394
PRIOR FILING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19

LENGTH: 660

TYPE: PRT

ORGANISM: Homo sapiens

US-09-391-104-19

Query Match 100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

DB 531 KAVFFA 536

RESULT 34

US-09-801-196-35
Sequence 35, Application US/09801196
Patent No. US20020037827A1
GENERAL INFORMATION:

APPLICANT: Wang, Kai
APPLICANT: Smith, Ryan
APPLICANT: Pajardo, Mark
APPLICANT: Moss, Patrick
TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
FILE REFERENCE: 240083.509
CURRENT APPLICATION NUMBER: US/09/801,196
CURRENT FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35

LENGTH: 660

TYPE: PRT

ORGANISM: Homo sapiens

US-09-801-196-35

Query Match 100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

RESULT 35
US-09-918-715-208
; Sequence 208, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
; APPLICANT: Bert Vogelstein
; APPLICANT: Brad St. Croix
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-918-715-208

Query Match 100.0%; Score 29; DB 3; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

RESULT 36
US-10-219-329-14
; Sequence 14, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443.035W01
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-14

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 37
US-10-301-822-125
; Sequence 125, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burt, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPW01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-125

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

RESULT 38
US-10-153-185-14
; Sequence 14, Application US/10153185
; Publication No. US20030148959A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-14

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 531 KAVFFA 536
|||||

RESULT 39
US-10-219-561-14
; Sequence 14, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Mailik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-14

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 40
US-10-131-985-25
; Sequence 25, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-25

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 41
US-10-447-315-3
; Sequence 3, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; APPLICANT: Heissig, Beate
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1676.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-315-3

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 42
US-10-032-376A-14
; Sequence 14, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-14

Query Match 100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 43
US-10-335-207-14
; Sequence 14, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207

```
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-14

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 44
US-10-480-621-1
; Sequence 1, Application US/10480621
; Publication No. US20040175817A1
; GENERAL INFORMATION:
; APPLICANT: Jepson, Holly
; APPLICANT: Minshull, Claire
; APPLICANT: Paupit, Richard
; APPLICANT: Rowsell, Sian
; TITLE OF INVENTION: A CRYSTALLISED CATALYTIC DOMAIN OF MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE 9 (MMP9) AND THE USE OF
; TITLE OF INVENTION: ITS THREE DIMENSIONAL STRUCTURE TO DESIGN
; TITLE OF INVENTION: MMP9 MODULATORS
; FILE REFERENCE: 06275-377US1
; CURRENT APPLICATION NUMBER: US/10/480,621
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/SE02/01266
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: SE 0102298-7
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-621-1

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 45
US-10-474-794-208
; Sequence 208, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
; APPLICANT: Carson-Walter, Eleanor
; APPLICANT: St. Croix, Brad
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00179
; CURRENT APPLICATION NUMBER: US/10/474,794
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/308,829
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 359

; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-794-208

Query Match      100.0%; Score 29; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 46
US-10-601-059-14
; Sequence 14, Application US/10601059
; Publication No. US20040259802A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Shu-Ping
; APPLICANT: Quirk, Stephen
; APPLICANT: Kimberly-Clark Worldwide, Inc.
; TITLE OF INVENTION: Anti-Chondrosarcoma Compounds
; FILE REFERENCE: 1443.064US1
; CURRENT APPLICATION NUMBER: US/10/601,059
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 10/335,207
; PRIOR FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/219,329
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: PCT/US02/26319
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-601-059-14

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 47
US-10-872-198-131
; Sequence 131, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMEIER
; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U4
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
```

```
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 0403058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-131

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 48
US-10-901-417-25
; Sequence 25, Application US/10901417
; Publication No. US20050026836A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Ocleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/901,417
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/10/131,985
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-901-417-25

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 49
US-10-979-159-208
; Sequence 208, Application US/10979159
; Publication No. US20050142138A1
; GENERAL INFORMATION:
; APPLICANT: Brad St. Croix
; APPLICANT: Bert Vogelstein
; APPLICANT: Kenneth Kinzler

; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/10/979,159
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: US/09/918,715
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/222,599
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/282,850
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 208
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-979-159-208

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 50
US-10-287-436A-489
; Sequence 489, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 489
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-489

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
Db      531 KAVFFA 536

RESULT 51
US-10-287-436A-1185
; Sequence 1185, Application US/10287436A
; Publication No. US20050202421A1
; GENERAL INFORMATION:
; APPLICANT: CHILDREN'S HOSPITAL MEDICAL CENTER
; TITLE OF INVENTION: METHOD FOR DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: RHEUMATOID ARTHRITIS
; FILE REFERENCE: 10872.514696
; CURRENT APPLICATION NUMBER: US/10/287,436A
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/336,220
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 1446
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1185
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-1185

Query Match      100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFEA 6
Db      531 KAVFEA 536

RESULT 52
US-11-021-951-131
; Sequence 131, Application US/11021951
; Publication No. US20050175581A1
; GENERAL INFORMATION:
; APPLICANT: HAUPTS, Ulrich
; APPLICANT: KOLTERMANN, Andre
; APPLICANT: SCHEIDIG, Andreas
; APPLICANT: VOTSMEIER, Christian
; APPLICANT: Kettling, Ulrich
; APPLICANT: COCO, Wayne Michael
; TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
; FILE REFERENCE: 04156.0002U5
; CURRENT APPLICATION NUMBER: US/11/021,951
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: 10/872,198
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-131

Query Match      100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFEA 6
Db      531 KAVFEA 536

RESULT 53
US-11-031-488-14
; Sequence 14, Application US/11031488
; Publication No. US20050239710A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034U51
; CURRENT APPLICATION NUMBER: US/11/031,488

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1185
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-436A-1185

; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: US/10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-488-14

Query Match      100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFEA 6
Db      531 KAVFEA 536

RESULT 54
US-10-115-223-30
; Sequence 30, Application US/10115223
; Publication No. US20030176334A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheres, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/10/115,223
; CURRENT FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US/09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-115-223-30

Query Match      100.0%; Score 29; DB 4; Length 663;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFEA 6
Db      534 KAVFEA 539

RESULT 55
US-10-402-212-30
; Sequence 30, Application US/10402212
; Publication No. US20040063790A1
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter C.
; APPLICANT: Cheres, David A.
; APPLICANT: Silletti, Steven A.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: METHODS FOR INHIBITION OF ANGIOGENESIS
; FILE REFERENCE: TSRI-419.3
; CURRENT APPLICATION NUMBER: US/10/402,212
```

; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 10/115,223
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 09/194,468
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,869
; PRIOR FILING DATE: 1996-05-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-402-212-30

Query Match 100.0%; Score 29; DB 4; Length 663;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 534 KAVFFA 539

RESULT 56
US-10-369-493-4873
; Sequence 4873, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4873
; LENGTH: 718
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4873

Query Match 100.0%; Score 29; DB 4; Length 718;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 576 KAVFFA 581

RESULT 57
US-10-369-493-7633
; Sequence 7633, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7633
; LENGTH: 737
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7633

Query Match 100.0%; Score 29; DB 4; Length 737;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 576 KAVFFA 581

RESULT 58
US-10-437-963-138526
; Sequence 138526, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138526
; LENGTH: 770
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39906C.1.pep
US-10-437-963-138526

Query Match 100.0%; Score 29; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
DB 555 KAVFFA 560

RESULT 59
US-10-450-763-54358
; Sequence 54358, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23

```
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 54358
; LENGTH: 1330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (579)..(616)
; OTHER INFORMATION: Type II fibronectin collagen-binding domain proteins domain
; OTHER INFORMATION: identified by eMATRIX, accession number BL00023, p-value=4.682e-3
; OTHER INFORMATION: raw score of 24.31
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (271)..(451)
; OTHER INFORMATION: Matrixin domain identified by Pfam, accession name
; OTHER INFORMATION: Peptidase_M10, E-value=3.7e-109, Pfam score of 376.1
US-10-450-763-54358

Query Match      100.0%; Score 29; DB 5; Length 1330;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      768 KAVFFA 773

RESULT 60
US-10-493-493-4941
; Sequence 4941, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4941
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4941

Query Match      96.6%; Score 28; DB 4; Length 383;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      167 KAVFFA 172

RESULT 61
US-10-369-493-7699
; Sequence 7699, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 4941
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-369-493-4941

; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 7699
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-369-493-7699

Query Match      96.6%; Score 28; DB 4; Length 383;
Best Local Similarity 83.3%; Pred. No. 6.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      164 KAVFFA 169

RESULT 62
US-10-424-599-278606
; Sequence 278606, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278606
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93603C.1.pep
US-10-424-599-278606

Query Match      89.7%; Score 26; DB 4; Length 49;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFFA 6
Db      15 KAVFFA 20

RESULT 63
US-10-424-599-150066
; Sequence 150066, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Cao Yongwei
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 150066
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
```


; OTHER INFORMATION: Clone ID: PAT_MRT3847_106530C.1.pep
US-10-424-599-150066

Query Match 89.7%; Score 26; DB 4; Length 61;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|:||||
Db 53 KSVFFA 58

RESULT 64

US-10-926-683-1595
; Sequence 1595, Application US/10926683
; Publication No. US20050106595A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/10/926,683
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US/09/471,276
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/057,719
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 09/069,047
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: PCT/IB99/00712
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1595
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-926-683-1595

Query Match 89.7%; Score 26; DB 5; Length 65;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|:||||
Db 54 KAVFFS 59

RESULT 65

US-10-425-115-359391
; Sequence 359391, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 359391
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_90934C.1.pep
US-10-425-115-359391

Query Match 89.7%; Score 26; DB 4; Length 89;

Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|:||||
Db 54 KAVFFS 59

RESULT 66

US-10-424-599-210814
; Sequence 210814, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 210814
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32392C.1.pep
US-10-424-599-210814

Query Match 89.7%; Score 26; DB 4; Length 103;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|:||||
Db 44 KALFFA 49

RESULT 67

US-10-437-963-114838
; Sequence 114838, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 114838
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(108)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_18490C.1.pep
US-10-437-963-114838

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
||||:|
Db 48 KAVFYA 53

RESULT 68

US-10-424-599-182643
; Sequence 182643, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182643
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(124)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13593C.1.pep
US-10-424-599-182643

Query Match 89.7%; Score 26; DB 4; Length 124;

Best Local Similarity 83.3%; Pred. No. 6.1e+02; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
||||:
Db 65 KAVFFS 70

RESULT 69

US-10-767-701-41102
; Sequence 41102, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53355)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 41102
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C1929_1.pep
US-10-767-701-41102

Query Match 89.7%; Score 26; DB 4; Length 131;

Best Local Similarity 83.3%; Pred. No. 6.4e+02; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
||||:
Db 42 KAVFFA 47

RESULT 70

US-10-450-763-39449
; Sequence 39449, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 39449
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-39449

Query Match 89.7%; Score 26; DB 5; Length 138;

Best Local Similarity 83.3%; Pred. No. 6.7e+02; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
:|||||
Db 49 RAVFFA 54

RESULT 71

US-10-437-963-172959
; Sequence 172959, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 172959
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_71044C.1.pep
US-10-437-963-172959

Query Match 89.7%; Score 26; DB 4; Length 172;

Best Local Similarity 83.3%; Pred. No. 8.4e+02; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
:|||||
Db 145 RAVFFA 150

RESULT 72

US-10-767-701-31699
; Sequence 31699, Application US/10767701

Publication No. US20040172684A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof For Plant Improvement

FILE REFERENCE: 38-21(53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 31699

LENGTH: 206

TYPE: PRT

ORGANISM: Sorghum bicolor

FEATURE:

OTHER INFORMATION: Clone ID: SORBI-28MAY03-C102839_1.pep

US-10-767-701-31699

Query Match 89.7%; Score 26; DB 4; Length 206;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 6 KAVFFS 11

RESULT 73

US-10-450-763-39451

Sequence 39451, Application US/10450763

Publication No. US20050196754A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790CIP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR FILING DATE: 2001-03-30

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR FILING DATE: 2000-03-31

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: Custom

SEQ ID NO 39451

LENGTH: 208

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: (1)-(208)

OTHER INFORMATION: Xaa = X or * as defined in Table 2

US-10-450-763-39451

Query Match

Best Local Similarity 89.7%; Score 26; DB 5; Length 208;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 37 RAVFFA 42

RESULT 74

US-10-282-122A-61639

Sequence 61639, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu

APPLICANT: Zamudio, Carlos

APPLICANT: Malone, Cheryl

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlsen, Kari

APPLICANT: Zyskind, Judith

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John

APPLICANT: Carr, Grant

APPLICANT: Yamamoto, Robert

APPLICANT: Forsyth, R.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 61639

LENGTH: 210

TYPE: PRT

ORGANISM: Mycobacterium avium

US-10-282-122A-61639

Query Match 89.7%; Score 26; DB 4; Length 210;

Best Local Similarity 83.3%; Pred. No. 1e+03; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 54 RAVFFA 59

RESULT 75

US-10-425-115-286732

Sequence 286732, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(53222)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 286732

LENGTH: 258

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: MRT4577_24595C.1.pep

US-10-425-115-286732

Query Match 89.7%; Score 26; DB 4; Length 258;
 Best Local Similarity 83.3%; Pred. No. 1.2e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 ||:||||
 Db 212 KAMFFA 217

Search completed: December 29, 2005, 18:49:47
 Job time : 67.2903 secs

GenCore version 5.1.6
Copyright (C) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:18:57 ; Search time 20.0323 Seconds
(without alignments)
24.763 Million cell updates/sec

Title: US-10-009-122-15

Perfect score: 29

Sequence: 1 KAVPPA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5 COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/6 COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/PTCTUS COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/baCkfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	6	2	US-09-747-408-7
2	29	100.0	6	2	US-09-747-408-15
3	29	100.0	74	2	US-09-194-468A-19
4	29	100.0	74	2	US-09-194-468A-25
5	29	100.0	108	2	US-09-194-468A-20
6	29	100.0	108	2	US-09-194-468A-26
7	29	100.0	193	2	US-09-194-468A-18
8	29	100.0	193	2	US-09-194-468A-24
9	29	100.0	222	2	US-09-194-468A-17
10	29	100.0	228	2	US-09-194-468A-23
11	29	100.0	429	2	US-09-194-468A-45
12	29	100.0	631	2	US-08-448-489-17
13	29	100.0	631	2	US-09-689-730-17
14	29	100.0	660	2	US-08-704-711A-18
15	29	100.0	660	2	US-09-521-220-18
16	29	100.0	660	2	US-09-391-104-19
17	29	100.0	660	2	US-09-917-254-89
18	29	100.0	660	2	US-09-949-016-6512
19	29	100.0	660	2	US-09-949-016-7937
20	29	100.0	660	2	US-10-153-185-14
21	29	100.0	663	2	US-09-194-468A-30
22	26	89.7	65	2	US-09-471-276-1595
23	26	89.7	128	2	US-09-540-236-2808
24	26	89.7	295	2	US-09-248-796A-18333
25	26	89.7	334	2	US-09-205-258-348
26	26	89.7	334	2	US-10-004-860-348
27	26	89.7	494	2	US-09-328-352-7729

28	89.7	535	2	US-09-902-540-10002	Sequence 10002, A
29	89.7	1507	2	US-08-929-329-5	Sequence 5, Appl1
30	86.2		2	US-09-095-106A-40	Sequence 40, Appl1
31	86.2	6	2	US-09-747-408-9	Sequence 9, Appl1
32	86.2	6	2	US-09-747-408-17	Sequence 17, Appl1
33	86.2	28	1	US-08-461-216-4	Sequence 4, Appl1
34	86.2	77	2	US-09-513-999C-6921	Sequence 6921, Ap
35	86.2	80	2	US-09-248-796A-27785	Sequence 27785, A
36	86.2	142	2	US-09-270-767-33756	Sequence 33756, A
37	86.2	142	2	US-09-270-767-48973	Sequence 48973, A
38	86.2	261	2	US-09-270-767-43456	Sequence 43456, A
39	86.2	281	2	US-09-252-991A-29199	Sequence 29199, A
40	86.2	282	2	US-09-845-713A-2	Sequence 2, Appl1
41	86.2	306	2	US-09-303-518D-676	Sequence 676, App
42	86.2	306	2	US-09-303-518D-678	Sequence 678, App
43	86.2	307	2	US-09-303-518D-680	Sequence 680, App
44	86.2	322	2	US-09-495-406-34	Sequence 34, Appl
45	86.2	322	2	US-09-816-028A-48	Sequence 48, Appl
46	86.2	322	2	US-10-303-163-48	Sequence 163, Appl
47	86.2	322	2	US-10-303-134-48	Sequence 48, Appl
48	86.2	322	2	US-10-303-118-48	Sequence 48, Appl
49	86.2	322	2	US-10-303-128-48	Sequence 48, Appl
50	86.2	334	2	US-09-270-767-43522	Sequence 43522, A
51	86.2	337	2	US-09-438-185A-960	Sequence 960, App
52	86.2	347	2	US-08-749-816-3	Sequence 3, Appl1
53	86.2	347	2	US-09-144-914-6	Sequence 6, Appl1
54	86.2	375	2	US-09-489-039A-11261	Sequence 11261, A
55	86.2	421	2	US-09-543-681A-5731	Sequence 5731, Ap
56	86.2	430	2	US-09-272-960-2	Sequence 2, Appl1
57	86.2	430	2	US-10-058-636-2	Sequence 2, Appl1
58	86.2	462	2	US-09-583-110-3587	Sequence 3587, Ap
59	86.2	473	2	US-09-107-433-3273	Sequence 3273, Ap
60	86.2	474	2	US-09-489-039A-13140	Sequence 13140, A
61	86.2	532	1	US-08-288-405A-10	Sequence 10, Appl
62	86.2	532	2	US-10-162-012-13	Sequence 13, Appl
63	86.2	547	2	US-09-605-703B-2398	Sequence 2398, Ap
64	86.2	560	1	US-08-594-031-90	Sequence 90, Appl
65	86.2	560	2	US-09-643-597-225	Sequence 225, App
66	86.2	560	2	US-09-480-884A-225	Sequence 225, App
67	86.2	560	2	US-09-542-615A-225	Sequence 225, App
68	86.2	560	2	US-09-606-421B-225	Sequence 225, App
69	86.2	560	2	US-09-476-496A-225	Sequence 225, App
70	86.2	560	2	US-09-630-940B-225	Sequence 225, App
71	86.2	560	2	US-09-943-075A-6	Sequence 6, Appl1
72	86.2	560	2	US-10-039-272A-2	Sequence 2, Appl1
73	86.2	560	2	US-10-007-700-225	Sequence 225, App
74	86.2	560	5	US-09-985-799-90	Sequence 90, Appl
75	86.2	560	5	US-09-977-371-90	Sequence 90, Appl
76	86.2	591	2	US-09-489-039A-12837	Sequence 12837, A
77	86.2	605	2	US-08-693-214-8	Sequence 8, Appl1
78	86.2	945	2	US-09-198-452A-1030	Sequence 1030, Ap
79	86.2	1144	1	US-08-147-812-5	Sequence 5, Appl1
80	86.2	1144	1	US-08-319-866-12	Sequence 12, Appl
81	86.2	1144	2	US-09-123-708-2	Sequence 2, Appl1
82	86.2	1144	2	US-09-123-624-2	Sequence 2, Appl1
83	86.2	1144	2	US-09-661-258-5	Sequence 5, Appl1
84	86.2	1144	2	US-08-809-917-12	Sequence 12, Appl
85	86.2	1144	2	US-09-419-371-12	Sequence 12, Appl
86	86.2	2343	2	US-09-324-867-2	Sequence 2, Appl1
87	82.8	5	1	US-08-612-785B-25	Sequence 25, Appl
88	82.8	5	2	US-08-703-675C-38	Sequence 38, Appl
89	82.8	5	2	US-08-617-267C-25	Sequence 25, Appl
90	82.8	6	1	US-08-612-785B-9	Sequence 9, Appl1
91	82.8	6	2	US-08-703-675C-32	Sequence 32, Appl
92	82.8	6	2	US-08-617-267C-9	Sequence 9, Appl1
93	82.8	6	2	US-09-747-408-1	Sequence 1, Appl1
94	82.8	6	2	US-09-747-408-3	Sequence 3, Appl1
95	82.8	6	2	US-09-747-408-10	Sequence 10, Appl
96	82.8	6	2	US-09-747-408-11	Sequence 11, Appl
97	82.8	7	1	US-08-127-904-14	Sequence 14, Appl
98	82.8	7	1	US-08-612-785B-7	Sequence 7, Appl1
99	82.8	7	2	US-08-703-675C-30	Sequence 30, Appl
100	82.8	7	2	US-08-617-267C-7	Sequence 7, Appl1

101	24	82.8	7	2	US-09-264-709A-13	Sequence 13, Appl	174	24	82.8	19	2	US-10-815-353-5	Sequence 5, Appl
102	24	82.8	7	2	US-09-747-408-2	Sequence 2, Appl	175	24	82.8	19	2	US-10-816-529-5	Sequence 5, Appl
103	24	82.8	7	2	US-09-747-408-18	Sequence 18, Appl	176	24	82.8	19	2	US-10-815-391-5	Sequence 5, Appl
104	24	82.8	7	2	US-09-747-408-19	Sequence 19, Appl	177	24	82.8	19	2	US-10-816-022-5	Sequence 5, Appl
105	24	82.8	7	4	PCT-US94-10475-14	Sequence 14, Appl	178	24	82.8	19	2	US-09-724-940-75	Sequence 75, Appl
106	24	82.8	8	1	US-08-612-785B-5	Sequence 5, Appl	179	24	82.8	19	2	US-10-934-609-5	Sequence 5, Appl
107	24	82.8	8	1	US-08-630-645-1	Sequence 1, Appl	180	24	82.8	19	2	US-10-884-892-5	Sequence 5, Appl
108	24	82.8	8	2	US-08-703-675C-28	Sequence 28, Appl	181	24	82.8	20	2	US-08-970-833-10	Sequence 10, Appl
109	24	82.8	8	2	US-08-617-267C-5	Sequence 5, Appl	182	24	82.8	20	2	US-09-724-953-33	Sequence 33, Appl
110	24	82.8	8	2	US-09-095-106A-44	Sequence 44, Appl	183	24	82.8	20	2	US-09-724-567-33	Sequence 33, Appl
111	24	82.8	8	2	US-08-766-596A-1	Sequence 1, Appl	184	24	82.8	20	2	US-09-979-952-33	Sequence 33, Appl
112	24	82.8	8	2	US-09-668-314C-73	Sequence 73, Appl	185	24	82.8	20	2	US-09-585-817-33	Sequence 33, Appl
113	24	82.8	8	4	PCT-US96-10220-1	Sequence 1, Appl	186	24	82.8	26	1	US-08-304-585-7	Sequence 7, Appl
114	24	82.8	9	2	US-08-766-596A-50	Sequence 50, Appl	187	24	82.8	28	1	US-08-346-849-4	Sequence 4, Appl
115	24	82.8	9	2	US-08-766-596A-64	Sequence 64, Appl	188	24	82.8	28	1	US-08-302-080-7	Sequence 7, Appl
116	24	82.8	9	2	US-09-747-408-20	Sequence 20, Appl	189	24	82.8	28	1	US-08-609-090-2	Sequence 2, Appl
117	24	82.8	9	2	US-10-014-658-15	Sequence 15, Appl	190	24	82.8	28	1	US-08-986-948-7	Sequence 7, Appl
118	24	82.8	10	2	US-08-970-833-3	Sequence 3, Appl	191	24	82.8	28	1	US-08-233-284A-4	Sequence 4, Appl
119	24	82.8	10	2	US-09-724-961-20	Sequence 20, Appl	192	24	82.8	28	1	US-08-461-216-2	Sequence 2, Appl
120	24	82.8	10	2	US-09-724-961-21	Sequence 21, Appl	193	24	82.8	28	2	US-09-388-890-2	Sequence 2, Appl
121	24	82.8	10	2	US-09-724-961-22	Sequence 22, Appl	194	24	82.8	28	2	US-09-388-890-3	Sequence 3, Appl
122	24	82.8	10	2	US-09-724-961-23	Sequence 23, Appl	195	24	82.8	28	2	US-09-388-890-4	Sequence 4, Appl
123	24	82.8	10	2	US-09-724-961-24	Sequence 24, Appl	196	24	82.8	28	2	US-09-388-890-5	Sequence 5, Appl
124	24	82.8	10	2	US-09-580-018-20	Sequence 20, Appl	197	24	82.8	28	2	US-09-388-890-6	Sequence 6, Appl
125	24	82.8	10	2	US-09-580-018-21	Sequence 21, Appl	198	24	82.8	28	2	US-09-388-890-7	Sequence 7, Appl
126	24	82.8	10	2	US-09-580-018-22	Sequence 22, Appl	199	24	82.8	28	2	US-09-388-890-8	Sequence 8, Appl
127	24	82.8	10	2	US-09-580-018-23	Sequence 23, Appl	200	24	82.8	28	2	US-09-388-890-9	Sequence 9, Appl
128	24	82.8	10	2	US-09-580-018-24	Sequence 24, Appl	201	24	82.8	28	2	US-09-388-890-10	Sequence 10, Appl
129	24	82.8	10	2	US-09-724-551-20	Sequence 20, Appl	202	24	82.8	28	2	US-09-388-890-12	Sequence 12, Appl
130	24	82.8	10	2	US-09-724-551-21	Sequence 21, Appl	203	24	82.8	28	2	US-09-388-890-13	Sequence 13, Appl
131	24	82.8	10	2	US-09-724-551-22	Sequence 22, Appl	204	24	82.8	28	2	US-09-388-890-14	Sequence 14, Appl
132	24	82.8	10	2	US-09-724-551-23	Sequence 23, Appl	205	24	82.8	28	2	US-08-264-709A-1	Sequence 1, Appl
133	24	82.8	10	2	US-09-724-551-24	Sequence 24, Appl	206	24	82.8	28	2	US-08-723-661B-2	Sequence 2, Appl
134	24	82.8	10	2	US-09-724-940-20	Sequence 20, Appl	207	24	82.8	28	2	US-09-660-954-2	Sequence 2, Appl
135	24	82.8	10	2	US-09-724-940-21	Sequence 21, Appl	208	24	82.8	28	2	US-09-660-954-3	Sequence 3, Appl
136	24	82.8	10	2	US-09-724-940-22	Sequence 22, Appl	209	24	82.8	28	2	US-09-660-954-4	Sequence 4, Appl
137	24	82.8	10	2	US-09-724-940-23	Sequence 23, Appl	210	24	82.8	28	2	US-09-660-954-5	Sequence 5, Appl
138	24	82.8	10	2	US-09-724-940-24	Sequence 24, Appl	211	24	82.8	28	2	US-09-660-954-6	Sequence 6, Appl
139	24	82.8	11	1	US-08-630-645-14	Sequence 14, Appl	212	24	82.8	28	2	US-09-660-954-7	Sequence 7, Appl
140	24	82.8	11	2	US-08-766-596A-14	Sequence 14, Appl	213	24	82.8	28	2	US-09-660-954-8	Sequence 8, Appl
141	24	82.8	11	2	US-09-988-842-9	Sequence 9, Appl	214	24	82.8	28	2	US-09-660-954-9	Sequence 9, Appl
142	24	82.8	11	4	PCT-US96-10220-14	Sequence 14, Appl	215	24	82.8	28	2	US-09-660-954-10	Sequence 10, Appl
143	24	82.8	11	4	US-09-594-366-5	Sequence 5, Appl	216	24	82.8	28	2	US-09-660-954-12	Sequence 12, Appl
144	24	82.8	14	2	US-09-992-800-5	Sequence 5, Appl	217	24	82.8	28	2	US-09-660-954-13	Sequence 13, Appl
145	24	82.8	14	2	US-08-612-785B-14	Sequence 14, Appl	218	24	82.8	28	2	US-09-660-954-14	Sequence 14, Appl
146	24	82.8	15	1	US-08-612-785B-37	Sequence 37, Appl	219	24	82.8	28	2	US-08-898-300-4	Sequence 4, Appl
147	24	82.8	15	2	US-08-617-267C-14	Sequence 14, Appl	220	24	82.8	28	2	US-08-824-513-4	Sequence 4, Appl
148	24	82.8	15	2	US-08-766-596A-56	Sequence 56, Appl	221	24	82.8	28	2	US-09-623-548A-959	Sequence 959, App
149	24	82.8	15	2	US-08-766-596A-57	Sequence 57, Appl	222	24	82.8	28	2	US-09-623-548A-965	Sequence 965, App
150	24	82.8	15	2	US-08-766-596A-58	Sequence 58, Appl	223	24	82.8	28	2	US-09-623-548A-976	Sequence 976, App
151	24	82.8	15	2	US-08-766-596A-60	Sequence 60, Appl	224	24	82.8	28	2	US-09-623-548A-992	Sequence 992, App
152	24	82.8	15	2	US-08-766-596A-61	Sequence 61, Appl	225	24	82.8	28	2	US-09-623-548A-1003	Sequence 1003, App
153	24	82.8	15	2	US-08-766-596A-63	Sequence 63, Appl	226	24	82.8	28	2	US-09-657-276-959	Sequence 959, App
154	24	82.8	15	2	US-08-766-596A-65	Sequence 65, Appl	227	24	82.8	28	2	US-09-657-276-965	Sequence 965, App
155	24	82.8	15	2	US-08-766-596A-63	Sequence 63, Appl	228	24	82.8	28	2	US-09-657-276-976	Sequence 976, App
156	24	82.8	17	2	US-09-264-709A-2	Sequence 2, Appl	229	24	82.8	28	2	US-09-657-276-1003	Sequence 1003, App
157	24	82.8	17	2	US-09-594-366-3	Sequence 3, Appl	230	24	82.8	28	2	US-09-657-276-1003	Sequence 1003, App
158	24	82.8	17	2	US-09-623-548A-950	Sequence 950, App	231	24	82.8	28	2	US-09-865-294A-66	Sequence 66, Appl
159	24	82.8	17	2	US-09-623-548A-983	Sequence 983, App	232	24	82.8	30	1	US-08-609-090-3	Sequence 3, Appl
160	24	82.8	17	2	US-09-992-800-3	Sequence 3, Appl	233	24	82.8	30	2	US-08-861-847A-1	Sequence 1, Appl
161	24	82.8	17	2	US-09-657-276-950	Sequence 950, App	234	24	82.8	33	1	US-08-609-090-4	Sequence 4, Appl
162	24	82.8	17	2	US-09-657-276-983	Sequence 983, App	235	24	82.8	34	1	US-08-475-579A-4	Sequence 4, Appl
163	24	82.8	19	2	US-08-970-833-11	Sequence 11, Appl	236	24	82.8	35	1	US-08-304-585-6	Sequence 6, Appl
164	24	82.8	19	2	US-09-723-384-5	Sequence 5, Appl	237	24	82.8	35	1	US-08-612-785B-16	Sequence 16, Appl
165	24	82.8	19	2	US-09-724-961-75	Sequence 75, Appl	238	24	82.8	35	1	US-08-612-785B-36	Sequence 36, Appl
166	24	82.8	19	2	US-09-724-552-5	Sequence 5, Appl	239	24	82.8	35	1	US-08-612-785B-38	Sequence 38, Appl
167	24	82.8	19	2	US-09-580-018-75	Sequence 75, Appl	240	24	82.8	35	1	US-08-612-785B-40	Sequence 40, Appl
168	24	82.8	19	2	US-09-723-927-5	Sequence 5, Appl	241	24	82.8	35	2	US-08-617-267C-16	Sequence 16, Appl
169	24	82.8	19	2	US-09-724-489-5	Sequence 5, Appl	242	24	82.8	35	2	US-09-623-548A-979	Sequence 979, App
170	24	82.8	19	2	US-09-724-477-5	Sequence 5, Appl	243	24	82.8	35	2	US-09-623-548A-1006	Sequence 1006, App
171	24	82.8	19	2	US-09-723-762-5	Sequence 5, Appl	244	24	82.8	35	2	US-09-657-276-979	Sequence 979, App
172	24	82.8	19	2	US-09-201-430-5	Sequence 5, Appl	245	24	82.8	35	2	US-09-657-276-1006	Sequence 1006, App
173	24	82.8	19	2	US-09-724-551-75	Sequence 75, Appl	246	24	82.8	36	1	US-08-609-090-6	Sequence 6, Appl

```
247 24 82.8 36 2 US-09-861-847A-6
248 24 82.8 36 2 US-09-861-847A-11
249 24 82.8 38 1 US-08-302-808-1
250 24 82.8 38 1 US-07-737-371B-68
251 24 82.8 38 1 US-08-986-948-1
252 24 82.8 38 1 US-09-623-548A-975
253 24 82.8 38 2 US-09-623-548A-1002
254 24 82.8 38 2 US-09-657-276-975
255 24 82.8 38 2 US-09-657-276-1002
256 24 82.8 39 1 US-08-304-585-5
257 24 82.8 39 1 US-08-302-808-2
258 24 82.8 39 1 US-08-609-090-7
259 24 82.8 39 1 US-08-682-245A-1
260 24 82.8 39 1 US-08-986-948-1
261 24 82.8 40 1 US-07-744-767A-1
262 24 82.8 40 1 US-08-235-400-2
263 24 82.8 40 1 US-08-476-464A-2
264 24 82.8 40 1 US-08-304-585-1
265 24 82.8 40 1 US-08-304-585-8
266 24 82.8 40 1 US-08-302-808-3
267 24 82.8 40 1 US-08-433-734-1
268 24 82.8 40 1 US-08-609-090-8
269 24 82.8 40 1 US-07-737-371B-69
270 24 82.8 40 1 US-08-682-245A-2
271 24 82.8 40 1 US-08-986-948-3
272 24 82.8 40 1 US-08-461-216-1
273 24 82.8 40 2 US-08-959-148-1
274 24 82.8 40 2 US-09-242-724-22
275 24 82.8 40 2 US-08-723-661B-1
276 24 82.8 40 2 US-09-062-365-3
277 24 82.8 40 2 US-09-133-866-1
278 24 82.8 40 2 US-09-861-847A-7
279 24 82.8 40 2 US-09-861-847A-8
280 24 82.8 40 2 US-09-988-842-3
281 24 82.8 40 2 US-10-455-218-1
282 24 82.8 40 2 US-10-151-614-1
283 24 82.8 40 2 US-09-623-548A-956
284 24 82.8 40 2 US-09-623-548A-962
285 24 82.8 40 2 US-09-623-548A-968
286 24 82.8 40 2 US-09-623-548A-978
287 24 82.8 40 2 US-09-623-548A-989
288 24 82.8 40 2 US-09-623-548A-995
289 24 82.8 40 2 US-09-623-548A-1005
290 24 82.8 40 2 US-09-657-276-956
291 24 82.8 40 2 US-09-657-276-962
292 24 82.8 40 2 US-09-657-276-968
293 24 82.8 40 2 US-09-657-276-978
294 24 82.8 40 2 US-09-657-276-989
295 24 82.8 40 2 US-09-657-276-995
296 24 82.8 40 2 US-09-657-276-1005
297 24 82.8 40 2 US-09-962-955D-36
298 24 82.8 40 4 PCT-US92-06700-1
299 24 82.8 41 1 US-07-819-361-1
300 24 82.8 41 1 US-08-302-808-4
```

ALIGNMENTS

```
RESULT 1
US-09-747-408-7
; Sequence 7, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
```

```
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-7

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 2
US-09-747-408-15
; Sequence 15, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-15

Query Match 100.0%; Score 29; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 3
US-09-194-468A-19
; Sequence 19, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Chersesh, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-19
```

Query Match 100.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 4
US-09-194-468A-25
; Sequence 25, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-25

Query Match 100.0%; Score 29; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 5
US-09-194-468A-20
; Sequence 20, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-20

Query Match 100.0%; Score 29; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 38;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 6
US-09-194-468A-26
; Sequence 26, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-26

Query Match 100.0%; Score 29; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 64 KAVFFA 69

RESULT 7
US-09-194-468A-18
; Sequence 18, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Cheresch, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; TITLE OF INVENTION: ANGIOGENESIS
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-194-468A-18

Query Match 100.0%; Score 29; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

Db 64 KAVFFA 69

RESULT 8

US-09-194-468A-24

; Sequence 24, Application US/09194468A

; Patent No. 6500924

; GENERAL INFORMATION:

; APPLICANT: Brooks, Peter

; APPLICANT: Cheresh, David A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF

; FILE REFERENCE: MER0049S

; CURRENT APPLICATION NUMBER: US/09/194,468A

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 60/018,773

; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: 60/015,896

; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: PCT/US97/09158

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 193

; TYPE: PRT

; ORGANISM: Gallus gallus

US-09-194-468A-24

Query Match

Best Local Similarity 100.0%; Score 29; DB 2; Length 193;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 64 KAVFFA 69

RESULT 9

US-09-194-468A-17

; Sequence 17, Application US/09194468A

; Patent No. 6500924

; GENERAL INFORMATION:

; APPLICANT: Brooks, Peter

; APPLICANT: Cheresh, David A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF

; FILE REFERENCE: MER0049S

; CURRENT APPLICATION NUMBER: US/09/194,468A

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 60/018,773

; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: 60/015,896

; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: PCT/US97/09158

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 222

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-194-468A-17

Query Match

Best Local Similarity 100.0%; Score 29; DB 2; Length 222;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 93 KAVFFA 98

RESULT 10

US-09-194-468A-23

; Sequence 23, Application US/09194468A

; Patent No. 6500924

; GENERAL INFORMATION:

; APPLICANT: Brooks, Peter

; APPLICANT: Cheresh, David A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF

; FILE REFERENCE: MER0049S

; CURRENT APPLICATION NUMBER: US/09/194,468A

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 60/018,773

; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: 60/015,896

; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: PCT/US97/09158

; PRIOR FILING DATE: 1997-05-30

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 228

; TYPE: PRT

; ORGANISM: Gallus gallus

US-09-194-468A-23

Query Match

Best Local Similarity 100.0%; Score 29; DB 2; Length 228;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 99 KAVFFA 104

RESULT 11

US-09-194-468A-45

; Sequence 45, Application US/09194468A

; Patent No. 6500924

; GENERAL INFORMATION:

; APPLICANT: Brooks, Peter

; APPLICANT: Cheresh, David A.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF

; FILE REFERENCE: MER0049S

; CURRENT APPLICATION NUMBER: US/09/194,468A

; CURRENT FILING DATE: 1999-03-23

; PRIOR APPLICATION NUMBER: 60/018,773

; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: 60/015,896

; PRIOR FILING DATE: 1996-05-31

; PRIOR APPLICATION NUMBER: PCT/US97/09158

; NUMBER OF SEQ ID NOS: 45

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 45

; LENGTH: 429

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-194-468A-45

Query Match

Best Local Similarity 100.0%; Score 29; DB 2; Length 429;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

Db 300 KAVFFA 305

RESULT 12

US-08-448-489-17

```
; Sequence 17, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-17

Query Match          100.0%; Score 29; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 502 KAVFFA 507

RESULT 13
US-09-689-730-17
; Sequence 17, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-09-689-730-17

Query Match          100.0%; Score 29; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 502 KAVFFA 507

RESULT 14
US-08-704-711A-18
; Sequence 18, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
US-08-704-711A-18
```

```
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 660 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-18

Query Match          100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 531 KAVFFA 536

RESULT 15
US-09-521-220-18
; Sequence 18, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
US-09-521-220-18

Query Match          100.0%; Score 29; DB 2; Length 500;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 531 KAVFFA 536

RESULT 16
US-08-704-711A-18
; Sequence 18, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
US-08-704-711A-18
```

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/521,220
;; FILING DATE: 08-Mar-2000
;; CLASSIFICATION: <Unknown>
;; 21-OCT-1994
;; 17-MAR-1994
;;
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: 08/704,711
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: DE 4438838.1
;; FILING DATE: 21-OCT-1994
;; APPLICATION NUMBER: DE 4409663.1
;; FILING DATE: 17-MAR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: GRANADOS, Patricia D.
;; REGISTRATION NUMBER: 33,683
;; REFERENCE/DOCKET NUMBER: 26083/124
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136
;;
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 660 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-521-220-18

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 531 KAVFFA 536

RESULT 16
US-09-391-104-19
; Sequence 19, Application US/09391104
; Patent No. 6393171
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; PRIOR FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-19

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 531 KAVFFA 536

RESULT 17
US-09-917-254-89
; Sequence 89, Application US/09917254
; Patent No. 6703204
; GENERAL INFORMATION:
; APPLICANT: Mutter, George
; APPLICANT: Baak, Jan
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer
; FILE REFERENCE: B0801/7224(JRV)
; CURRENT APPLICATION NUMBER: US/09/917,254
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/222,093
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-917-254-89

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 531 KAVFFA 536

RESULT 18
US-09-949-016-6512
; Sequence 6512, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6512
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6512

Query Match 100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||
DB 531 KAVFFA 536

RESULT 19
US-09-949-016-7937
; Sequence 7937, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7937
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7937
```

```
Query Match          100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KAVFFA 6
Db      531 KAVFFA 536
```

```
RESULT 20
US-10-153-185-14
; Sequence 14, Application US/10153185
; Patent No. 6906036
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-14
```

```
Query Match          100.0%; Score 29; DB 2; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KAVFFA 6
Db      531 KAVFFA 536
```

```
RESULT 21
US-09-194-468A-30
; Sequence 30, Application US/09194468A
; Patent No. 6500924
; GENERAL INFORMATION:
; APPLICANT: Brooks, Peter
; APPLICANT: Chereah, David A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR INHIBITION OF
; FILE REFERENCE: MER0049S
; CURRENT APPLICATION NUMBER: US/09/194,468A
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/018,773
; PRIOR FILING DATE: 1996-05-31
; PRIOR APPLICATION NUMBER: 60/015,896
; PRIOR FILING DATE: 1996-05-31
```

```
; PRIOR APPLICATION NUMBER: PCT/US97/09158
; PRIOR FILING DATE: 1997-05-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Gallus gallus
US-09-194-468A-30
```

```
Query Match          100.0%; Score 29; DB 2; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KAVFFA 6
Db      534 KAVFFA 539
```

```
RESULT 22
US-09-471-276-1595
; Sequence 1595, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471.276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 1595
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-471-276-1595
```

```
Query Match          89.7%; Score 26; DB 2; Length 65;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 KAVFFA 6
Db      54 KAVFFS 59
```

```
RESULT 23
US-09-540-236-2808
; Sequence 2808, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2808
; LENGTH: 128
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2808
```

```
Query Match      89.7%; Score 26; DB 2; Length 128;
Best Local Similarity 83.3%; Pred. No. 1.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0;

QY      1 KAVFFA 6
      |||||
Db      55 KAVFYA 60

RESULT 24
US-09-248-796A-18333
; Sequence 18333, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18333
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18333

Query Match      89.7%; Score 26; DB 2; Length 295;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||
Db      31 KAVFYA 36

RESULT 25
US-09-205-258-348
; Sequence 348, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 348
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (288)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (334)
; OTHER INFORMATION: Xaa equals stop translation
;
US-09-205-258-348
```

```
Query Match      89.7%; Score 26; DB 2; Length 334;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||:|
Db      273 KAVFYA 278

RESULT 26
US-10-004-860-348
; Sequence 348, Application US/10004860
; Patent No. 6914047
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007PI
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 348
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; FEATURE:
; LOCATION: (288)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (334)
; OTHER INFORMATION: Xaa equals stop translation
US-10-004-860-348

Query Match      89.7%; Score 26; DB 2; Length 334;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||:|
Db      273 KAVFYA 278

RESULT 27
US-09-328-352-7729
; Sequence 7729, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 7729
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7729

Query Match      89.7%; Score 26; DB 2; Length 494;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||:|
Db      79 KSVFFA 84

RESULT 28
```

```
US-09-902-540-10002
; Sequence 10002, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10002
; LENGTH: 535
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10002

Query Match      89.7%; Score 26; DB 2; Length 535;
Best Local Similarity 83.3%; Pred. No. 7.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
      |||||:|
Db      131 KALFFA 136

RESULT 29
US-08-929-329-5
; Sequence 5, Application US/08929329
; Patent No. 6120770
; GENERAL INFORMATION:
; APPLICANT: Adams, John H
; APPLICANT: Dalton, John P
; APPLICANT: Kappe, Stefan
; TITLE OF INVENTION: Plasmodium Proteins Useful for Preparing
; TITLE OF INVENTION: Vaccine Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 S Meridian
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,329
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 835910-28685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1507 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
```

```
; ORIGINAL SOURCE:
; ORGANISM: Plasmodium yoelii
US-08-929-329-5

Query Match      89.7%; Score 26; DB 2; Length 1507;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1454 KAVYFA 1459

RESULT 30
US-09-095-106A-40
; Sequence 40, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVPFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386
; PRIOR FILING DATE: 1995-12-29
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Amyloidosis
US-09-095-106A-40

Query Match      86.2%; Score 25; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 1 KAVFF 5

RESULT 31
US-09-747-408-9
; Sequence 9, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-9

Query Match      86.2%; Score 25; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; ORIGINAL SOURCE:
; ORGANISM: Plasmodium yoelii
US-08-929-329-5

Query Match      89.7%; Score 26; DB 2; Length 1507;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1454 KAVYFA 1459

RESULT 32
US-09-747-408-17
; Sequence 17, Application US/09747408
; Patent No. 6670399
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; TITLE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-17

Query Match      86.2%; Score 25; DB 2; Length 6;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
Db 1 KAVFFA 6

RESULT 33
US-08-461-216-4
; Sequence 4, Application US/08461216
; Patent No. 5958883
; GENERAL INFORMATION:
; APPLICANT: Snow, A.D.
; TITLE OF INVENTION: ANIMAL MODELS OF HUMAN AMYLOIDOSES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
; STREET: 1420 Fifth Avenue, Suite 2800
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101-2347
; MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage
; COMPUTER: IBM PC/386 Compatible
; OPERATING SYSTEM: MS-DOS 4.01
; SOFTWARE: Word for Windows-t
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,216
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/969,734
; FILING DATE: October 23, 1992
; APPLICATION NUMBER: 07/950,417
; FILING DATE: September 23, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Broderick, Thomas F.
; REGISTRATION NUMBER: 31,332
; REFERENCE/DOCKET NUMBER: UOFW-1-6707
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 1-206-682-8100; 1-206-224-0709 (direct)
; TELEFAX: 1-206-224-0779
```

```
/
/
/ TELEX: 4938023
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ DESCRIPTION: {SYMBOL 98 \f "Symbol"}/A4(1-28) mutant;
/ DESCRIPTION: page 83, lines 27-28
US-08-461-216-4

Query Match      86.2%; Score 25; DB 1; Length 28;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      16 KGVFFA 21

RESULT 34
US-09-513-999C-6921
; Sequence 6921, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6921
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6921

Query Match      86.2%; Score 25; DB 2; Length 77;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      38 KVVFFA 43

RESULT 35
US-09-248-796A-27785
; Sequence 27785, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27785
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Candida albicans

US-09-248-796A-27785
Query Match      86.2%; Score 25; DB 2; Length 80;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      31 RA1FFA 36

RESULT 36
US-09-270-767-33756
; Sequence 33756, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33756
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-33756

Query Match      86.2%; Score 25; DB 2; Length 142;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      99 KGVFFA 104

RESULT 37
US-09-270-767-48973
; Sequence 48973, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48973
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-48973

Query Match      86.2%; Score 25; DB 2; Length 142;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVFFA 6
DB      99 KGVFFA 104

RESULT 38
US-09-270-767-43456
; Sequence 43456, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
```



```
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 43456
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-43456

Query Match      86.2%; Score 25; DB 2; Length 261;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVVFF 5
Db      184 KAVVFF 188

RESULT 39
US-09-252-991A-29199
; Sequence 29199, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29199
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29199

Query Match      86.2%; Score 25; DB 2; Length 281;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVVFF 6
Db      257 EAVVFF 262

RESULT 40
US-09-845-713A-2
; Sequence 2, Application US/09845713A
; Patent No. 6660476
; GENERAL INFORMATION:
; APPLICANT: MacMurray, James P.
; TITLE OF INVENTION: Polymorphisms in the PNMT Gene
; FILE REFERENCE: 1954-327-11
; CURRENT APPLICATION NUMBER: US/09/845,713A
; CURRENT FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,310
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-713A-2
```

```
Query Match      86.2%; Score 25; DB 2; Length 282;
Best Local Similarity 83.3%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KAVVFF 6
Db      270 KGVVFF 275

RESULT 41
US-09-303-518D-676
; Sequence 676, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scariato, Vincenzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 676
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-303-518D-676

Query Match      86.2%; Score 25; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KAVVFF 5
Db      155 KAVVFF 159

RESULT 42
US-09-303-518D-678
; Sequence 678, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scariato, Vincenzo
; APPLICANT: Masignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 678
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (67)..(67)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (203)..(203)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc_feature
; LOCATION: (208)..(208)
; OTHER INFORMATION: Xaa= any amino acid
```

```
; NAME/KEY: misc.feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc.feature
; LOCATION: (269)..(269)
; OTHER INFORMATION: Xaa= any amino acid
US-09-303-518D-678

Query Match      86.2%; Score 25; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 155 KAVPF 159

RESULT 43
US-09-303-518D-680
; Sequence 680, Application US/09303518D
; Patent No. 6914131
; GENERAL INFORMATION:
; APPLICANT: Scarlato, Vincenzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Neisserial Antigens
; FILE REFERENCE: CHIR0160
; CURRENT APPLICATION NUMBER: US/09/303,518D
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1098
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 680
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-303-518D-680

Query Match      86.2%; Score 25; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 155 KAVPF 159

RESULT 44
US-09-495-406-34
; Sequence 34, Application US/09495406
; Patent No. 6503744
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000110US
; CURRENT APPLICATION NUMBER: US/09/495,406
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (cstI)
; OTHER INFORMATION: from C. jejuni OH4384
US-09-495-406-34

; NAME/KEY: misc.feature
; LOCATION: (227)..(227)
; OTHER INFORMATION: Xaa= any amino acid
; NAME/KEY: misc.feature
; LOCATION: (269)..(269)
; OTHER INFORMATION: Xaa= any amino acid
US-09-303-518D-678

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 61 KAVPF 65

RESULT 45
US-09-816-028A-48
; Sequence 48, Application US/09816028A
; Patent No. 6699705
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/09/816,028A
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-09-816-028A-48

Query Match      86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVPF 5
Db 61 KAVPF 65

RESULT 46
US-10-303-162-48
; Sequence 48, Application US/10303162
; Patent No. 6723545
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,162
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (cstI)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-162-48
```

; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-162-48

Query Match 86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFP 5
Db 61 KAVFP 65

RESULT 47

US-10-303-134-48
; Sequence 48, Application US/10303134
; Patent No. 6825019
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,134
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-134-48

Query Match 86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFP 5
Db 61 KAVFP 65

RESULT 48

US-10-303-118-48
; Sequence 48, Application US/10303118
; Patent No. 6905867
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,118
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-118-48

Query Match 86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFP 5
Db 61 KAVFP 65

RESULT 49

US-10-303-128-48
; Sequence 48, Application US/10303128
; Patent No. 6911337
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Campylobacter Glycosyltransferases for Biosynthesis of
; TITLE OF INVENTION: Gangliosides and Ganglioside Mimics
; FILE REFERENCE: 019633-000111US
; CURRENT APPLICATION NUMBER: US/10/303,128
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/816,028
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/118,213
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: US 09/495,406
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Campylobacter jejuni
; FEATURE:
; OTHER INFORMATION: Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
; OTHER INFORMATION: from C. jejuni OH4384
US-10-303-128-48

Query Match 86.2%; Score 25; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFP 5
Db 61 KAVFP 65

RESULT 50

US-09-270-767-43522
; Sequence 43522, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43522
; LENGTH: 334
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*

US-09-270-767-43522

Query Match 86.2%; Score 25; DB 2; Length 334;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
[:|||
Db 282 KSIFPA 287

RESULT 51

US-09-438-185A-960
; Sequence 960, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 960
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0958
US-09-438-185A-960

Query Match 86.2%; Score 25; DB 2; Length 337;
Best Local Similarity 66.7%; Pred. No. 7.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
[:|||
Db 284 RAIFPA 289

RESULT 52

US-08-749-816-3
; Sequence 3, Application US/08749816
; Patent No. 6013470
; GENERAL INFORMATION:
; APPLICANT: Lesage, Florian
; APPLICANT: Guillemare, Eric
; APPLICANT: Fink, Michel
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lazdunski, Michel
; APPLICANT: Romey, Georges
; APPLICANT: Barhanin, Jacques
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
; TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,816
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 989.6351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-749-816-3

Query Match 86.2%; Score 25; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
[:|||
Db 111 KAIFFS 116

RESULT 53

US-09-144-914-6
; Sequence 6, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 347
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog
US-09-144-914-6

Query Match 86.2%; Score 25; DB 2; Length 347;
Best Local Similarity 66.7%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
[:|||
Db 111 KAIFFS 116

RESULT 54

US-09-489-039A-11261

; Sequence 11261, Application US/09489039A
; Patent No. 6610836

GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11261
; LENGTH: 375
; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11261

Query Match 86.2%; Score 25; DB 2; Length 375;

Best Local Similarity 100.0%; Pred. No. 8.5e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 KAVFF 5

Db 19 KAVFF 23

RESULT 55

US-09-543-681A-5731
; Sequence 5731, Application US/09543681A
; Patent No. 6605709

GENERAL INFORMATION:

; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5731
; LENGTH: 421
; TYPE: PRT

; ORGANISM: Proteus mirabilis
US-09-543-681A-5731

Query Match 86.2%; Score 25; DB 2; Length 421;

Best Local Similarity 66.7%; Pred. No. 9.5e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0;

Qy 1 KAVFFA 6

Db 334 RAFFA 339

RESULT 56

US-09-272-960-2
; Sequence 2, Application US/09272960
; Patent No. 6689604

GENERAL INFORMATION:

; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
; TITLE OF INVENTION: Campylobacter jejuni and Its Uses
; FILE REFERENCE: 014137-013210US
; CURRENT APPLICATION NUMBER: US/09/272,960
; CURRENT FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: US 60/078,891
; EARLIER FILING DATE: 1998-03-20
; EARLIER APPLICATION NUMBER: US 09/272,960
; EARLIER FILING DATE: 1999-03-18

; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

; LENGTH: 430
; TYPE: PRT

; ORGANISM: Campylobacter jejuni
US-09-272-960-2

Query Match 86.2%; Score 25; DB 2; Length 430;

Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 KAVFF 5

Db 61 KAVFF 65

RESULT 57

US-10-058-636-2
; Sequence 2, Application US/10058636
; Patent No. 6709834

GENERAL INFORMATION:

; APPLICANT: Gilbert, Michel
; APPLICANT: Wakarchuk, Warren W.
; APPLICANT: National Research Council of Canada
; TITLE OF INVENTION: Lipopolysaccharide alpha-2,3 Sialyltransferase of
; TITLE OF INVENTION: Campylobacter jejuni and Its Uses
; FILE REFERENCE: 014137-013210US
; CURRENT APPLICATION NUMBER: US/10/058,636
; CURRENT FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: US/09/272,960
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: US 60/078,891
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/272,960
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 430

; TYPE: PRT

; ORGANISM: Campylobacter jejuni

US-10-058-636-2

Query Match 86.2%; Score 25; DB 2; Length 430;

Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 KAVFF 5

Db 61 KAVFF 65

RESULT 58

US-09-583-110-3587
; Sequence 3587, Application US/09583110
; Patent No. 6699703

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3587
; LENGTH: 462

```
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3587

Query Match      86.2%; Score 25; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
   |||||
Db 4 KAVFF 8

RESULT 59
US-09-107-433-3273
; Sequence 3273, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENE THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3273:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...473
; SEQUENCE DESCRIPTION: SEQ ID NO: 3273:
US-09-107-433-3273

Query Match      86.2%; Score 25; DB 2; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
   |||||
Db 15 KAVFF 19

; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-489-039A-13140
; Sequence 13140, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13140
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13140

Query Match      86.2%; Score 25; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
   |||||
Db 362 KAVFF 366

RESULT 61
US-08-288-405A-10
; Sequence 10, Application US/08288405A
; Patent No. 5559009
; GENERAL INFORMATION:
; APPLICANT: Chandoy, Kanianthara G.
; APPLICANT: Kalman, Katalin
; APPLICANT: Chandoy, Grischa
; APPLICANT: Gutman, George A.
; TITLE OF INVENTION: A No. 5559009e1 Voltage-Gated Potassium Channel
; TITLE OF INVENTION: Gene
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert,
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/288,405A
; FILING DATE: 10-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/207,431
; FILING DATE: 04-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-59844-1/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 532 amino acids
```

TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-288-405A-10

Query Match 86.2%; Score 25; DB 1; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
DB 310 KAVFF 314

RESULT 62
US-10-162-012-13
; Sequence 13, Application US/10162012
; Patent No. 6682597
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J., Immaculada
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: NOVEL HUMAN ION CHANNEL AND TRANSPORTER FAMILY MEMBERS
; FILE REFERENCE: 10448-190001
; CURRENT APPLICATION NUMBER: US/10/162,012
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/209,845
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 09/875,321
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: PCT/US01/18340
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,257
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,423
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18398
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,238
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: US 09/875,363
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: PCT/US01/18247
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/227,068
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 09/928,530
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: PCT/US01/25475
; PRIOR FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/226,770
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/934,421
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26096
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/279,281
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 10/109,029
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: PCT/US02/09728
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/290,288
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US (not assigned)
; PRIOR FILING DATE: 2002-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-162-012-13

Query Match 86.2%; Score 25; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
DB 310 KAVFF 314

RESULT 63
US-09-605-703B-2398
; Sequence 2398, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: BGI-129CP
; CURRENT APPLICATION NUMBER: US/09/605,703B
; CURRENT FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: 60/142,764
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: 60/152,318
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 2398
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-605-703B-2398

Query Match 86.2%; Score 25; DB 2; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
DB 454 KAVFF 458

RESULT 64
US-08-594-031-90
; Sequence 90, Application US/08594031
; Patent No. 5783182
; GENERAL INFORMATION:
; APPLICANT: THOMPSON, Timothy C.
; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BAKER & BOTTS, L.L.P.
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,031
; FILING DATE: 30-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/006,838
; FILING DATE: 16-NOV-1995
; ATTORNEY/AGENT INFORMATION:

; NAME: Remenick, James
; REGISTRATION NUMBER: 36,902
; REFERENCE/DOCKET NUMBER: 0A146-0110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-639-7700
; TELEFAX: 202-639-7890
; TELEX:
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-594-031-90

Query Match 86.2%; Score 25; DB 1; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 537 KAVFF 541

RESULT 65
US-09-643-597-225
; Sequence 225, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643.597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-643-597-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 537 KAVFF 541

RESULT 66
US-09-480-884A-225
; Sequence 225, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-480-884A-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 537 KAVFF 541

RESULT 67
US-09-542-615A-225
; Sequence 225, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-542-615A-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
Db 537 KAVFF 541

RESULT 68
US-09-606-421B-225
; Sequence 225, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606,421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-606-421B-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 537 KAVFF 541

RESULT 69

US-09-476-496A-225
; Sequence 225, Application US/09476496A
; Patent No. 6706262
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
; FILE REFERENCE: 210121.455C5
; CURRENT APPLICATION NUMBER: US/09/476,496A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-476-496A-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 537 KAVFF 541

RESULT 70

US-09-630-940B-225
; Sequence 225, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Ligu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B

; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 225
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-630-940B-225

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 537 KAVFF 541

RESULT 71

US-09-943-075A-6
; Sequence 6, Application US/09943075A
; Patent No. 6812002
; GENERAL INFORMATION:
; APPLICANT: Popoff, Steven N.
; APPLICANT: Safado, Favez F.
; APPLICANT: Owen, Thomas A.
; APPLICANT: Smock, Steven L.
; TITLE OF INVENTION: Osteoactivin Protein and Nucleic Acids Encoding the Same,
; FILE REFERENCE: 71369.262
; CURRENT APPLICATION NUMBER: US/09/943,075A
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,006
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Human
US-09-943-075A-6

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFF 5
Db 537 KAVFF 541

RESULT 72

US-10-039-272A-2
; Sequence 2, Application US/10039272A
; Patent No. 6939955
; GENERAL INFORMATION:
; APPLICANT: RAMESHWAR, Pranela
; TITLE OF INVENTION: HEMATOPOIETIC GROWTH FACTOR INDUCIBLE NEUROKININ-TYPE
; FILE REFERENCE: 267/033 (UMD-0055)
; CURRENT APPLICATION NUMBER: US/10/039,272A
; CURRENT FILING DATE: 2001-10-20
; PRIOR APPLICATION NUMBER: US 60/241,881
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 560
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-272A-2

Query Match 86.2%; Score 25; DB 2; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
 Db 537 KAVFF 541

RESULT 73

US-10-007-700-225
 ; Sequence 225, Application US/10007700
 ; Patent No. 6960570
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Fanger, Neil
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Durham, Margarita
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Peckman, David W.
 ; APPLICANT: Cai, Feng
 ; APPLICANT: FOY, Teresa M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.455C17
 ; CURRENT APPLICATION NUMBER: US/10/007,700
 ; CURRENT FILING DATE: 2001-11-30
 ; NUMBER OF SEQ ID NOS: 469
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 225
 ; LENGTH: 560
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-007-700-225

Query Match 86.2%; Score 25; DB 2; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
 Db 537 KAVFF 541

RESULT 74

US-09-985-799-90
 ; Sequence 90, Application US/09985799
 ; Patent No. RE38392
 ; GENERAL INFORMATION:
 ; APPLICANT: THOMPSON, Timothy C.
 ; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
 ; NUMBER OF SEQUENCES: 175
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BAKER & BOTTS, L.L.P.
 ; STREET: 1299 Pennsylvania Avenue, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004-2400
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/985,799
 ; FILING DATE: 16-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/594,031
 ; FILING DATE: 30-JAN-1996
 ; APPLICATION NUMBER: 60/006,838
 ; FILING DATE: 16-NOV-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remenick, James
 ; REGISTRATION NUMBER: 36,902
 ; REFERENCE/DOCKET NUMBER: 0A146-0110
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-639-7700

FILING DATE: 06-No. RE38392-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/594,031
 FILING DATE: 30-JAN-1996
 APPLICATION NUMBER: 60/006,838
 FILING DATE: 16-NOV-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Remenick, James
 REGISTRATION NUMBER: 36,902
 REFERENCE/DOCKET NUMBER: 0A146-0110
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-639-7700
 TELEFAX: 202-639-7890
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 90:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 560 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 SEQUENCE DESCRIPTION: SEQ ID NO: 90:
 US-09-985-799-90

Query Match 86.2%; Score 25; DB 5; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFF 5
 Db 537 KAVFF 541

RESULT 75

US-09-977-371-90
 ; Sequence 90, Application US/09977371
 ; Patent No. RE38490
 ; GENERAL INFORMATION:
 ; APPLICANT: THOMPSON, Timothy C.
 ; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
 ; NUMBER OF SEQUENCES: 175
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BAKER & BOTTS, L.L.P.
 ; STREET: 1299 Pennsylvania Avenue, N.W.
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004-2400
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/977,371
 ; FILING DATE: 16-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/594,031
 ; FILING DATE: 30-JAN-1996
 ; APPLICATION NUMBER: 60/006,838
 ; FILING DATE: 16-NOV-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Remenick, James
 ; REGISTRATION NUMBER: 36,902
 ; REFERENCE/DOCKET NUMBER: 0A146-0110
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-639-7700

```

;
; TELEPAX: 202-639-7890
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 560 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 90:
;
US-09-977-371-90

```

```

Query Match      86.2%; Score 25; DB 5; Length 560;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KAVFF 5
Db      537 KAVFF 541

```

Search completed: December 29, 2005, 17:52:38
 Job time : 20.1323 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 16:51:32 ; Search time 81.7742 Seconds
(without alignments)
32.238 Million cell updates/sec

Title: US-10-009-122-15
Perfect score: 29
Sequence: 1 KAVFPA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	6	4	AAB48480
2	29	100.0	6	4	AAB48488
3	29	100.0	6	4	AAB82636
4	29	100.0	6	4	AAB82628
5	29	100.0	6	5	AAU96824
6	29	100.0	6	5	AAU96816
7	29	100.0	6	5	AAU11662
8	29	100.0	6	5	AAU11654
9	29	100.0	6	6	AAE35450
10	29	100.0	6	6	AAE35443
11	29	100.0	6	8	ADQ37275
12	29	100.0	6	8	ADQ37267
13	29	100.0	6	8	ADQ37319
14	29	100.0	6	8	ADQ37327
15	29	100.0	6	9	ADY37934
16	29	100.0	6	9	ADY37926
17	29	100.0	37	3	AA05909
18	29	100.0	37	8	ADK34079
19	29	100.0	37	8	ADL70726
20	29	100.0	42	8	ADG17617
21	29	100.0	42	8	ADG17612
22	29	100.0	74	2	AAW41091
23	29	100.0	74	2	AAW41085
24	29	100.0	74	2	AAW41230

25	29	100.0	74	8	ADT05998	Modified
26	29	100.0	74	8	ADT05965	Human mat
27	29	100.0	74	8	ADT05971	Chicken m
28	29	100.0	108	2	AAW41086	Human mat
29	29	100.0	108	2	AAW41092	Chicken m
30	29	100.0	108	2	AAW41231	Alpha-v-b
31	29	100.0	108	2	AAW41237	Alpha-v-b
32	29	100.0	108	8	ADT05972	Chicken m
33	29	100.0	108	8	ADT05966	Human mat
34	29	100.0	108	8	ADT05999	Modified
35	29	100.0	122	2	AAW41238	Alpha-v-b
36	29	100.0	152	2	AAW41232	Alpha-v-b
37	29	100.0	193	2	AAW41090	Chicken m
38	29	100.0	193	2	AAW41084	Human mat
39	29	100.0	193	2	AAW41229	Human mat
40	29	100.0	193	2	AAW41235	Alpha-v-b
41	29	100.0	193	8	ADT05964	Human mat
42	29	100.0	193	8	ADT05970	Chicken m
43	29	100.0	222	2	AAW41083	Human mat
44	29	100.0	222	2	AAW41228	Alpha-v-b
45	29	100.0	222	8	ADT05963	Human mat
46	29	100.0	228	2	AAW41089	Chicken m
47	29	100.0	228	2	AAW41234	Alpha-v-b
48	29	100.0	228	8	ADT05969	Chicken m
49	29	100.0	261	8	ADT05661	Haemophil
50	29	100.0	429	2	AAW41112	Human mat
51	29	100.0	429	8	ADT05991	Human mat
52	29	100.0	468	4	ABG24001	Novel hum
53	29	100.0	623	8	ABM84057	Human dia
54	29	100.0	626	8	ADG17622	Modified
55	29	100.0	631	1	ADG17627	Modified
56	29	100.0	631	1	AAFP96143	Sequence
57	29	100.0	631	1	AAFP91139	Human typ
58	29	100.0	631	2	AAFP07969	Complete
59	29	100.0	631	2	AAFP07350	Human typ
60	29	100.0	631	7	AAW41226	Human mat
61	29	100.0	631	7	ADM48668	Human mat
62	29	100.0	631	8	ADT05996	Human mat
63	29	100.0	633	8	ADT05997	Mouse mat
64	29	100.0	644	4	AAAB20490	Human mat
65	29	100.0	660	2	AAAB06420	Type IV c
66	29	100.0	660	4	AAAB84607	Amino aci
67	29	100.0	660	4	AAAE10431	Human mat
68	29	100.0	660	5	ABBY79413	Human mat
69	29	100.0	660	5	ABBY90738	Human Tum
70	29	100.0	660	5	AAU84348	Protein M
71	29	100.0	660	6	ABU54445	Human tum
72	29	100.0	660	6	ABP971136	Human mat
73	29	100.0	660	6	AAO16608	Human mat
74	29	100.0	660	6	ABG76322	Human mat
75	29	100.0	660	7	ADP18578	Human dis
76	29	100.0	660	7	ADP65244	Human mat
77	29	100.0	660	8	ADN07697	Human mat
78	29	100.0	660	8	ADQ17097	Human mat
79	29	100.0	660	9	ADV90301	Protease-
80	29	100.0	660	9	ADV68478	Human mat
81	29	100.0	662	7	ADDE62857	Rat Prote
82	29	100.0	662	7	ADDA46270	Rat Prote
83	29	100.0	663	2	AAW41111	Chicken m
84	29	100.0	663	2	AAW41227	Chicken m
85	29	100.0	663	8	ADT05976	Chicken m
86	29	100.0	663	8	ADT05995	Chicken m
87	29	100.0	708	7	ADPF60554	Human con
88	29	100.0	708	9	AEA20970	Novel hum
89	29	100.0	718	8	ADN22220	Bacterial
90	29	100.0	737	8	ADN24980	Bacterial
91	29	100.0	1147	2	AAW02571	Rat induc
92	29	100.0	1330	4	ABG23999	Novel hum
93	28	96.6	383	8	ADN25046	Bacterial
94	28	96.6	383	8	ADN22288	Bacterial
95	26	89.7	65	3	AAV65434	Human 5'
96	26	89.7	65	8	ADU72998	Non-signa
97	26	89.7	65	9	ADZ73989	Human com

98	26	89.7	128	8	ADJ05122	AdJ05122 M. catarr	171	25	86.2	117	4	AAW17468	Aaw17468 Peptide #
99	26	89.7	138	4	ABG09090	Abg09090 Novel hum	172	25	86.2	117	4	ABB36488	Abb36488 Peptide #
100	26	89.7	149	9	AEBA1486	Aeb14186 L. pneumo	173	25	86.2	117	4	AAW29987	Aaw29987 Peptide #
101	26	89.7	166	9	AEB38197	Aeb38197 L. pneumo	174	25	86.2	117	4	ABB31282	Abb31282 Peptide #
102	26	89.7	208	4	ABG09092	Abg09092 Novel hum	175	25	86.2	117	4	ABB21830	Abb21830 Protein #
103	26	89.7	210	6	ABU33715	Abu33715 Protein e	176	25	86.2	117	4	AAW69653	Aaw69653 Human bon
104	26	89.7	238	4	AAUJ1660	Aauj1660 Novel hum	177	25	86.2	117	4	AAW57251	Aaw57251 Human bra
105	26	89.7	292	4	AAW42075	Aaw42075 Human pol	178	25	86.2	117	4	ABG51335	Abg51335 Human liv
106	26	89.7	296	3	AAW43372	Aaw43372 Human ORF	179	25	86.2	117	4	AAW51146	Aaw51146 Peptide #
107	26	89.7	320	8	ADY08844	Ady08844 Plant ful	180	25	86.2	117	5	ABG39273	Abg39273 Human pep
108	26	89.7	320	8	ADY73944	Ady73944 Plant ful	181	25	86.2	132	8	ABO55307	AbO55307 Human gen
109	26	89.7	322	5	ABO66558	AbO66558 G protein	182	25	86.2	141	7	ADL06701	AdL06701 Carassius
110	26	89.7	329	4	AAW40289	Aaw40289 Human pol	183	25	86.2	150	2	AAW20912	Aaw20912 H. pylori
111	26	89.7	334	2	AAW86833	Aaw86833 Secreted	184	25	86.2	160	4	AAU60292	Aau60292 Propionib
112	26	89.7	334	6	ABO50400	AbO50400 Human sec	185	25	86.2	170	6	ABM56811	Abm56811 Propionib
113	26	89.7	334	6	ABO44657	AbO44657 Novel hum	186	25	86.2	164	3	AAW23502	Aaw23502 Arabidops
114	26	89.7	334	7	ABO26137	AbO26137 Human pro	187	25	86.2	174	3	AAW39522	Aaw39522 Arabidops
115	26	89.7	352	8	ADP29738	Adp29738 Human sec	188	25	86.2	175	4	AAO11219	Aao11219 Human pol
116	26	89.7	358	8	ADQ96208	Adq96208 T cell ac	189	25	86.2	186	7	ADC07962	Adc07962 Rice prot
117	26	89.7	358	8	ADQ96310	Adq96310 T cell ac	190	25	86.2	186	7	ADC07948	Adc07948 Rice prot
118	26	89.7	421	4	AAW98352	Aaw98352 Escherich	191	25	86.2	190	4	AAW83792	Aaw83792 Human imm
119	26	89.7	421	6	ABU14827	Abu14827 Protein e	192	25	86.2	200	7	ABM89622	Abm89622 Rice abio
120	26	89.7	441	3	AAV53014	Aav53014 Human sec	193	25	86.2	201	8	ADY12035	Ady12035 Plant ful
121	26	89.7	494	6	ADA36442	Ada36442 Acinetoba	194	25	86.2	202	8	ADU05630	AdU05630 H. pylori
122	26	89.7	535	9	AAW90803	Aaw90803 M. xanthu	195	25	86.2	206	3	AAW39521	Aaw39521 Arabidops
123	26	89.7	555	4	AAW93388	Aaw93388 Human pol	196	25	86.2	207	3	AAW23501	Aaw23501 Arabidops
124	26	89.7	555	8	AAW66415	Aaw66415 Human maj	197	25	86.2	210	6	ABP79894	Abp79894 N. gonorr
125	26	89.7	555	8	ADL30943	Adl30943 Human pro	198	25	86.2	210	6	ABU37523	Abu37523 Protein e
126	26	89.7	555	8	ADQ96132	Adq96132 T cell ac	199	25	86.2	210	6	ABU38175	Abu38175 Protein e
127	26	89.7	555	3	ADY07709	Ady07709 Cyclin-de	200	25	86.2	213	3	AAW51077	Aaw51077 Arabidops
128	26	89.7	556	3	AAW87342	Aaw87342 Human sig	201	25	86.2	239	8	ADN46479	Adn46479 Thermococ
129	26	89.7	564	4	AAW88362	Aaw88362 Human mem	202	25	86.2	243	3	AAW51076	Aaw51076 Arabidops
130	26	89.7	564	8	ADQ96212	Adq96212 T cell ac	203	25	86.2	243	3	AAW12759	Aaw12759 Arabidops
131	26	89.7	564	9	ADY63089	Ady63089 Human clo	204	25	86.2	246	3	AAW51075	Aaw51075 Arabidops
132	26	89.7	715	6	ABU47623	Abu47623 Protein e	205	25	86.2	246	4	ABW58652	Abw58652 Drosophil
133	26	89.7	1042	6	ABU33394	Abu33394 Protein e	206	25	86.2	247	2	AAW20248	Aaw20248 H. pylori
134	26	89.7	1172	4	ABG06613	Abg06613 Novel hum	207	25	86.2	249	8	ADS21551	Ads21551 Bacterial
135	26	89.7	1507	3	AAW24128	Aaw24128 Plasmodiu	208	25	86.2	254	8	ADS27681	Ads27681 Bacterial
136	25	86.2	5	2	AAW45963	Aaw45963 Peptide d	209	25	86.2	255	4	ABW67621	Abw67621 Drosophil
137	25	86.2	6	4	AAW48482	Aaw48482 Antifibri	210	25	86.2	256	6	ABW68528	Abw68528 Phototrab
138	25	86.2	6	4	AAW48490	Aaw48490 Antifibri	211	25	86.2	268	8	ADS41641	Ads41641 Bacterial
139	25	86.2	6	4	AAW82630	Aaw82630 All-D pep	212	25	86.2	272	3	AAW12758	Aaw12758 Arabidops
140	25	86.2	6	4	AAW82638	Aaw82638 All-D pep	213	25	86.2	276	3	AAW12757	Aaw12757 Arabidops
141	25	86.2	6	5	AAU96818	Aau96818 Amyloid t	214	25	86.2	281	7	ABO80453	AbO80453 Pseudomon
142	25	86.2	6	5	AAU96826	Aau96826 Amyloid t	215	25	86.2	282	1	AAW90422	Aaw90422 Human phe
143	25	86.2	6	5	AAU11664	Aau11664 Peptide #	216	25	86.2	282	6	ABU09405	Abu09405 Human phe
144	25	86.2	6	5	AAU11656	Aau11656 Peptide #	217	25	86.2	282	8	ADH13186	Adh13186 Human mal
145	25	86.2	6	6	AAW35452	Aaw35452 Abeta pep	218	25	86.2	282	9	AEA15073	Aea15073 Human pol
146	25	86.2	6	8	ADQ37277	Adq37277 Vaccine a	219	25	86.2	282	9	AEA08357	Aea08357 Human phe
147	25	86.2	6	8	ADQ37321	Adq37321 Antifibri	220	25	86.2	285	4	AAW39174	Aaw39174 Human pol
148	25	86.2	6	8	ADQ37329	Adq37329 Antifibri	221	25	86.2	297	8	ADY25262	Ady25262 Plant ful
149	25	86.2	6	9	ADY37928	Ady37928 Amyloid-t	222	25	86.2	303	6	ABR40195	AbR40195 alpha-2,3
150	25	86.2	6	9	ADY37936	Ady37936 Amyloid-t	223	25	86.2	306	2	AAW38837	Aaw38837 Neisseria
151	25	86.2	22	8	ADQ09761	Adq09761 Rice 26kD	224	25	86.2	306	2	AAW38836	Aaw38836 Neisseria
152	25	86.2	23	8	ABU33984	Abu33984 Rice 26 k	225	25	86.2	306	4	AAW71923	Aaw71923 Human Olf
153	25	86.2	25	4	ABO33313	AbO33313 Human mus	226	25	86.2	306	9	ABE49486	Aeb49486 N. mening
154	25	86.2	25	6	ABU12607	Abu12607 Novel hum	227	25	86.2	306	9	ABE49484	Aeb49484 N. mening
155	25	86.2	28	8	ADY28633	Ady28633 Human mus	228	25	86.2	307	9	AAW39838	Aaw39838 Neisseria
156	25	86.2	28	8	AAW39806	Aaw39806 Beta-amyl	229	25	86.2	307	9	ABE49488	Aeb49488 N. gonorr
157	25	86.2	34	7	ADW72404	Adw72404 Human end	230	25	86.2	309	5	ABO66559	AbO66559 G protein
158	25	86.2	37	3	AAW05910	Aaw05910 Mouse ind	231	25	86.2	314	5	AAU83579	Aau83579 Human nov
159	25	86.2	37	8	ADK34080	Adk34080 Human nNO	232	25	86.2	314	7	ADM29640	Adm29640 Novel hum
160	25	86.2	37	8	ADL70727	Adl70727 Mouse iNO	233	25	86.2	319	7	ABM87620	Abm87620 Rice abio
161	25	86.2	42	3	AAW04347	Aaw04347 Arabidops	234	25	86.2	322	4	AAU24642	Aau24642 Human olf
162	25	86.2	50	3	AAW04346	Aaw04346 Arabidops	235	25	86.2	322	5	ABW06657	Abw06657 G protein
163	25	86.2	65	8	ABO55025	AbO55025 Human gen	236	25	86.2	322	5	ABP95886	Abp95886 Human GPC
164	25	86.2	69	3	AAW24897	Aaw24897 Arabidops	237	25	86.2	322	5	AAU95597	Aau95597 Human Olf
165	25	86.2	77	3	AAW02840	Aaw02840 Human sec	238	25	86.2	322	5	AAU85262	Aau85262 G-coupled
166	25	86.2	80	6	ABO00562	AbO00562 Novel hum	239	25	86.2	322	6	ABU11149	Abu11149 Human G-p
167	25	86.2	83	4	AAW92860	Aaw92860 Human dig	240	25	86.2	322	7	ADC85681	Adc85681 Human GPC
168	25	86.2	90	4	AAU47327	Aau47327 Propionib	241	25	86.2	322	8	ADG83362	Adg83362 Human Olf
169	25	86.2	90	6	ABW43846	Abw43846 Propionib	242	25	86.2	332	5	ABG07514	Abg07514 Human dru
170	25	86.2	105	4	AAO00117	Aao00117 Human pol	243	25	86.2	332	8	ADS44454	Ads44454 Bacterial

244	25	86.2	332	8	ADS22134	Bacterial
245	25	86.2	347	3	AAV79676	Caenorhab
246	25	86.2	354	4	ABBS59799	Drosophila
247	25	86.2	371	3	AAG31391	Arabidops
248	25	86.2	372	3	AAB10940	L. donova
249	25	86.2	372	3	AAB10944	L. major
250	25	86.2	372	3	AAB10939	L. infant
251	25	86.2	372	3	AAB10938	L. anazon
252	25	86.2	372	3	AAB10943	L. tropic
253	25	86.2	372	3	AAB10941	L. chagas
254	25	86.2	372	3	AAB10937	L. mexicana
255	25	86.2	372	3	AAB10942	L. aethio
256	25	86.2	372	3	AAG31390	Arabidops
257	25	86.2	375	7	ABO64744	Klebsiell
258	25	86.2	380	8	ADN25333	Bacterial
259	25	86.2	382	8	ADS22130	Bacterial
260	25	86.2	411	3	AAG13578	Arabidops
261	25	86.2	411	6	ABU49877	Protein e
262	25	86.2	412	3	AAG13577	Arabidops
263	25	86.2	415	6	ABU40846	Protein e
264	25	86.2	420	3	AAG31389	Arabidops
265	25	86.2	421	7	ADF05446	Bacterial
266	25	86.2	430	2	AAV45221	Campylob
267	25	86.2	454	5	ABG31335	Marine KC
268	25	86.2	460	3	AAG13576	Arabidops
269	25	86.2	460	5	ABP27238	Streptoco
270	25	86.2	460	8	ADV89577	Streptoco
271	25	86.2	460	8	ADV82984	Streptoco
272	25	86.2	460	8	ADV80830	Streptoco
273	25	86.2	462	5	ABP27239	Streptoco
274	25	86.2	462	5	ABBS4050	Lactococc
275	25	86.2	462	8	ADK47072	Streptoco
276	25	86.2	466	5	ABP26930	Streptoco
277	25	86.2	466	8	ADV81295	Streptoco
278	25	86.2	472	6	ABU02501	S. pneumo
279	25	86.2	473	8	ADR94638	Novel S.
280	25	86.2	473	9	AEA58508	Streptoco
281	25	86.2	474	7	ABO66623	Klebsiell
282	25	86.2	475	3	ABAB1368	1-deoxy-D
283	25	86.2	481	4	ABBS58790	Drosophila
284	25	86.2	507	6	ABG76432	Sindbis p
285	25	86.2	512	8	ADO26827	Human rec
286	25	86.2	532	2	AAR82937	Mouse Kv1
287	25	86.2	532	6	ABP98780	Mouse Kv1
288	25	86.2	539	6	ABU20239	Protein e
289	25	86.2	544	2	AAR82213	Talaromyc
290	25	86.2	552	6	ABU21210	Protein e
291	25	86.2	558	6	ABU22708	Protein e
292	25	86.2	560	2	AAW35382	Murine me
293	25	86.2	560	3	AAB11329	Human lun
294	25	86.2	560	4	AAG91711	C glutami
295	25	86.2	560	5	ABB78200	Amino aci
296	25	86.2	560	5	ABB74961	Human lun
297	25	86.2	560	5	ABP61881	Human lun
298	25	86.2	560	6	ABU56592	Lung canc
299	25	86.2	560	6	ABG72962	Human ost
300	25	86.2	560	6	ABU70852	Human adi

ALIGNMENTS

RESULT 1
ID AAB48480 standard; peptide; 6 AA.
XX AC

XX AAB48480;

DT 02-MAR-2001 (first entry)

XX Antifibrillogenic peptide #7.

DE Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
XX KW

KW cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KW Alzheimer's disease.
OS Homo sapiens.
PN WO200068263-A2.
PD 16-NOV-2000.
XX 04-MAY-2000; 2000WO-CA000515.
PF 05-MAY-1999; 99US-0132592P.
PR (NEUR-) NEUROCHEM INC.
PA Chalfour R, Gervais F, Gupta A;
PI WPI; 2001-031852/04.
DR Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
XX cytoprotection for treating amyloidosis disorders, comprises a peptide,
XX its isomer or peptidomimetic.
PS Claim 7; Page 25; 46pp; English.
CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
CC useful for treating amyloidosis disorders such as Alzheimer's disease.
CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
CC binding region and the prot-prot interaction region of the human amyloid
CC protein
XX Sequence 6 AA;
SQ Query Match 100.0%; Score 29; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
QY 1 KAVFFA 6
Db 1 KAVFFA 6
RESULT 2
ID AAB48480
XX AAB48488 standard; peptide; 6 AA.
AC AAB48488;
DT 02-MAR-2001 (first entry)
XX Antifibrillogenic peptide #15.
DE Nootropic; neuroprotective; antifibrillogenic; amyloidosis inhibition;
XX cytoprotection; amyloid deposit degradation; amyloidosis disorder;
KW Alzheimer's disease.
XX Homo sapiens.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Modified-site 6
FT /note= "C-terminal amide"
PN WO200068263-A2.
XX 16-NOV-2000.
XX 04-MAY-2000; 2000WO-CA000515.
PF 05-MAY-1999; 99US-0132592P.
PR (NEUR-) NEUROCHEM INC.
PA

XX PI Chalifour R, Gervais F, Gupta A;
 XX WPI; 2001-031852/04.
 XX
 XX Antifibrillogenic agent useful for inhibiting amyloidosis and/or for
 PT cytoprotection for treating amyloidosis disorders, comprises a peptide,
 FT its isomer or peptidomimetic.
 XX
 XX Claim 7; Page 25; 46pp; English.
 XX
 CC Peptides AAB48474-B48496 are antifibrillogenic agents that can be used
 CC for inhibiting amyloidosis and/or for cytoprotection. The peptides of
 CC AAB48474-B48496 cause the breakdown of amyloid deposits and are therefore
 CC useful for treating amyloidosis disorders such as Alzheimer's disease.
 CC Peptides AAB48474-B48496 were identified from the glycosaminoglycan
 CC binding region and the prot-prot interaction region of the human amyloid
 CC protein
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db |||||
 1 KAVFFA 6
 RESULT 3
 AAB82636
 ID AAB82636 standard; peptide; 6 AA.
 AC AAB82636;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX
 KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "all D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT
 XX WO200139796-A2.
 PN
 XX 07-JUN-2001.
 PD
 XX 29-NOV-2000; 2000WO-CA001413.
 PF
 XX 29-NOV-1999; 99US-0168594P.
 PR
 XX 28-NOV-2000; 2000US-00724842.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalifour R, Hebert L, Kong X, Gervais F;
 XX
 DR WPI; 2001-441458/47.
 XX
 PT Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX
 XX Disclosure; Page 11; 31pp; English.
 PS
 XX

CC The present sequence is that of an all-D peptide suitable for use in
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AAB82622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AAB82623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalopathy, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db |||||
 1 KAVFFA 6
 RESULT 4
 AAB82628
 ID AAB82628 standard; peptide; 6 AA.
 AC AAB82628;
 XX
 DT 02-OCT-2001 (first entry)
 XX
 DE All-D peptide used in Alzheimer's disease vaccine.
 XX
 KW Alzheimer's disease; amyloidosis; amyloid-related disease; vaccine;
 KW therapy; antigen.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..6 /note= "all D-form residues"
 FT
 XX WO200139796-A2.
 PN
 XX 07-JUN-2001.
 PD
 XX 29-NOV-2000; 2000WO-CA001413.
 PF
 XX 29-NOV-1999; 99US-0168594P.
 PR
 XX 28-NOV-2000; 2000US-00724842.
 XX
 PA (NEUR-) NEUROCHEM INC.
 XX
 PI Chalifour R, Hebert L, Kong X, Gervais F;
 XX
 DR WPI; 2001-441458/47.
 XX
 PT Preventing/treating amyloid-related disease, especially Alzheimer's
 PT disease, comprises administering antigenic all-D peptide, eg. as vaccine,
 PT which elicits production of antibodies to prevent fibrillogenesis and
 PT associated cellular toxicity.
 XX
 XX Disclosure; Page 11; 31pp; English.
 PS
 XX

PT which elicits production of antibodies to prevent fibrillogenesis and
 XX associated cellular toxicity.

PS Disclosure; Page 11; 31pp; English.

XX The present sequence is that of an all-D peptide suitable for use for
 CC preparing vaccines for preventing or treating Alzheimer's disease and
 CC other amyloid related disorders in humans. It is based on a portion of
 CC amyloid-beta peptide (see AA882622), and may be modified by removing or
 CC inserting 1 or more amino acid residues, or by substituting 1 or more
 CC amino acid residues with other amino acid residues or non-amino acid
 CC fragments. Vaccines of the invention are produced using 'non-self'
 CC peptides synthesised from the unnatural D-configuration amino acids to
 CC avoid the drawbacks of 'self' proteins. The all-D peptides need not be
 CC aggregated to be operative or immunogenic. They preferably interact with
 CC at least 1 region of an amyloid protein, e.g. the beta-sheet region or
 CC GAG-binding site region, the amyloid-beta peptide, or their immunogenic
 CC fragments, protein conjugates, immunogenic derivative peptides and
 CC immunogenic peptidomimetics. Examples include all-D peptides
 CC corresponding to residues 1-42, 1-40, 1-35, 1-28, 1-7, 10-16, 16-21 and
 CC 36-42 of the amyloid-beta peptide and the all-D derivative peptides given
 CC in AA882623-64. The vaccine elicits a preferential TH-2 or TH-1 response,
 CC preventing fibrillogenesis and associated cellular toxicity. The amyloid
 CC related diseases may be localised amyloidosis, e.g. diabetes type II,
 CC neurodegenerative diseases, e.g. bovine spongiform encephalitis, and
 CC Creutzfeldt-Jakob disease, scrapie, cerebral amyloid angiopathy, and
 CC prion protein related disorders, or systemic amyloidosis associated with
 CC chronic infection (e.g. tuberculosis) or chronic inflammation (e.g.
 CC rheumatoid arthritis), familial Mediterranean fever (FMF) and systemic
 CC amyloidosis found in long-term haemodialysis patients

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 4; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 DB |||||
 1 KAVFFPA 6

RESULT 5
 AAU96824
 ID AAU96824 standard; peptide; 6 AA.

XX AAU96824;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #14.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1. .6

XX FT /note= "Preferably D-form residue"

XX FT Modified-site 6

XX FT /note= "Ala is amidated"

XX WO200207781-A2.

XX 31-JAN-2002.

PF 25-JUL-2001; 2001WO-CA001071.
 XX
 PR 25-JUL-2000; 2000US-0220808P.
 PR 24-JUL-2001; 2001US-00915092.
 XX
 PA (NEUR-) NEUROCHEM INC.

PI Gervais F, Kong X, Chalifour R, Migneault D;
 XX
 XX WPI; 2002-371447/40.

XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
 PT plaques and/or for the treatment of amyloidosis disorders.

XX Claim 49; Page 21; 57pp; English.

XX The invention relates to an amyloid-targeting imaging agent comprising an
 CC amyloid targeting moiety, a linker moiety and a labelling moiety. The
 CC agent is of general formula A t-(A 1 n k) z-A 1 a b (I) where z = 0 - 1;
 CC A t = an amyloid targeting moiety; A 1 n k = a linker moiety; and A 1 a b
 CC = a labelling moiety. Also included are imaging amyloid deposition or
 CC diagnosing an amyloid-related condition in a patient involving
 CC administering (I) to the patient, and ultrasound imaging (I) in the
 CC patient to determine the presence of amyloid or amyloid-related condition
 CC ; and a kit for preparing a radiopharmaceutical preparation comprising
 CC (I), a reducing agent, a buffering agent, a transchelating agent, and
 CC instructions for the preparation and use of the radiopharmaceutical in
 CC the imaging of amyloid or an amyloid-related condition. The agents are
 CC used for imaging amyloid deposition and for diagnosing an amyloid related
 CC condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
 CC cerebral amyloidosis (transmissible virus dementia), familial CJD,
 CC scrapie, transmissible mink encephalopathy, bovine spongiform
 CC encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
 CC primary amyloidosis, feline spongiform encephalopathy, non-transmissible
 CC cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
 CC dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
 CC amyloid angiopathy. The agents are capable of crossing the blood-brain
 CC barrier and are capable of binding specifically to amyloid plaques. The
 CC present sequence is a peptide forming the amyloid targeting moiety of the
 CC agent of the invention

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 DB |||||
 1 KAVFFPA 6

RESULT 6

AAU96816

ID AAU96816 standard; peptide; 6 AA.

XX AAU96816;

XX 30-JUL-2002 (first entry)

XX Amyloid targeting peptide #6.

XX Amyloid; imaging agent; Creutzfeldt-Jakob disease; Kuru; CJD;
 KW transmissible cerebral amyloidosis; transmissible virus dementia;
 KW scrapie; transmissible mink encephalopathy; BSE; type II diabetes;
 KW bovine spongiform encephalopathy; inflammation associated amyloid;
 KW primary amyloidosis; feline spongiform encephalopathy;
 KW Alzheimer's disease; prion-mediated disease; blood-brain barrier;
 KW dialysis-related amyloidosis; light chain-related amyloidosis;
 KW cerebral amyloid angiopathy.

XX Synthetic.

```

FH Key                               Location/Qualifiers
FT Misc-difference 1..6
XX /note= "Preferably D-form residue"
XX WO200207781-A2.
XX 31-JAN-2002.
XX
XX 25-JUL-2001; 2001WO-CA001071.
XX
XX 25-JUL-2000; 2000US-0220808P.
XX
XX 24-JUL-2001; 2001US-00915092.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D,
XX WPI; 2002-371447/40.
XX
XX New amyloid-targeting imaging agents useful for in vivo imaging amyloid
XX plaques and/or for the treatment of amyloidosis disorders.
XX
XX Claim 49; Page 21; 57pp; English.
XX
XX The invention relates to an amyloid-targeting imaging agent comprising an
XX amyloid targeting moiety, a linker moiety and a labelling moiety. The
XX agent is of general formula A_t-(A_1)_n_k z-A_1 a_b (t) where z = 0 - 1;
XX A_t is an amyloid targeting moiety; A_1_n_k is a linker moiety; and A_1 a_b
XX is a labelling moiety. Also included are imaging amyloid deposition or
XX diagnosing an amyloid-related condition in a patient involving
XX administering (I) to the patient, and ultrasound imaging (I) in the
XX patient to determine the presence of amyloid or amyloid-related condition
XX ; and a kit for preparing a radiopharmaceutical preparation comprising
XX (I), a reducing agent, a buffering agent, a transchelating agent, and
XX instructions for the preparation and use of the radiopharmaceutical in
XX the imaging of amyloid or an amyloid-related condition. The agents are
XX used for imaging amyloid deposition and for diagnosing an amyloid related
XX condition e.g. Creutzfeldt-Jakob disease (CJD), kuru, transmissible
XX cerebral amyloidoses (transmissible virus dementias), familial CJD,
XX scrapie, transmissible mink encephalopathy, bovine spongiform
XX encephalopathy (BSE), inflammation-associated amyloid, type II diabetes,
XX primary amyloidosis, feline spongiform encephalopathy, non-transmissible
XX cerebral amyloidosis, Alzheimer's disease, prion-mediated diseases,
XX dialysis-related amyloidosis, light chain-related amyloidosis, cerebral
XX amyloid angiopathy. The agents are capable of crossing the blood-brain
XX barrier and are capable of binding specifically to amyloid plaques. The
XX present sequence is a peptide forming the amyloid targeting moiety of the
XX agent of the invention
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFFA 6
DB 1 KAVFFFA 6
RESULT 7
AAU11662
ID AAU11662 standard; peptide; 6 AA.
XX
XX AAU11662;
XX
XX 09-APR-2002 (first entry)
XX
XX Peptide #15, used as carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; nontropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX Synthetic.
XX WO200185093-A2.
XX 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.
XX
XX (NEUR-) NEUROCHEM INC.
XX
XX Green AM, Gervais F;
XX WPI; 2002-075222/10.
XX
XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
XX disease comprises contacting blood vessel wall cell with amyloid-beta 40
XX inhibitor.
XX
XX Disclosure; Page 10; 60pp; English.
XX
XX The present invention relates to a new method of inhibiting cerebral
XX amyloid angiopathy. The new method of the invention involves contacting a
XX blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
XX can be used for treating disease states characterised by cerebral amyloid
XX angiopathy, particularly Alzheimer's disease, hereditary cerebral
XX haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
XX The present sequence represents one of a group of peptides (AAU11648-
XX AAU11669, AAU11910 & AAU11911) that were used in the invention as a
XX carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
XX was used in the invention to treat a disease state characterised by
XX cerebral amyloid angiopathy (CAA)
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 29; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFFA 6
DB 1 KAVFFFA 6
RESULT 8
AAU11654
ID AAU11654 standard; peptide; 6 AA.
XX
XX AAU11654;
XX
XX 09-APR-2002 (first entry)
XX
XX Peptide #7, used as a carrier for the amyloid-beta40 (Abeta40) inhibitor.
XX
XX Amyloid-beta40 inhibitor; Abeta40 inhibitor; cerebral amyloid angiopathy;
XX CAA; nontropic; neuroprotective; cerebroprotective; Alzheimer's disease;
XX cerebral haemorrhage; amyloidosis; haemorrhagic stroke.
XX
XX Synthetic.
XX WO200185093-A2.
XX
XX 15-NOV-2001.
XX
XX 22-DEC-2000; 2000WO-IB002078.
XX
XX 23-DEC-1999; 99US-0171877P.
XX
XX

```

XX PA (NEUR-) NEUROCHEM INC.
 XX PI Green AM, Gervais F;
 XX PT WPI; 2002-075222/10.
 XX DR
 XX XX Inhibiting cerebral amyloid angiopathy used for treating e.g. Alzheimer's
 PT disease comprises contacting blood vessel wall cell with amyloid-beta 40
 PT inhibitor.
 XX XX
 XX PS Disclosure; Page 10; 68pp; English.
 XX XX The present invention relates to a new method of inhibiting cerebral
 CC amyloid angiopathy. The new method of the invention involves contacting a
 CC blood vessel wall cell with an amyloid-beta40 inhibitor. The invention
 CC can be used for treating disease states characterised by cerebral amyloid
 CC angiopathy, particularly Alzheimer's disease, hereditary cerebral
 CC haemorrhage with amyloidosis of the Dutch type and haemorrhagic stroke.
 CC The present sequence represents one of a group of peptides (AAU11648-
 CC AAU11669, AAU11910 & AAU11911) that were used in the invention as a
 CC carrier for the amyloid-beta40 (Abeta40) inhibitor. The Abeta40 inhibitor
 CC was used in the invention to treat a disease state characterised by
 CC cerebral amyloid angiopathy (CAA)
 XX CC
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 5; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFPA 6
 |||||
 Db 1 KAVFFPA 6
 |||||
 RESULT 9
 AAE35450
 ID AAE35450 standard; peptide; 6 AA.
 XX AC AAE35450;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #21.
 XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX XX
 XX XX Key Location/Qualifiers
 XX Misc-difference 1. .6 /note= "D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT FT
 XX XX WO200296937-A2.
 XX XX
 XX PD 05-DEC-2002.
 XX XX
 XX PF 29-MAY-2002; 2002WO-CA000763.
 XX XX
 XX PR 29-MAY-2001; 2001US-00867847.
 XX XX
 XX PA (NEUR-) NEUROCHEM INC.
 XX PI Gervais F, Hebert L, Chalifour RJ, Kong X;

XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 PT Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX PT
 XX PS Claim 1; Page 59; 44pp; English.
 XX XX The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFPA 6
 |||||
 Db 1 KAVFFPA 6
 |||||
 RESULT 10
 AAE35443
 ID AAE35443 standard; peptide; 6 AA.
 XX AC AAE35443;
 XX DT 17-JUN-2003 (first entry)
 XX DE Abeta peptide #14.
 XX KW All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
 KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
 KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
 KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; nontropic;
 KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
 KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
 KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
 XX OS Unidentified.
 XX XX
 XX XX Key Location/Qualifiers
 XX Misc-difference 1. .6 /note= "D-form residues"
 FT Modified-site 6 /note= "C-terminal amide"
 FT FT
 XX XX WO200296937-A2.
 XX XX
 XX PD 05-DEC-2002.
 XX XX
 XX PF 29-MAY-2002; 2002WO-CA000763.
 XX XX
 XX PR 29-MAY-2001; 2001US-00867847.
 XX XX
 XX PA (NEUR-) NEUROCHEM INC.
 XX PI Gervais F, Hebert L, Chalifour RJ, Kong X;

PI Gervais F, Hebert L, Chalifour RJ, Kong X;
 XX WPI; 2003-201269/19.
 XX Prevention and/or treatment of an amyloid-related disease e.g.
 XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
 XX
 PS Claim 1; Page 59; 44pp; English.
 XX
 CC The invention relates to a method for prevention and/or treatment of an
 CC amyloid-related disease which comprises administration of an all-D -
 CC amyloid-beta peptide. The method is used for preventing and/or treating
 CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
 CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
 CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
 CC the mammal; and reducing or inhibiting the formation of plaques. It is
 CC also used for treating AA (reactive) amyloid diseases including
 CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
 CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
 CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
 CC disease. AA deposits are also produced as a result of chronic microbial
 CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
 CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
 CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
 CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
 CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
 CC present sequence is an Abeta peptide used to illustrate the method of the
 CC invention
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 6; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db |||||
 1 KAVFFA 6
 RESULT 11
 ADQ37275
 ID ADQ37275 standard; peptide; 6 AA.
 XX
 AC ADQ37275;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uteropic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1..6
 FT /note= "D-form residues"
 FT Modified-site 6
 FT /note= "amidated"

XX WO2004058239-A1.
 XX 15-JUL-2004.
 XX 24-DEC-2003; 2003WO-CA002021.
 XX 24-DEC-2003; 2002US-0436379P.
 XX 23-JUN-2003; 2003US-0482214P.
 XX (NEUR-) NEUROCHEM INT LTD.
 XX Gervais F, Bellini F;
 WPI; 2004-543342/52.
 PT Composition for treating e.g. Alzheimer's disease comprises first agent
 PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 67; 143pp; English.
 XX
 CC The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uteropic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt)) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as a vaccine antigen in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 6 AA;
 Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db |||||
 1 KAVFFA 6
 RESULT 12

ADQ37267
 ID ADQ37267 standard; peptide; 6 AA.
 AC ADQ37267;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Vaccine antigen amyloid-beta related amino acid sequence.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uterapathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FT Misc-difference 1. .6
 FT /note= "D-form residues"
 XX
 PN WO2004058239-A1.
 XX
 PD 15-JUL-2004.
 XX
 XX 24-DEC-2003; 2003WO-CA002021.
 XX
 PR 24-DEC-2002; 2002US-0436379P.
 PR 23-JUN-2003; 2003US-0482214P.
 XX
 PA (NEUR-) NEUROCHEM INT LTD.
 XX
 PI Gervais P, Bellini F;
 XX
 DR WPI; 2004-543342/52.
 XX
 PT Composition for treating e.g. Alzheimer's disease comprises first agent that prevents or treats amyloid-beta related disease and second agent that is either a peptide or peptidomimetic or an immune system modulator.
 XX
 PS Disclosure; Page 67; 143pp; English.
 XX
 CC The present invention describes compositions (C) comprising: (a) a first agent (a1) that prevents or treats amyloid-beta related disease; and (b) a second agent (a2) that is: (i) a peptide or peptidomimetic that modulates amyloid-beta fibril formation or induces a prophylactic or therapeutic immune response against amyloid-beta fibril formation; or (ii) an immune system modulator that prevents or inhibits amyloid-beta fibril formation. Also described is a kit comprising (C). (C) have neurotropic, neuroprotective, cerebroprotective, haemostatic, ophthalmological, anticonvulsant, anti-HIV, antiparkinsonian, muscular, uterapathic, cardiant, antidepressant, endocrine and hypnotic activities, and can be used as amyloid-beta fibril formation modulators, and as immune system modulators. (C) can be used for preventing or treating an amyloid-beta related disease e.g. Alzheimer's disease (including sporadic (non-hereditary) or familial (hereditary)), mild cognitive impairment, mild-to-moderate cognitive impairment, vascular dementia, cerebral amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia, Down's syndrome, inclusion body myositis, age-related macular degeneration, or a condition associated with Alzheimer's disease (including hypothyroidism, cerebrovascular disease, cardiovascular disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,

CC aggression, or incontinence), a neurological condition (e.g. Huntington's disease, amyotrophic lateral sclerosis, acquired immunodeficiency, Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia with Lewy bodies, altered muscle tone, seizures, sensory loss, visual field deficits, incoordination, gait disturbance, transient ischaemic attack or stroke, transient alertness, attention deficit, frequent falls, syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural haematoma, brain tumour, posttraumatic brain injury, or postrhypoxic damage), or a psychological condition (e.g. depression, delusions, illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep disturbance, insomnia, behavioural disinhibition, poor insight, suicidal ideation, depressed mood, irritability, anhedonia, social withdrawal, or excessive guilt) in a subject e.g. human having a genomic mutation in an amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide that can be used as a vaccine antigen in the exemplification of the present invention.
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 DB 1 KAVFFPA 6

RESULT 13

ADQ37319
 ID ADQ37319 standard; peptide; 6 AA.
 XX
 AC ADQ37319;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Antifibrillogenic amyloidosis inhibiting peptide.
 XX
 KW amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; neurotropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uterapathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;
 KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.

Synthetic.

OS
 PN WO2004058239-A1.
 XX

PD 15-JUL-2004.
 XX

PF 24-DEC-2003; 2003WO-CA002021.
 XX

PR 24-DEC-2002; 2002US-0436379P.
 XX

PR 23-JUN-2003; 2003US-0482214P.
 XX

PA (NEUR-) NEUROCHEM INT LTD.
 XX

PI Gervais P, Bellini F;
 XX

DR WPI; 2004-543342/52.
 XX

PT Composition for treating e.g. Alzheimer's disease comprises first agent

PT that prevents or treats amyloid-beta related disease and second agent
 PT that is either a peptide or peptidomimetic or an immune system modulator.
 PS Disclosure; Page 69; 143pp; English.

XX The present invention describes compositions (C) comprising: (a) a first
 CC agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 CC a second agent (a2) that is: (i) a peptide or peptidomimetic that
 CC modulates amyloid-beta fibril formation or induces a prophylactic or
 CC therapeutic immune response against amyloid-beta fibril formation; or
 CC (ii) an immune system modulator that prevents or inhibits amyloid-beta
 CC fibril formation. Also described is a kit comprising (C). (C) have
 CC nootropic, neuroprotective, cerebroprotective, haemostatic,
 CC ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 CC uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 CC neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 CC and can be used as amyloid-beta fibril formation modulators, and as
 CC immune system modulators. (C) can be used for preventing or treating an
 CC amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 CC (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 CC mild-to-moderate cognitive impairment, vascular dementia, cerebral
 CC amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 CC Down's syndrome, inclusion body myositis, age-related macular
 CC degeneration, or a condition associated with Alzheimer's disease
 CC (including hypothyroidism, cerebrovascular disease, cardiovascular
 CC disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 CC aggression, or incontinence), a neurological condition (e.g. Huntington's
 CC disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 CC Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 CC with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 CC field deficits, incoordination, gait disturbance, transient ischaemic
 CC attack or stroke, transient alertness, attention deficit, frequent falls,
 CC syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

XX Sequence 6 AA;

Query Match 100.0%; Score 29; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KAVFFA 6

Db 1 KAVFFA 6

RESULT 14

ADQ37327

ID ADQ37327 standard; peptide; 6 AA.

XX ADQ37327;

AC ADQ37327;

DT 07-OCT-2004 (first entry)

XX Antifibrillogenic amyloidosis inhibiting peptide.

XX amyloid-beta; amyloid-beta related disease;
 KW amyloid-beta fibril formation; immune response; nootropic;
 KW neuroprotective; cerebroprotective; haemostatic; ophthalmological;
 KW antithyroid; vasotropic; cardiovascular; tranquilliser; uropathic;
 KW anticonvulsant; anti-HIV; antiparkinsonian; muscular; neuroleptic;
 KW cardiant; antidepressant; endocrine; hypnotic;
 KW amyloid-beta fibril formation modulator; immune system modulator;
 KW Alzheimer's disease; mild cognitive impairment;

KW mild-to-moderate cognitive impairment; vascular dementia;
 KW cerebral amyloid angiopathy; hereditary cerebral haemorrhage;
 KW senile dementia; Down's syndrome; inclusion body myositis;
 KW age-related macular degeneration; hypothyroidism;
 KW cerebrovascular disease; cardiovascular disease; memory loss; anxiety;
 KW behavioural dysfunction; neurological condition; psychological condition;
 KW vaccine antigen.
 XX Synthetic.

Key Location/Qualifiers
 Modified-site 6 /note= "amidated"

WO2004058239-A1.

15-JUL-2004.

24-DEC-2003; 2003WO-CA002021.

24-DEC-2002; 2002US-0436379P.

23-JUN-2003; 2003US-0482214P.

(NEUR-) NEUROCHEM INT LTD.

Gervais F, Bellini F;

WPI; 2004-543342/52.

Composition for treating e.g. Alzheimer's disease comprises first agent
 that prevents or treats amyloid-beta related disease and second agent
 that is either a peptide or peptidomimetic or an immune system modulator.
 Disclosure; Page 70; 143pp; English.

The present invention describes compositions (C) comprising: (a) a first
 agent (a1) that prevents or treats amyloid-beta related disease; and (b)
 a second agent (a2) that is: (i) a peptide or peptidomimetic that
 modulates amyloid-beta fibril formation or induces a prophylactic or
 therapeutic immune response against amyloid-beta fibril formation; or
 (ii) an immune system modulator that prevents or inhibits amyloid-beta
 fibril formation. Also described is a kit comprising (C). (C) have
 nootropic, neuroprotective, cerebroprotective, haemostatic,
 ophthalmological, antithyroid, vasotropic, cardiovascular, tranquilliser,
 uropathic, anticonvulsant, anti-HIV, antiparkinsonian, muscular,
 neuroleptic, cardiant, antidepressant, endocrine and hypnotic activities,
 and can be used as amyloid-beta fibril formation modulators, and as
 immune system modulators. (C) can be used for preventing or treating an
 amyloid-beta related disease e.g. Alzheimer's disease (including sporadic
 (non-hereditary) or familial (hereditary)), mild cognitive impairment,
 mild-to-moderate cognitive impairment, vascular dementia, cerebral
 amyloid angiopathy, hereditary cerebral haemorrhage, senile dementia,
 Down's syndrome, inclusion body myositis, age-related macular
 degeneration, or a condition associated with Alzheimer's disease
 (including hypothyroidism, cerebrovascular disease, cardiovascular
 disease, memory loss, anxiety, a behavioural dysfunction (e.g. apathy,
 aggression, or incontinence), a neurological condition (e.g. Huntington's
 disease, amyotrophic lateral sclerosis, acquired immunodeficiency,
 Parkinson's disease, aphasia, apraxia, agnosia, Pick disease, dementia
 with Lewy bodies, altered muscle tone, seizures, sensory loss, visual
 field deficits, incoordination, gait disturbance, transient ischaemic
 attack or stroke, transient alertness, attention deficit, frequent falls,
 syncope, neuroleptic sensitivity, normal pressure hydrocephalus, subdural
 CC haematoma, brain tumour, posttraumatic brain injury, or posthypoxic
 CC damage), or a psychological condition (e.g. depression, delusions,
 CC illusion, hallucination, sexual disorder, weight loss, psychosis, a sleep
 CC disturbance, insomnia, behavioural disinhibition, poor insight, suicidal
 CC ideation, depressed mood, irritability, anhedonia, social withdrawal, or
 CC excessive guilt) in a subject e.g. human having a genomic mutation in an
 CC amyloid precursor protein gene, an ApoE gene, or a presenilin gene;
 CC having amyloid-beta deposits. The present sequence represents a peptide
 CC that can be used as an antifibrillogenic amyloidosis inhibiting peptide
 CC in the exemplification of the present invention.

CC amyloid-related conditions, thereby allowing earlier treatment and hence
CC prevention of the undesirable effects of such disorders. Sequences
CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
CC the amyloid-targeting moiety in an imaging agent of the invention.
XX
XX
SQ Sequence 6 AA;

Query Match	100.0%;	Score 29;	DB 9;	Length 6;
Best Local Similarity	100.0%;	Pred. No. 2e+06;		
Matches 6;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 KAVFFFA 6
 |||||
DB 1 KAVFFFA 6

RESULT 16
ADY37926
ID ADY37926 standard; peptide; 6 AA.
XX
AC
XX ADY37926;
XX
DT 19-MAY-2005 (first entry)
XX
DE Amyloid-targeting peptide, SEQ ID NO:6, for use in imaging agent.
XX
XX
KW Diagnosis; imaging; amyloid; Creutzfeldt Jakob disease; Kuru;
KW transmissible spongiform encephalopathy; scrapie; BSE;
KW Alzheimer's disease; neurological disease; amyloidosis;
KW non-insulin dependent diabetes; metabolic disorder.
XX
OS Synthetic.
XX
XX US2005048000-A1.
XX
XX 03-MAR-2005.
XX
XX 03-DEC-2003; 2003US-00728028.
XX
XX 25-JUL-2000; 2000US-0220808P.
PR 24-JUL-2001; 2001US-00915092.
PR 29-JAN-2003; 2003US-0443291P.
XX
XX (NEUR-) NEUROCHEM INT LTD.
XX
XX Gervais F, Kong X, Chalifour R, Migneault D;
XX
XX WPI; 2005-212201/22.
XX
XX
PT New amyloid-targeting imaging agent, useful for diagnosing an amyloid-
PT related condition, e.g. Creutzfeld-Jakob disease, bovine spongiform
PT encephalopathy, primary amyloidosis or Alzheimer's disease.
XX
XX
XX Disclosure; SEQ ID NO 6; 34pp; English.
XX
XX
CC The invention relates to an amyloid-targeting imaging agent. The imaging
CC agent comprises an amyloid targeting moiety (such as a peptide) joined to
CC a labeling moiety via a linking moiety, and is preferably able to cross
CC the blood-brain barrier. The invention also relates to a kit for
CC preparing a radiopharmaceutical preparation from the imaging agent of the
CC invention, a method for imaging amyloid deposition in a patient and a
CC method for diagnosing an amyloid-related condition in a patient. The
CC amyloid-targeting imaging agent is useful in imaging to diagnose amyloid-
CC related conditions such as Creutzfeld-Jakob disease (CJD), Kuru,
CC transmissible cerebral amyloidoses (also known as transmissible virus
CC dementias), familial CJD, scrapie, transmissible mink encephalopathy,
CC bovine spongiform encephalopathy (BSE), inflammation-associated amyloid,
CC type II diabetes, primary amyloidosis, feline spongiform encephalopathy,
CC non-transmissible cerebral amyloidosis (e.g. Alzheimer's disease), prion-
CC mediated diseases, dialysis-related amyloidosis, light chain-related
CC amyloidosis, cerebral amyloid angiopathy or Alzheimer's disease in a
CC patient. The agent does not exhibit excessive toxicity or irritation,
CC does not induce an allergic response, and permits an earlier diagnosis of

CC amyloid-related conditions, thereby allowing earlier treatment and hence
 CC prevention of the undesirable effects of such disorders. Sequences
 CC ADY37921-ADY37947 and ADY37949 represent peptides which may be used as
 CC the amyloid-targeting moiety in an imaging agent of the invention.
 XX
 SQ Sequence 6 AA;

Query Match 100.0%; Score 29; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 1 KAVFFA 6

RESULT 17

AAB05909
 ID AAB05909 standard; peptide; 37 AA.

XX AC AAB05909;

XX 16-OCT-2000 (first entry)

DE Rat inducible nitric oxide synthase calmodulin-binding region.

XX Rat; inducible nitric oxide synthase; iNOS;
 KW endothelial nitric oxide synthase; eNOS; vasotropic; hypertensive;
 KW AMP-activated protein kinase; AMPK; calmodulin; CaM;
 KW eNOS phosphorylation; ischaemic heart disease; pulmonary hypertension;
 KW obstructive airways disease.

XX Rattus sp.

XX WO200028076-A1.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-AU000968.

XX 06-NOV-1998; 98AU-00006976.

XX (SVIN-) ST VINCENTS INST MEDICAL RES.

XX Stapleton DI, Chen Z, Mitchell BU, Kemp BE, Mitchellhill KI;

XX WPI; 2000-376583/32.

XX Identifying modulators of AMP-activated protein kinase-mediated
 PT activation of a nitric oxide synthase (NOS), for use in ischemic heart
 PT disease, comprises testing for the increase or decrease in
 PT phosphorylation of NOS.

XX Example 4; Fig 5; 41pp; English.

XX The present sequence is the calmodulin (CaM)-binding region of rat
 CC inducible nitric oxide synthase (iNOS). iNOS is one of three isoforms of
 CC the enzyme NOS, which synthesises nitric oxide from the amino acid L-
 CC arginine. The sequence is provided for comparison with endothelial nitric
 CC oxide synthase (eNOS). The threonine residue at position 495 of eNOS is
 CC phosphorylated by AMP-activated protein kinase (AMPK) in the absence of
 CC Ca2+-CaM. Phosphorylation results in inhibition of eNOS. In the presence
 CC of Ca2+-CaM, phosphorylation by AMPK occurs predominantly at Ser-1177 and
 CC eNOS is activated. Modulators which activate AMPK may be used in the
 CC treatment of ischaemic heart disease by promoting glucose and fatty acid
 CC metabolism, and improving nutrient and oxygen supply to the myocytes.
 CC They may also be used for the treatment of pulmonary hypertension and
 CC obstructive airways disease

XX Sequence 37 AA;

Query Match 100.0%; Score 29; DB 3; Length 37;
 Best Local Similarity 100.0%; Pred. No. 43;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 |||||
 Db 18 KAVFFA 23

RESULT 18

ADK34079
 ID ADK34079 standard; peptide; 37 AA.

XX AC ADK34079;

XX 20-MAY-2004 (first entry)

XX Mouse iNOS calmodulin binding domain peptide seqid 6.

XX vasotropic; antiangiogenic; gene therapy; critical limb ischaemia; CLI;
 KW eNOS; endothelial nitric oxide synthase; angiogenesis;
 KW microvascular dysfunction; mouse; calmodulin binding domain;
 KW inducible nitric oxide; iNOS.

XX Mus musculus.

XX WO2004016761-A2.

XX 26-FEB-2004.

XX 15-AUG-2003; 2003WO-US025626.

XX 16-AUG-2002; 2002US-0403637P.

XX (SCHD) SCHERING AG.

XX Dole WP, Kauser K, Qian HS, Rubanyi G;

XX WPI; 2004-203789/19.

XX Treating critical limb ischemia (CLI), or angiogenesis comprises
 PT administering to a patient a polynucleotide encoding a mammalian
 PT endothelial nitric oxide synthase (eNOS) polypeptide.

XX Example 1; SEQ ID NO 6; 82pp; English.

XX The invention describes a method of creating critical limb ischaemia
 CC (CLI) comprising administering to a patient a polynucleotide encoding a
 CC mammalian eNOS (endothelial nitric oxide synthase) polypeptide. Also
 CC described are: a method for treating angiogenesis by administering to a
 CC patient a polynucleotide encoding eNOS; and ameliorating microvascular
 CC dysfunction by administering to the patient the polynucleotide encoding
 CC the eNOS polypeptide. The method is useful for treating critical limb
 CC ischaemia or angiogenesis, or ameliorating a microvascular dysfunction.
 CC This is the amino acid sequence of a mouse inducible nitric synthase
 CC (iNOS) calmodulin binding domain peptide.

XX Sequence 37 AA;

Query Match 100.0%; Score 29; DB 8; Length 37;
 Best Local Similarity 100.0%; Pred. No. 43;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 18 KAVFFA 23

RESULT 19

ADL70726
 ID ADL70726 standard; peptide; 37 AA.

XX AC ADL70726;

XX 20-MAY-2004 (first entry)

XX DE Rat iNOS calmodulin-binding site amino acid sequence SEQ ID NO:6.
 XX rat; endothelial nitric oxide synthase; eNOS; enzyme; mutant;
 KW calmodulin-binding domain; vasotropic; antiarteriosclerotic; hypotensive;
 KW antidiabetic; vulnary; antilipemic; anorectic;
 KW reduced calcium dependence; ischaemia; atherosclerosis; hypertension;
 KW diabetes; Raynaud's phenomenon; poor wound healing; hyperlipidaemia;
 XX obesity; iNOS.
 XX Rattus rattus.
 XX OS
 XX WO2004016764-A2.
 XX 26-FEB-2004.
 XX 15-AUG-2003; 2003WO-US025745.
 XX 16-AUG-2002; 2002US-0403638P.
 XX (SCHD) SCHERING AG.
 XX Blasko E, Kauser K, Parkinson J;
 XX WPI; 2004-203792/19.
 XX New isolated endothelial nitric oxide synthase polypeptide mutant, useful
 PT for diagnosing or treating ischemia, atherosclerosis, hypertension,
 PT diabetes, Raynaud's phenomenon, poor wound healing, hyperlipidemia or
 PT obesity.
 XX Example 1; SEQ ID NO 6; 57pp; English.

XX The present sequence represents the calmodulin-binding site of rat iNOS
 CC amino acid sequence. The present invention describes endothelial nitric
 CC oxide synthase (eNOS) mutants having one or more mutations in an amino
 CC acid sequence corresponding to a functional domain of a mammalian eNOS.
 CC At least one of the mutations is at a position corresponding to an amino
 CC acid residue in a calmodulin-binding domain that is phosphorylated in
 CC mammalian cells, and not an amino acid substitution to Ala or Asp. Also
 CC described: (1) an isolated eNOS polypeptide mutant that is substantially
 CC homologous, or has a 95-99% sequence identity to the amino acid sequence
 CC of the novel eNOS polypeptide mutant; (2) an isolated polynucleotide
 CC encoding the polypeptide mutant; (3) a recombinant vector comprising the
 CC polynucleotide operably linked to at least one regulatory sequence; (4) a
 CC pharmaceutical composition comprising the polypeptide mutant or the
 CC polynucleotide; (5) a binding partner of the polypeptide mutant; (6)
 CC modulating eNOS activity in a cell by administering to the cell the
 CC polypeptide mutant; (7) modulating eNOS activity in a cell by
 CC administering the polypeptide mutant or the polynucleotide to the cell,
 CC such that the polypeptide mutant is expressed in the cell; (8) diagnosing
 CC a condition associated with aberrant eNOS activity by contacting a cell
 CC of a patient with the polynucleotide, and detecting a level of eNOS
 CC activity indicative of the medical condition; and (9) prophylactic and
 CC therapeutic methods of treating a condition associated with aberrant eNOS
 CC activity by administering the polypeptide mutant or polynucleotide to the
 CC patient. The eNOS mutant has vasotropic, antiarteriosclerotic,
 CC hypotensive, antidiabetic, vulnary, antilipemic and anorectic
 CC activities, and has reduced calcium dependence and increased activity.
 CC The polypeptide mutant, polynucleotide and methods are useful for
 CC diagnosing or treating a condition associated with aberrant eNOS
 CC activity, e.g. ischaemia, atherosclerosis, hypertension, diabetes,
 CC Raynaud's phenomenon, poor wound healing, hyperlipidaemia or obesity.

XX Sequence 37 AA;
 XX Query Match 100.0%; Score 29; DB 8; Length 37;
 XX Best Local Similarity 100.0%; Pred. No. 43;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB 18 KAVFFA 23

XX RESULT 20
 XX ADG17617
 XX ID ADG17617 standard; protein; 42 AA.
 XX AC ADG17617;
 XX DT 26-FEB-2004 (first entry)
 XX XX Modified amyloid beta precursor protein-related partial protein SeqID8.
 XX amyloid beta precursor protein; APP; beta-selectase cleavage;
 KW alpha-selectase cleavage; Alzheimer's disease; dementia.
 XX OS Unidentified.
 XX XX WO2003102177-A1.
 XX 11-DEC-2003.
 XX 21-MAY-2003; 2003WO-JP006319.
 XX 31-MAY-2002; 2002JP-00159472.
 XX (SAXA) OTSUKA PHARM CO LTD.
 XX Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T;
 XX WPI; 2004-053473/05.
 XX Amyloid beta precursor protein cleaved by beta- but not alpha-selectase
 PT for screening for treatments for Alzheimers disease.
 XX Claim 14; SEQ ID NO 8; 89pp; Japanese.
 XX This invention relates to a novel modified amyloid beta precursor protein
 CC (APP) which contains a beta-selectase cleavage site and a modification
 CC which prevents cleavage by alpha-selectase. The invention may be useful
 CC for screening for, treating and preventing Alzheimer's disease and
 CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.
 XX Sequence 42 AA;
 XX Query Match 100.0%; Score 29; DB 8; Length 42;
 XX Best Local Similarity 100.0%; Pred. No. 48;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 DB 18 KAVFFA 23
 XX RESULT 21
 XX ADG17612
 XX ID ADG17612 standard; protein; 42 AA.
 XX AC ADG17612;
 XX DT 26-FEB-2004 (first entry)
 XX XX Modified amyloid beta precursor protein-related partial protein SeqID3.
 XX amyloid beta precursor protein; APP; beta-selectase cleavage;
 KW alpha-selectase cleavage; Alzheimer's disease; dementia.
 XX OS Unidentified.
 XX XX WO2003102177-A1.
 XX 11-DEC-2003.

PF 21-MAY-2003; 2003WO-JP006319.
 PR 31-MAY-2002; 2002JP-00159472.
 XX (SAKA) OTSUKA PHARM CO LTD.
 PA Shinabuku A, Ogino K, Taki T, Shin R, Kitamoto T;
 PI WPI; 2004-053473/05.
 DR Amyloid beta precursor protein cleaved by beta- but not alpha-selectase
 XX for screening for treatments for Alzheimers disease.
 PT Claim 13; SEQ ID NO 3; 89pp; Japanese.
 PS This invention relates to a novel modified amyloid beta precursor protein
 XX (APP) which contains a beta-selectase cleavage site and a modification
 CC which prevents cleavage by alpha-selectase. The invention may be useful
 CC for screening for, treating and preventing Alzheimer's disease and
 CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.
 XX
 SQ Sequence 42 AA;

Query Match 100.0%; Score 29; DB 8; Length 42;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db |||||
 18 KAVFFA 23

RESULT 22
 AAW41091
 ID AAW41091 standard; protein; 74 AA.
 AC AAW41091;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Chicken matrix metalloproteinase chMMP-2 (aa445-518).
 XX
 KW Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.
 XX
 OS Gallus sp.
 XX
 PN WO9745137-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 30-MAY-1997; 97WO-US009158.
 XX
 PR 31-MAY-1996; 96US-0015869P.
 XX
 PR 31-MAY-1996; 96US-0018733P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Brooks P, Cheres DA;
 XX
 DR WPI; 1998-032334/03.
 XX
 PT Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 XX
 PS Claim 2; Page 159-160; 234pp; English.
 XX
 CC This polypeptide comprises amino acid residues 445-518 of chicken mature
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by

CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.
 CC The invention relates to the discovery that angiogenesis is mediated by
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of
 CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
 CC organic mimetic compound. The antagonists are used to inhibit
 CC angiogenesis in: inflamed tissue for treatment of arthritis or
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
 CC tumour regression or inhibit growth of tumours; and in ocular disorders
 CC such as diabetic retinopathy or macular degeneration (all claimed). They
 CC can also be used to treat restenosis caused by migration of smooth muscle
 CC cells following angioplasty and to reduce blood supply to selected
 CC tissues (claimed). The new antagonists are highly selective for
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
 CC vessels are unaffected, and the antagonists should be of low toxicity
 XX
 SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db |||||
 64 KAVFFA 69

RESULT 23
 AAW41085
 ID AAW41085 standard; protein; 74 AA.
 XX
 AC AAW41085;
 XX
 DT 08-JUN-1998 (first entry)
 XX
 DE Human matrix metalloproteinase huMMP-2 (aa439-512).
 XX
 KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9745137-A1.
 XX
 PD 04-DEC-1997.
 XX
 PF 30-MAY-1997; 97WO-US009158.
 XX
 PR 31-MAY-1996; 96US-0015869P.
 XX
 PR 31-MAY-1996; 96US-0018733P.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Brooks P, Cheres DA;
 XX
 DR WPI; 1998-032334/03.
 XX
 PT Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 XX
 PS Claim 2; Page 153; 234pp; English.
 XX
 CC This polypeptide comprises amino acid residues 439-512 of human mature
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant
 CC methods such as PCR amplification of huMMP-2 coding sequence and cloning
 CC into e.g. pGEX-3X vector for expression in E. coli as a fusion protein

CC with glutathione-S-transferase. The invention relates to the discovery
 CC that angiogenesis is mediated by the specific vitronectin receptor alpha-
 CC v beta-3, and that inhibition of alpha-v beta-3 function inhibits
 CC angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-terminal
 CC fragments (see AAW41083-94) of human or chicken MMP-2, fusion
 CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
 CC or metastases, particularly to induce regression or to inhibit growth of
 CC tumours; and in ocular disorders such as diabetic retinopathy or macular
 CC degeneration (all claimed). They can also be used to treat restenosis
 CC caused by migration of smooth muscle cells following angioplasty and to
 CC reduce blood supply to selected tissues (claimed). The new antagonists
 CC are highly selective for angiogenesis. Only new blood vessels express
 CC alpha-v beta-3, so mature vessels are unaffected, and the antagonists
 CC should be of low toxicity

SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 24

AAW41230
 ID AAW41230 standard; protein; 74 AA.

AC AAW41230;

DT 09-JUN-1998 (first entry)

DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

KW Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

OS Synthetic.

OS Homo sapiens.

PN WO9745447-A1.

PD 04-DEC-1997.

PP 30-MAY-1997; 97WO-US009099.

PR 31-MAY-1996; 96US-0015859P.

PR 31-MAY-1996; 96US-0018733P.

PA (SCRI) SCRIPPS RES INST.

PI Brooks P, Cheres DA, Friedlander M;

DR WPI; 1998-041758/04.

FT Packaging material containing polypeptide antagonist of alphav, beta5
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

PS Claim 2; Page; 117pp; English.

CC Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloprotease-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 439-512. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an

CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 2; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 25

ADT05998

ID ADT05998 standard; protein; 74 AA.

AC ADT05998;

DT 30-DEC-2004 (first-entry)

DE Modified chicken MMP-2 Y517C, residues 445-518.

KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytotatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken;
 KW mutant; mutein; cyclic.

OS Gallus gallus.

OS Synthetic.

Key Location/Qualifiers

Disulfide-bond 2..73

Misc-difference 73

/note= "Cys replaces wild-type Tyr. This residue
 corresponds to residue 517 of the mature MMP-2 protein"

WO2004087057-A2.

PD 14-OCT-2004.

PP 26-MAR-2004; 2004WO-US009321.

PR 28-MAR-2003; 2003US-00402212.

PA (SCRI) SCRIPPS RES INST.

PI Brooks PC, Cheres DA;

DR WPI; 2004-737508/72.

CC Administration of composition comprising organic peptidomimetic alpha-v
 CC beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 CC angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

PS Example 2; Page; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADT05963-ADT06001 represent C-terminal (hemopexin
CC domain) fragments of chicken matrix metalloprotease 2 (MMP-2, gelatinase)
CC containing the amino acid substitutions Y517C and/or W551C which are
CC components of glutathione-S-transferase (GST)/MMP-2 fusion proteins used
CC in an example of the invention. Note: The present sequence is not shown
CC in the specification, but was derived from the wild-type chicken MMP-2 C-
CC terminal fragment ADT05971 and the information given on page 49.

XX Sequence 74 AA;

Query Match 100.0%; Score 29; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db |||||
64 KAVFFA 69

RESULT 26

ADT05965
ID ADT05965 standard; protein; 74 AA.

XX AC ADT05965;

DT 30-DEC-2004 (first entry)

XX Human matrix metalloprotease (MMP-2) residues 439-512, SEQ ID NO:19.

XX Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cystostatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX Homo sapiens.

OS WO2004087057-A2.

XX PN 14-OCT-2004.

XX PD 26-MAR-2004; 2004WO-US009321.

XX PF 28-MAR-2003; 2003US-00402212.

XX PR (Scri) SCRIPPS RES INST.

XX PA Brooks PC, Cheres DA;

XX PI WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v
XX beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
XX angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX

PS Example 1A; SEQ ID NO 19; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
CC gelatinase) used in an example of the invention in assays of inhibition
CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-
CC receptor binding.

XX Sequence 74 AA;

Query Match 100.0%; Score 29; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
Db |||||
64 KAVFFA 69

RESULT 27

ADT05971
ID ADT05971 standard; protein; 74 AA.

XX AC ADT05971;

DT 30-DEC-2004 (first entry)

XX Chicken matrix metalloprotease (MMP-2) residues 445-518, SEQ ID NO:25.

XX Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cystostatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.

OS Gallus gallus.

XX WO2004087057-A2.

XX PN 14-OCT-2004.

XX PD 26-MAR-2004; 2004WO-US009321.

XX PF 28-MAR-2003; 2003US-00402212.

XX PR (Scri) SCRIPPS RES INST.

XX PA Brooks PC, Cheres DA;

XX PI WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v
XX beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
XX angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX Example 1A; SEQ ID NO 25; 184pp; English.

XX

CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
 CC domain) fragments of human and chicken matrix metalloproteinase 2 (MMP-2,
 CC gelatinase) used in an example of the invention in assays of inhibition
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-
 CC receptor binding.

SQ Sequence 74 AA;

Query Match 100.0%; Score 29; DB 8; Length 74;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 28

AAW41086
 ID AAW41086 standard; protein; 108 AA.

AC AAW41086;

DT 08-JUN-1998 (first entry)

DE Human matrix metalloproteinase huMMP-2 (aa439-546).

KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.

OS Homo sapiens.

PN WO9745137-A1.

PD 04-DEC-1997.

PF 30-MAY-1997; 97WO-US009158.

PR 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

PA (SCRI) SCRIPPS RES INST.

PI Brooks P, Cheresch DA;

PI WPI; 1998-032334/03.

PT Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

PS Claim 2; Page 154; 234pp; English.

CC This polypeptide comprises amino acid residues 439-546 of human mature
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant
 CC methods such as PCR amplification of huMMP-2 coding sequence and cloning
 CC into e.g. pGEX-3X vector for expression in E. coli as a fusion protein
 CC with glutathione-S-transferase. The invention relates to the discovery

CC that angiogenesis is mediated by the specific vitronectin receptor alpha-
 CC v beta-3, and that inhibition of alpha-v beta-3 function inhibits
 CC angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-terminal
 CC fragments (see AAW41083-94) of human or chicken MMP-2, fusion
 CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
 CC or metastases, particularly to induce regression or to inhibit growth of
 CC tumours; and in ocular disorders such as diabetic retinopathy or macular
 CC degeneration (all claimed). They can also be used to treat restenosis
 CC caused by migration of smooth muscle cells following angioplasty and to
 CC reduce blood supply to selected tissues (claimed). The new antagonists
 CC are highly selective for angiogenesis. Only new blood vessels express
 CC alpha-v beta-3, so mature vessels are unaffected, and the antagonists
 CC should be of low toxicity

SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 29

AAW41092

ID AAW41092 standard; protein; 108 AA.

AC AAW41092;

DT 08-JUN-1998 (first entry)

DE Chicken matrix metalloproteinase chMMP-2 (aa445-552).

KW Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.

OS Gallus sp.

PN WO9745137-A1.

PD 04-DEC-1997.

PF 30-MAY-1997; 97WO-US009158.

PR 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

PA (SCRI) SCRIPPS RES INST.

PI Brooks P, Cheresch DA;

PI WPI; 1998-032334/03.

PT Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

PS Claim 2; Page 160; 234pp; English.

CC This polypeptide comprises amino acid residues 445-552 of chicken mature
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by
 CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.
 CC The invention relates to the discovery that angiogenesis is mediated by
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of

CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
 CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
 CC organic mimetic compound. The antagonists are used to inhibit
 CC angiogenesis in: inflamed tissue for treatment of arthritis or
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
 CC tumour regression or inhibit growth of tumours; and in ocular disorders
 CC such as diabetic retinopathy or macular degeneration (all claimed). They
 CC can also be used to treat restenosis caused by migration of smooth muscle
 CC cells following angioplasty and to reduce blood supply to selected
 CC tissues (claimed). The new antagonists are highly selective for
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
 CC vessels are unaffected, and the antagonists should be of low toxicity
 XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 30

AAW41231
 ID AAW41231 standard; protein; 108 AA.

XX AC AAW41231;
 XX

DT 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

XX Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

XX Synthetic.
 OS Homo sapiens.

XX WO9745447-A1.

XX 04-DEC-1997.

PF 30-MAY-1997; 97WO-US009099.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheres DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, beta5
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 439-546. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX Sequence 108 AA;

Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 31

AAW41237
 ID AAW41237 standard; protein; 108 AA.

XX AC AAW41237;
 XX

DT 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

XX Synthetic.
 OS Gallus sp.

XX WO9745447-A1.

XX 04-DEC-1997.

PF 30-MAY-1997; 97WO-US009099.

PR 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheres DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, beta5
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41234-39 are derived from the chicken matrix metalloproteinase-
 CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino
 CC acids 445-552. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to

CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX
 SQ Sequence 108 AA;
 Query Match 100.0%; Score 29; DB 2; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 90 KAVFFA 95

RESULT 32

ADT05972
 ID ADT05972 standard; protein; 108 AA.

XX
 AC ADT05972;

XX
 DT 30-DEC-2004 (first entry)

XX
 DE Chicken matrix metalloprotease (MMP-2) residues 445-552, SEQ ID NO:26.

KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.

XX
 OS Gallus gallus.

XX
 PN WO2004087057-A2.

XX
 PD 14-OCT-2004.

XX
 PF 26-MAR-2004; 2004WO-US009321.

XX
 PR 28-MAR-2003; 2003US-00402212.

XX
 PA (SCRI) SCRIPPS RES INST.

XX
 PI Brooks PC, Cheres DA;

XX
 DR WPI; 2004-737508/72.

XX
 PT Administration of composition comprising organic peptidomimetic alpha-v
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX
 PS Example 1A; SEQ ID NO 26; 184pp; English.

XX
 CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to

CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
 CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
 CC gelatinase) used in an example of the invention in assays of inhibition
 CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-
 CC receptor binding.

XX
 SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 33

ADT05966
 ID ADT05966 standard; protein; 108 AA.

XX
 AC ADT05966;

XX
 DT 30-DEC-2004 (first entry)

XX
 DE Human matrix metalloprotease (MMP-2) residues 439-546, SEQ ID NO:20.

KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX
 OS Homo sapiens.

XX
 PN WO2004087057-A2.

XX
 PD 14-OCT-2004.

XX
 PF 26-MAR-2004; 2004WO-US009321.

XX
 PR 28-MAR-2003; 2003US-00402212.

XX
 PA (SCRI) SCRIPPS RES INST.

XX
 PI Brooks PC, Cheres DA;

XX
 DR WPI; 2004-737508/72.

XX
 PT Administration of composition comprising organic peptidomimetic alpha-v
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX
 PS Example 1A; SEQ ID NO 20; 184pp; English.

XX
 CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin

CC domain) fragments of human and chicken matrix metalloproteinase 2 (MMP-2, CC gelatinase) used in an example of the invention in assays of inhibition CC of integrin alpha-v beta-3-mediated cell attachment and of ligand- CC receptor binding.

XX Sequence 108 AA;

SQ

Query Match 100.0%; Score 29; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||

Db 64 KAVFFA 69

RESULT 34
 ADT05999
 ID ADT05999 standard; protein; 108 AA.

XX

AC ADT05999;

XX

DT 30-DEC-2004 (first entry)

XX

DE Modified chicken MMP-2 Y517C/W551C, residues 445-552.

XX

KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 cytostatic; antiinflammatory; antiarthritic; antineumatic;
 ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 peptidomimetic; matrix metalloproteinase 2; MMP-2; gelatinase;
 hemopexin domain; cell attachment assay; ligand binding assay; chicken;
 mutant; mutein.

XX

OS Gallus gallus.

OS Synthetic.

XX

XX

FH Key Location/Qualifiers

FT Misc-difference 73
 /note= "Cys replaces wild-type Tyr. This residue
 corresponds to residue 517 of the mature MMP-2 protein"

FT

FT

FT Misc-difference 107
 /note= "Cys replaces wild-type Trp. This residue
 corresponds to residue 551 of the mature MMP-2 protein"

FT

XX

PN WO2004087057-A2.

XX

PD 14-OCT-2004.

XX

PF 26-MAR-2004; 2004WO-US009321.

XX

PR 28-MAR-2003; 2003US-00402212.

XX

PA (SCRI) SCRIPPS RES INST.

XX

PI Brooks PC, Cheres DA;

XX

DR WPI; 2004-737508/72.

XX

PT Administration of composition comprising organic peptidomimetic alpha-v
 beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

PT

PS Example 2; Page; 184pp; English.

XX

XX The invention relates to a method of inhibiting angiogenesis in a tissue
 by the administration of a composition comprising an organic
 peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 receptor). The integrin alpha-v beta-3 antagonist and compositions
 containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression

CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC treat neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC retinopathy); to treat restenosis in a tissue (e.g., in diabetic
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05998-ADT06001 represent C-terminal (hemopexin
 CC domain) fragments of chicken matrix metalloproteinase 2 (MMP-2, gelatinase)
 CC containing the amino acid substitutions Y517C and/or W551C which are
 CC components of glutathione-S-transferase (GST)/MMP-2 fusion proteins used
 CC in an example of the invention. Note: The present sequence is not shown
 CC in the specification, but was derived from the wild-type chicken MMP-2 C-
 CC terminal fragment ADT05971 and the information given on page 49.

XX

SQ Sequence 108 AA;

Query Match 100.0%; Score 29; DB 8; Length 108;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||

Db 64 KAVFFA 69

RESULT 35

AAW41238

ID AAW41238 standard; protein; 122 AA.

AC AAW41238;

DT 09-JUN-1998 (first entry)

DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

OS Synthetic.
 OS Gallus sp.

FN WO9745447-A1.

PD 04-DEC-1997.

XX 30-MAY-1997; 97WO-US0090999.

XX 31-MAY-1996; 96US-0015869P.

XX 31-MAY-1996; 96US-0018733P.

PA (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheres DA, Friedlander M;
 PI WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, beta5
 integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

PS Claim 2; Page; 117pp; English.

XX Peptides AAW41234-39 are derived from the chicken matrix metalloproteinase-
 CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino
 CC acids 516-637. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX Sequence 122 AA;

SQ Query Match 100.0%; Score 29; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 |||||
 DB 19 KAVFFPA 24

RESULT 36

AAW41232

ID AAW41232 standard; protein; 152 AA.

AC AAW41232;

DT 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.

DE Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.

XX Synthetic.

OS Homo sapiens.

XX WO9745447-A1.

PD 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009099.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

PI Brooks P, Cheres DA, Friedlander M;

XX WPI; 1998-041758/04.

DR Packaging material containing polypeptide antagonist of alphav, betas
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 510-631. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to

CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using
 CC information provided

XX Sequence 152 AA;

SQ Query Match 100.0%; Score 29; DB 2; Length 152;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
 |||||
 DB 23 KAVFFPA 28

RESULT 37

AAW41090

ID AAW41090 standard; protein; 193 AA.

AC AAW41090;

XX 08-JUN-1998 (first entry)

XX Chicken matrix metalloproteinase chMMP-2 (aa445-637).

XX Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; Chicken;
 KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
 KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
 KW diabetic retinopathy; macular degeneration; restenosis; therapy.

XX Gallus sp.

XX WO9745137-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009158.

XX 31-MAY-1996; 96US-0015869P.

PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheres DA;

XX WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, betas
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.

XX Claim 2; Page 158-159; 234pp; English.

XX This polypeptide comprises amino acid residues 445-637 of chicken mature
 CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by
 CC recombinant methods such as PCR amplification (see AAV12502) of chMMP-2
 CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
 CC expression in E. coli as a fusion protein with glutathione-S-transferase.
 CC The invention relates to the discovery that angiogenesis is mediated by
 CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of
 CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
 CC alpha-v beta-3 comprise C-terminal fragments (see AAW41083-94) of human
 CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
 CC also AAW41098-110), derivatised polypeptides, a monoclonal antibody or
 CC organic mimetic compound. The antagonists are used to inhibit
 CC angiogenesis in: inflamed tissue for treatment of arthritis or
 CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
 CC tumour regression or inhibit growth of tumours; and in ocular disorders

CC such as diabetic retinopathy or macular degeneration (all claimed). They
 CC can also be used to treat restenosis caused by migration of smooth muscle
 CC cells following angioplasty and to reduce blood supply to selected
 CC tissues (claimed). The new antagonists are highly selective for
 CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
 CC vessels are unaffected, and the antagonists should be of low toxicity

XX Sequence 193 AA;
 SQ Query Match 100.0%; Score 29; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 38
 AAW41084
 ID AAW41084 standard; protein; 193 AA.
 XX AC AAW41084;
 XX DT 08-JUN-1998 (first entry)
 XX DE Human matrix metalloproteinase huMMP-2 (aa439-631).
 XX KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.
 XX OS Homo sapiens.
 XX PN WO9745137-A1.
 XX PD 04-DEC-1997.
 XX PF 30-MAY-1997; 97WO-US009158.
 XX PR 31-MAY-1996; 96US-0015869P.
 XX PR 31-MAY-1996; 96US-0018733P.
 XX PA (SCRI) SCRIPPS RES INST.
 XX PI Brooks P, Cheres DA;
 XX DR WPI; 1998-032334/03.
 XX PT Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 XX PS Claim 2; Page 152-153; 234pp; English.

CC This polypeptide comprises amino acid residues 439-631 of human mature
 CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant
 CC methods such as PCR amplification (see AAV12510) of huMMP-2 coding
 CC sequence and cloning into e.g. pGEX-3X vector for expression in E. coli
 CC as a glutathione-S-transferase fusion protein. The invention relates to
 CC the discovery that angiogenesis is mediated by the specific vitronectin
 CC receptor alpha-v beta-3, and that inhibition of alpha-v beta-3 function
 CC inhibits angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-
 CC terminal fragments (see AAW41083-94) of human or chicken MMP-2, fusion
 CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),
 CC derivatised polypeptides, a monoclonal antibody or organic mimetic
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
 CC or metastases, particularly to induce tumour regression or inhibit growth
 CC of tumours; and in ocular disorders such as diabetic retinopathy or
 CC macular degeneration (all claimed). They can also be used to treat
 CC restenosis caused by migration of smooth muscle cells following

CC angioplasty and to reduce blood supply to selected tissues (claimed). The
 CC new antagonists are highly selective for angiogenesis. Only new blood
 CC vessels express alpha-v beta-3, so mature vessels are unaffected, and the
 CC antagonists should be of low toxicity

XX Sequence 193 AA;
 SQ Query Match 100.0%; Score 29; DB 2; Length 193;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 64 KAVFFA 69

RESULT 39
 AAW41229
 ID AAW41229 standard; protein; 193 AA.
 XX AC AAW41229;
 XX DT 09-JUN-1998 (first entry)
 XX DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.
 XX KW Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
 KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
 KW restenosis; neovascularisation.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO9745447-A1.
 XX PD 04-DEC-1997.
 XX PF 30-MAY-1997; 97WO-US009099.
 XX PR 31-MAY-1996; 96US-0015869P.
 XX PR 31-MAY-1996; 96US-0018733P.
 XX PA (SCRI) SCRIPPS RES INST.
 XX PI Brooks P, Cheres DA, Friedlander M;
 XX DR WPI; 1998-041758/04.
 XX PT Packaging material containing polypeptide antagonist of alphav, beta5
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 XX PS Claim 2; Page; 117pp; English.

CC Peptides AAW41228-33 are derived from the mature protein of human matrix
 CC metalloproteinase-2 (MMP-2) (AAW41226). The present peptide is derived from
 CC amino acids 439-631. The peptides are able to act as alpha-v-beta-5
 CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
 CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
 CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
 CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
 CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
 CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
 CC tumours or metastases, and in a wide range of ocular disorders (e.g.
 CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
 CC transplants). They are particularly used to induce regression or to
 CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
 CC used to treat restenosis caused by migration of smooth muscle cells
 CC following angioplasty and to reduce blood supply to selected tissues. The
 CC antagonists particularly inhibit neovascularisation where this is induced
 CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
 CC factor or especially vascular endothelial growth factor. note: this
 CC sequence does not appear in the specification; it was created using

CC Information provided

XX Sequence 193 AA;

Query Match 100.0%; Score 29; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 0;

QY 1 KAVFFA 6

DB 64 KAVFFA 69

RESULT 40

AAW41235
ID AAW41235 standard; protein; 193 AA.

AC AAW41235;

DT 09-JUN-1998 (first entry)

XX Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.

XX Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;

XX vitronectin receptor; inhibition; angiogenesis; tumour growth;

XX restenosis; neovascularisation.

XX Synthetic.

XX Gallus sp.

XX WO9745447-A1.

XX 04-DEC-1997.

XX 30-MAY-1997; 97WO-US009099.

XX 31-MAY-1996; 96US-0015869P.

XX 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.

XX Brooks P, Cheres DA, Friedlander M;

XX WPI; 1998-041758/04.

XX Packaging material containing polypeptide antagonist of alphav, betas

XX integrin - used for inhibition of angiogenesis, and for treating tumours,

XX inflammation, eye diseases etc.

XX Claim 2; Page; 117pp; English.

XX Peptides AAW41234-39 are derived from the chicken matrix metalloprotease-

XX 2 (MMP-2) protein (AAW41237). The present peptide is derived from amino

XX acids 445-637. The peptides are able to act as alpha-v-beta-5

XX antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of

XX alpha-v-beta-5 can inhibit angiogenesis. The specification describes a

XX novel labelled package that contains an inhibitor of angiogenesis i.e. an

XX alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-

XX beta-5 and includes a part of the C-terminal domain of MMP-2. The

XX antagonists are used to inhibit angiogenesis in inflamed tissue, in solid

XX tumours or metastases, and in a wide range of ocular disorders (e.g.

XX diabetic or other forms of retinopathy, neovascular glaucoma, or corneal

XX transplants). They are particularly used to induce regression or to

XX inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be

XX used to treat restenosis caused by migration of smooth muscle cells

XX following angioplasty and to reduce blood supply to selected tissues. The

XX antagonists particularly inhibit neovascularisation where this is induced

XX by cytokines, e.g. transforming growth factor alpha, epidermal growth

XX factor or especially vascular endothelial growth factor. note: this

XX sequence does not appear in the specification; it was created using

XX information provided

XX Sequence 193 AA;

Query Match

Best Local Similarity 100.0%; Score 29; DB 2; Length 193;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6

DB 90 KAVFFA 95

RESULT 41

ADT05964
ID ADT05964 standard; protein; 193 AA.

XX AC ADT05964;

XX 30-DEC-2004 (first entry)

XX Human matrix metalloprotease (MMP-2) residues 439-631, SEQ ID NO:18.

XX Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;

XX vitronectin receptor antagonist; neovascularisation; cancer; tumour;

XX inflammation; rheumatoid arthritis; retina; diabetic retinopathy;

XX restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;

XX cytostatic; antiinflammatory; antiarthritic; antirheumatic;

XX ophthalmological; antidiabetic; vasotropic; muscular-gen.;

XX peptidomimetic; matrix metalloprotease 2; MMP-2; Gelatinase;

XX hemopexin domain; cell attachment assay; ligand binding assay; human.

XX Homo sapiens.

XX WO2004087057-A2.

XX 14-OCT-2004.

XX 26-MAR-2004; 2004WO-US009321.

XX 28-MAR-2003; 2003US-00402212.

XX (SCRI) SCRIPPS RES INST.

XX Brooks PC, Cheres DA;

XX WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v

XX beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue

XX angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX Example 1A; SEQ ID NO 18; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue

XX by the administration of a composition comprising an organic

XX peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin

XX receptor). The integrin alpha-v beta-3 antagonist and compositions

XX containing it are useful for inhibiting angiogenesis in a variety of

XX medical conditions. The antagonist may be used to induce the regression

XX of solid tumours or solid tumour metastases; to inhibit the growth of

XX solid tumours undergoing neovascularisation; to treat inflamed tissue in

XX which neovascularisation is occurring (e.g., in rheumatoid arthritis); to

XX treat neovascularisation in retinal tissue (e.g., in diabetic

XX retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle

XX cell migration (such as that which occurs following angioplasty); and to

XX reduce the blood supply to a tissue required to support new growth of the

XX tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin

XX domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,

XX gelatinase) used in an example of the invention in assays of inhibition

XX of integrin alpha-v beta-3-mediated cell attachment and of ligand-

XX receptor binding.

XX Sequence 193 AA;

Query Match

100.0%; Score 29; DB 8; Length 193;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 KAVFFA 6
|||||
Db 64 KAVFFA 69

RESULT 42
ADT05970
ID ADT05970 standard; protein; 193 AA.

XX AC ADT05970;
XX DT 30-DEC-2004 (first entry)
XX DE Chicken matrix metalloproteinase (MMP-2) residues 445-637, SEQ ID NO:24.
XX KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cytostatic; antiinflammatory; antiarthritic; antirheumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloproteinase 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.
XX OS Gallus gallus.
XX PN WO2004087057-A2.
XX PD 14-OCT-2004.

PF 26-MAR-2004; 2004WO-US009321.

PR 28-MAR-2003; 2003US-00402212.

PA (SCRI) SCRIPPS RES INST.

PI Brooks PC, Cheresh DA;

DR WPI; 2004-737508/72.

XX Administration of composition comprising organic peptidomimetic alpha-v
PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

PS Example 1A; SEQ ID NO 24; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
CC receptor). The integrin alpha-V beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
CC domain) fragments of human and chicken matrix metalloproteinase 2 (MMP-2,
CC gelatinase) used in an example of the invention in assays of inhibition
CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-
CC receptor binding.

XX SQ Sequence 193 AA;

Query Match 100.0%; Score 29; DB 8; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 KAVFFA 6
|||||
Db 64 KAVFFA 69

RESULT 43
AAW41083
ID AAW41083 standard; protein; 222 AA.

XX AC AAW41083;
XX DT 08-JUN-1998 (first entry)
XX DE Human matrix metalloproteinase huMMP-2 (aa410-631).

XX KW Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
KW macular degeneration; restenosis; therapy.

XX OS Homo sapiens.

PN WO9745137-A1.

XX PD 04-DEC-1997.

XX PF 30-MAY-1997; 97WO-US009158.

XX PR 31-MAY-1996; 96US-0015869P.

XX PR 31-MAY-1996; 96US-0018733P.

XX PA (SCRI) SCRIPPS RES INST.

XX PI Brooks P, Cheresh DA;

XX DR WPI; 1998-032334/03.

XX Packaging material containing polypeptide antagonist of alphav, beta3
PT integrin - used for inhibition of angiogenesis, and for treating tumours,
PT inflammation, eye diseases etc.

PS Claim 2; Page 150-151; 234pp; English.

XX This polypeptide comprises amino acid residues 410-631 of human mature
CC matrix metalloproteinase 2 (huMMP-2). It can be produced by recombinant
CC methods such as PCR amplification of huMMP-2 coding sequence and cloning
CC into e.g. pGEX-3X vector for expression in E. coli as a fusion protein
CC with glutathione-S-transferase. The invention relates to the discovery
CC that angiogenesis is mediated by the specific vitronectin receptor alpha-
CC v beta-3, and that inhibition of alpha-v beta-3 function inhibits
CC angiogenesis. Claimed antagonists of alpha-v beta-3 comprise C-terminal
CC fragments (see AAW41083-94) of human or chicken MMP-2, fusion
CC polypeptides, cyclic or linear polypeptides (see also AAW41098-110),
CC derivatised polypeptides, a monoclonal antibody or organic mimetic
CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
CC or metastases, particularly to induce regression or to inhibit growth of
CC tumours; and in ocular disorders such as diabetic retinopathy or macular
CC degeneration (all claimed). They can also be used to treat restenosis
CC caused by migration of smooth muscle cells following angioplasty and to
CC reduce blood supply to selected tissues (claimed). The new antagonists
CC are highly selective for angiogenesis. Only new blood vessels express
CC alpha-v beta-3, so mature vessels are unaffected, and the antagonists
CC should be of low toxicity

XX SQ Sequence 222 AA;

Query Match 100.0%; Score 29; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 KAVFFA 6

Db |||||
93 KAVFFA 98

RESULT 44
AAW41228
ID AAW41228 standard; protein; 222 AA.

AC XX
XX AAW41228;
DT 09-JUN-1998 (first entry)

DE Alpha-v-beta-5 antagonistic peptide derived from human MMP-2.
XX Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
KW restenosis; neovascularisation.

XX Synthetic.
OS Homo sapiens.
XX WO9745447-A1.
PN 04-DEC-1997.

PD 30-MAY-1997; 97WO-US009099.
PF 31-MAY-1996; 96US-0015869P.
PR 31-MAY-1996; 96US-0018733P.

XX (SCRI) SCRIPPS RES INST.
PA Brooks P, Cheresh DA, Friedlander M;
XX WPI; 1998-041758/04.

DR Packaging material containing polypeptide antagonist of alphav, beta5
XX integrin - used for inhibition of angiogenesis, and for treating tumours,
PT inflammation, eye diseases etc.
XX Claim 2; Page; 117pp; English.

XX Peptides AAW41228-33 are derived from the mature protein of human matrix
CC metalloprotease-2 (MMP-2) (AAW41226). The present peptide is derived from
CC amino acids 410-631. The peptides are able to act as alpha-v-beta-5
CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
CC tumours or metastases, and in a wide range of ocular disorders (e.g.
CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
CC transplants). They are particularly used to induce regression or to
CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
CC used to treat restenosis caused by migration of smooth muscle cells
CC following angioplasty and to reduce blood supply to selected tissues. The
CC antagonists particularly inhibit neovascularisation where this is induced
CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
CC factor or especially vascular endothelial growth factor. note: this
CC information does not appear in the specification; it was created using
CC information provided

XX Sequence 222 AA;
SQ Query Match 100.0%; Score 29; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||
Db 93 KAVFFA 98

RESULT 45
ADT05963
ID ADT05963 standard; protein; 222 AA.

AC XX
XX ADT05963;
DT 30-DEC-2004 (first entry)

DE Human matrix metalloprotease (MMP-2) residues 410-631, SEQ ID NO:17.
XX Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
KW cystostatic; antiinflammatory; antiarthritic; antineumatic;
KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase;
KW hemopexin domain; cell attachment assay; ligand binding assay; human.

XX Homo sapiens.
XX WO2004087057-A2.
PN 14-OCT-2004.

PD 26-MAR-2004; 2004WO-US009321.
PF 28-MAR-2003; 2003US-00402212.
PR (SCRI) SCRIPPS RES INST.

XX Brooks PC, Cheresh DA;
XX WPI; 2004-737508/72.

DR Administration of composition comprising organic peptidomimetic alpha-v
XX beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
XX angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
XX Example 1A; SEQ ID NO 17; 184pp; English.

XX The invention relates to a method of inhibiting angiogenesis in a tissue
CC by the administration of a composition comprising an organic
CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
CC receptor). The integrin alpha-v beta-3 antagonist and compositions
CC containing it are useful for inhibiting angiogenesis in a variety of
CC medical conditions. The antagonist may be used to induce the regression
CC of solid tumours or solid tumour metastases; to inhibit the growth of
CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
CC treat neovascularisation in retinal tissue (e.g., in diabetic
CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
CC cell migration (such as that which occurs following angioplasty); and to
CC reduce the blood supply to a tissue required to support new growth of the
CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
CC gelatinase) used in an example of the invention in assays of inhibition
CC of integrin alpha-v beta-3-mediated cell attachment and of ligand-
CC receptor binding.

XX Sequence 222 AA;
SQ Query Match 100.0%; Score 29; DB 8; Length 222;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
|||
Db 93 KAVFFA 98

RESULT 46

```

AAW41089
ID AAW41089 standard; protein; 228 AA.
XX AC AAW41089;
XX DT 08-JUN-1998 (first entry)
XX DE Chicken matrix metalloproteinase chMMP-2 (aa410-637).
XX DE Matrix metalloproteinase; MMP-2; chMMP-2; gelatinase; chicken;
XX KW angiogenesis; inhibitor; antagonist; integrin alpha-v beta-3;
XX KW vitronectin receptor; rheumatoid arthritis; tumour; metastasis;
XX KW diabetic retinopathy; macular degeneration; restenosis; therapy.
XX OS Gallus sp.
XX PN WO9745137-A1.
XX PD 04-DEC-1997.
XX PF 30-MAY-1997; 97WO-US009158.
XX PR 31-MAY-1996; 96US-0015869P.
XX PR 31-MAY-1996; 96US-0018733P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Brooks P, Cheres DA;
XX PI WPI; 1998-032334/03.
XX DR Packaging material containing polypeptide antagonist of alphav, beta3
XX PT integrin - used for inhibition of angiogenesis, and for treating tumours,
XX PT inflammation, eye diseases etc.
XX PS Claim 2; Page 157-158; 234pp; English.
XX CC This polypeptide comprises amino acid residues 410-637 of chicken mature
XX CC matrix metalloproteinase 2 (chMMP-2, see AAW41111). It can be produced by
XX CC recombinant methods such as PCR amplification (see AAV12501) of chMMP-2
XX CC coding sequence (see AAV03995) and cloning into e.g. pGEX-3X vector for
XX CC expression in E. coli as a fusion protein with glutathione-S-transferase.
XX CC The invention relates to the discovery that angiogenesis is mediated by
XX CC the specific vitronectin receptor alpha-v beta-3, and that inhibition of
XX CC alpha-v beta-3 function inhibits angiogenesis. Claimed antagonists of
XX CC alpha-v beta-3 comprise C-terminal fragments (see AAW1083-94) of human
XX CC or chicken MMP-2, fusion polypeptides, cyclic or linear polypeptides (see
XX CC also AAW1098-110), derivatised polypeptides, a monoclonal antibody or
XX CC organic mimetic compound. The antagonists are used to inhibit
XX CC angiogenesis in: inflamed tissue for treatment of arthritis or
XX CC rheumatoid arthritis; solid tumours or metastases, particularly to induce
XX CC tumour regression or inhibit growth of tumours; and in ocular disorders
XX CC such as diabetic retinopathy or macular degeneration (all claimed). They
XX CC can also be used to treat restenosis caused by migration of smooth muscle
XX CC cells following angioplasty and to reduce blood supply to selected
XX CC tissues (claimed). The new antagonists are highly selective for
XX CC angiogenesis. Only new blood vessels express alpha-v beta-3, so mature
XX CC vessels are unaffected, and the antagonists should be of low toxicity
XX SQ Sequence 228 AA;
Query Match 100.0%; Score 29; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
DB 99 KAVFFA 104
RESULT 47
AAW41234
ID AAW41234 standard; protein; 228 AA.
XX AC AAW41234;
XX DT 09-JUN-1998 (first entry)
XX DE Alpha-v-beta-5 antagonistic peptide derived from chicken MMP-2.
XX DE Matrix metalloproteinase-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
XX KW vitronectin receptor; inhibition; angiogenesis; tumour growth;
XX KW restenosis; neovascularisation.
XX OS Synthetic.
XX OS Gallus sp.
XX PN WO9745447-A1.
XX PD 04-DEC-1997.
XX PF 30-MAY-1997; 97WO-US009099.
XX PR 31-MAY-1996; 96US-0015869P.
XX PR 31-MAY-1996; 96US-0018733P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Brooks P, Cheres DA, Friedlander M;
XX PI WPI; 1998-041758/04.
XX DR Packaging material containing polypeptide antagonist of alphav, beta5
XX PT integrin - used for inhibition of angiogenesis, and for treating tumours,
XX PT inflammation, eye diseases etc.
XX PS Claim 2; Page; 117pp; English.
XX CC Peptides AAW41234-39 are derived from the chicken matrix metalloproteinase-
XX CC 2 (MMP-2) protein (AAW41227). The present peptide is derived from amino
XX CC acids 410-637. The peptides are able to act as alpha-v-beta-5
XX CC antagonists. Alpha-v-beta-5 is a vitronectin receptor. Inhibitors of
XX CC alpha-v-beta-5 can inhibit angiogenesis. The specification describes a
XX CC novel labelled package that contains an inhibitor of angiogenesis i.e. an
XX CC alpha-v-beta-5 antagonising polypeptide that binds to integrin alpha-v-
XX CC beta-5 and includes a part of the C-terminal domain of MMP-2. The
XX CC antagonists are used to inhibit angiogenesis in inflamed tissue, in solid
XX CC tumours or metastases, and in a wide range of ocular disorders (e.g.
XX CC diabetic or other forms of retinopathy, neovascular glaucoma, or corneal
XX CC transplants). They are particularly used to induce regression or to
XX CC inhibit growth of tumours. The alpha-v-beta-5 antagonists can also be
XX CC used to treat restenosis caused by migration of smooth muscle cells
XX CC following angioplasty and to reduce blood supply to selected tissues. The
XX CC antagonists particularly inhibit neovascularisation where this is induced
XX CC by cytokines, e.g. transforming growth factor alpha, epidermal growth
XX CC factor or especially vascular endothelial growth factor. Note: this
XX CC sequence does not appear in the specification; it was created using
XX CC information provided
XX SQ Sequence 228 AA;
Query Match 100.0%; Score 29; DB 2; Length 228;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KAVFFA 6
DB 125 KAVFFA 130
RESULT 48
ADT05969
ID ADT05969 standard; protein; 228 AA.
XX AC ADT05969;
XX XX

```

DT 30-DEC-2004 (first entry)
 XX Chicken matrix metalloprotease (MMP-2) residues 410-637, SEQ ID NO:23.
 DE
 KW
 XX
 KW Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cytostatic; anti-inflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; Gelatinase;
 KW hemopexin domain; cell attachment assay; ligand binding assay; chicken.
 XX
 OS Gallus gallus.
 XX
 XX WO2004087057-A2.
 PN
 XX
 XX 14-OCT-2004.
 PD
 XX
 XX 26-MAR-2004; 2004WO-US009321.
 PF
 XX
 XX 28-MAR-2003; 2003US-00402212.
 PR
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX
 XX Brooks FC, Cheresch DA;
 PI
 XX
 XX WPI; 2004-737508/72.
 DR
 XX
 XX Administration of composition comprising organic peptidomimetic alpha-v
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
 XX
 XX Example 1A; SEQ ID NO 23; 184pp; English.
 PS
 XX
 CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
 CC receptor). The integrin alpha-V beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. Sequences ADT05963-ADT05974 represent C-terminal (hemopexin
 CC domain) fragments of human and chicken matrix metalloprotease 2 (MMP-2,
 CC gelatinase) used in an example of the invention in assays of inhibition
 CC of integrin alpha-V beta-3-mediated cell attachment and of ligand-
 CC receptor binding.
 XX
 XX Sequence 228 AA;
 SQ
 Query Match 100.0%; Score 29; DB 8; Length 228;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 |||||
 Db 99 KAVFFA 104
 RESULT 49
 ADT05661
 ID ADT05661 standard; protein; 261 AA.
 XX
 XX ADT05661;
 AC
 XX 02-DEC-2004 (first entry)
 DT
 XX

DE Haemophilus influenzae (NTHI) protein - SEQ ID 697.
 XX middle ear bacterial infection; nasopharynx bacterial infection.
 KW
 XX Haemophilus influenzae.
 OS
 XX WO2004078949-A2.
 PN
 XX 16-SEP-2004.
 PD
 XX 05-MAR-2004; 2004WO-US007001.
 PF
 XX 06-MAR-2003; 2003US-0453134P.
 PR
 XX (CHIL-) CHILDRENS HOSPITAL INC.
 PA
 XX Bakaletz LO, Munson RS, Dyer DW;
 PI
 XX WPI; 2004-662422/64.
 DR
 XX N-PSDB; ADT05660.
 XX
 XX New polynucleotides of nontypeable strain of Haemophilus influenzae,
 PT useful for treating or preventing NTHI bacterial infections of the middle
 PT ear and/or nasopharynx.
 PT
 XX Claim 3; SEQ ID NO 697; 88pp; English.
 PS
 XX The invention comprises nucleotide sequences (genes) from the genome of a
 CC nontypeable strain of Haemophilus influenzae (NTHI). The NTHI DNA
 CC sequences of the invention are useful for treating or preventing NTHI
 CC bacterial infections of the middle ear and/or nasopharynx. The present
 CC amino acid sequence represents an NTHI protein of the invention.
 XX
 XX Sequence 261 AA;
 SQ
 Query Match 100.0%; Score 29; DB 8; Length 261;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 |||||
 Db 205 KAVFFA 210
 RESULT 50
 AAW41112
 ID AAW41112 standard; protein; 429 AA.
 XX
 XX AAW41112;
 AC
 XX 08-JUN-1998 (first entry)
 DT
 XX Human matrix metalloproteinase huMMP-2 (aa203-631).
 DE
 XX Matrix metalloproteinase; MMP-2; huMMP-2; human; angiogenesis; inhibitor;
 KW antagonist; integrin alpha-v beta-3; vitronectin receptor;
 KW rheumatoid arthritis; tumour; metastasis; diabetic retinopathy;
 KW macular degeneration; restenosis; therapy.
 KW
 XX Homo sapiens.
 OS
 XX WO9745137-A1.
 PN
 XX 04-DEC-1997.
 PD
 XX 30-MAY-1997; 97WO-US009158.
 PF
 XX 31-MAY-1996; 96US-0015869P.
 PR
 XX 31-MAY-1996; 96US-0018733P.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Brooks P, Cheresch DA;
 XX PI

XX WPI; 1998-032334/03.
 XX
 XX Packaging material containing polypeptide antagonist of alphav, beta3
 PT integrin - used for inhibition of angiogenesis, and for treating tumours,
 PT inflammation, eye diseases etc.
 XX
 XX Example 4; Page 177-179; 234pp; English.
 PS
 PS This polypeptide comprises amino acid residues 203-631 of human mature
 CC matrix metalloproteinase 2 (hMMP-2). It was produced by recombinant
 CC methods involving PCR amplification (see AAV12509) of hMMP-2 coding
 CC sequence and cloning into e.g. pGEX-lambda vector for expression in E.
 CC coli as a glutathione-S-transferase fusion protein. The invention relates
 CC to the discovery that angiogenesis is mediated by the specific
 CC vitronectin receptor alpha-v beta-3, and that inhibition of alpha-v beta-
 CC 3 function inhibits angiogenesis. Claimed antagonists of alpha-v beta-3
 CC comprise C-terminal fragments (see AAW1083-94) of human or chicken MMP-
 CC 2, fusion polypeptides, cyclic or linear polypeptides (see also AAW41098-
 CC 110), derivatised polypeptides, a monoclonal antibody or organic mimetic
 CC compound. The antagonists are used to inhibit angiogenesis in: inflamed
 CC tissue for treatment of arthritis or rheumatoid arthritis; solid tumours
 CC or metastases, particularly to induce tumour regression or inhibit growth
 CC of tumours; and in ocular disorders such as diabetic retinopathy or
 CC macular degeneration (all claimed). They can also be used to treat
 CC restenosis caused by migration of smooth muscle cells following
 CC angioplasty and to reduce blood supply to selected tissues (claimed). The
 CC new antagonists are highly selective for angiogenesis. Only new blood
 CC vessels express alpha-v beta-3, so mature vessels are unaffected, and the
 CC antagonists should be of low toxicity

XX Sequence 429 AA;

Query Match 100.0%; Score 29; DB 2; Length 429;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 Db 300 KAVFFFA 305

RESULT 51
 ADT05991
 ID ADT05991 standard; protein; 429 AA.

XX AC ADT05991;

XX DT 30-DEC-2004 (first entry)

XX DE Human matrix metalloproteinase (MMP-2) residues 203-631, SEQ ID NO:45.

XX KW Angiogenesis inhibitor; integrin alpha-v beta-3 antagonist;
 KW vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 KW inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 KW restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 KW cystostatic; antiinflammatory; antiarthritic; antirheumatic;
 KW ophthalmological; antidiabetic; vasotropic; muscular-gen.
 KW peptidomimetic; matrix metalloproteinase 2; MMP-2; progelatinase; human;
 KW C-terminal fragment; glutathione-S-transferase; GST fusion protein.

XX OS Homo sapiens.

XX PN WO2004087057-A2.

XX PD 14-OCT-2004.

XX PF 26-MAR-2004; 2004WO-US009321.

XX PR 28-MAR-2003; 2003US-00402212.

XX PA (Scripps) SCRIPPS RES INST.

XX

PI Brooks PC, Cheresch DA;

XX WPI; 2004-737508/72.

XX
 XX Administration of composition comprising organic peptidomimetic alpha-v
 PT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.

XX Example 2; SEQ ID NO 45; 184pp; English.

XX
 XX The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. The present sequence represents residues 203-631 of human MMP-2
 CC which is a component of a glutathione-S-transferase (GST)/MMP-2 fusion
 CC protein produced in an example of the invention.

XX Sequence 429 AA;

Query Match 100.0%; Score 29; DB 8; Length 429;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFFA 6
 |||||
 Db 300 KAVFFFA 305

RESULT 52

ABG24001
 ID ABG24001 standard; protein; 468 AA.

XX AC ABG24001;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #23992.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS88188.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.
 XX
 SQ Sequence 626 AA;

Query Match 100.0%; Score 29; DB 8; Length 626;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 543 KAVFFA 548

RESULT 55
 ADG17627
 ID ADG17627 standard; protein; 626 AA.
 XX
 AC ADG17627;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Modified amyloid beta precursor protein-related fusion protein SeqID18.
 XX
 XX amyloid beta precursor protein; APP; beta-selectase cleavage;
 KW alpha-selectase cleavage; Alzheimer's disease; dementia.
 XX
 OS Unidentified.
 XX
 PN WO2003102177-A1.
 XX
 PD 11-DEC-2003.
 XX
 PF 21-MAY-2003; 2003WO-JP006319.
 XX
 PR 31-MAY-2002; 2002JP-00159472.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 PI Shimabuku A, Ogino K, Taki T, Shin R, Kitamoto T;
 XX
 DR WPI; 2004-053473/05.
 XX
 XX Amyloid beta precursor protein cleaved by beta- but not alpha-selectase
 PT for screening for treatments for Alzheimers disease.
 XX
 PS Claim 16; SEQ ID NO 18; 89pp; Japanese.
 XX
 CC This invention relates to a novel modified amyloid beta precursor protein
 CC (APP) which contains a beta-selectase cleavage site and a modification
 CC which prevents cleavage by alpha-selectase. The invention may be useful
 CC for screening for, treating and preventing Alzheimer's disease and
 CC dementia. The present sequence is that of a protein which is related to
 CC the modified amyloid beta precursor proteins of the invention.
 XX
 SQ Sequence 626 AA;

Query Match 100.0%; Score 29; DB 8; Length 626;
 Best Local Similarity 100.0%; Pred. No. 6.7e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 543 KAVFFA 548

RESULT 56
 AAP96143
 ID AAP96143 standard; protein; 631 AA.
 XX
 AC AAP96143;
 XX
 DT 25-MAR-2003 (revised)

DT 09-MAY-1991 (first entry)
 XX
 DE Sequence of human type IV collagenase (gelatinase) in pGEL 186.2.
 XX
 KW Hypertrophic scar; keloid; intervertebral disc disease; enzyme.
 XX
 OS Homo sapiens.
 XX
 PN GB2209526-A.
 XX
 PD 17-MAY-1989.
 XX
 PF 02-SEP-1988; 88GB-00820803.
 XX
 PR 04-SEP-1987; 87US-00093421.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Eisen AZ, Goldberg GI;
 XX
 DR WPI; 1989-147011/20.
 DR N-PSDB; AAN91700.
 XX
 PT DNA encoding human type IV collagenase (gelatinase) - for use in the
 PT treatment of hypertrophic scars, keloids and intervertebral disc disease.
 PS Disclosure; Fig 3; 36pp; English.
 XX
 CC The original source of the protein material was H-ras transformed human
 CC bronchial epithelial cells (TBE-1). The AA sequence was then used to
 CC develop oligonucleotide probes which were used to screen a cDNA library
 CC of human skin fibroblast mRNA. The longest clone, pGEL 186.2, represented
 CC almost the full gelatinase mRNA sequence except the leader sequence
 CC encoding the first few AA's of the signal peptide. (Updated on 25-MAR-
 CC 2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 631 AA;

Query Match 100.0%; Score 29; DB 1; Length 631;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 |||||
 DB 502 KAVFFA 507

RESULT 57
 AAP91139
 ID AAP91139 standard; protein; 631 AA.
 XX
 AC AAP91139;
 XX
 DT 25-MAR-2003 (revised)
 DT 18-DEC-1989 (first entry)
 XX
 XX Human type IV collagenase (gelatinase).
 DE
 XX Human type IV collagenase; gelatinase; hypertrophic scars; keloids;
 KW intervertebral disc disease; extracellular matrix metalloprotease;
 KW bronchial epithelial cells; TBE-1 cells; pGEL186.2; type II motif;
 KW fibonectin; collagen-binding domain.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Domain 1..192
 FT Domain 193..367
 FT Duplication 197..254
 FT Duplication 255..312
 FT Duplication 313..368
 FT Domain 368..631

XX GB2209526-A.
 PN 17-MAY-1989.
 XX 02-SEP-1988; 88GB-00820803.
 XX 04-SEP-1987; 87US-00093421.
 PR (UNIW) UNIV WASHINGTON.
 PA Eisen AZ, Goldberg GI;
 PI WPI; 1989-147011/20.
 XX
 XX DNA encoding human type IV collagenase (gelatinase) - for use in the
 PT treatment of hypertrophic scars, keloids and intervertebral disc disease.
 PT
 XX
 XX Claim 2; Fig 6; 36pp; English.
 PS
 XX Human type IV collagenase (gelatinase). Protein source was H-ras
 CC transformed human bronchial epithelial cells (TBE-1). The sequence was
 CC determined from clone pGel 186.2 which represents almost the full mRNA
 CC sequence. Feature 1 is the N-terminal domain. I; feature 2 is a middle
 CC domain, II, which is organised into 3 x 58 amino acid long head to tail
 CC repeats (features 4,5, and 6). These show homology to the type II motif
 CC collagen binding domain of fibronectin. Feature 3 is the C-terminal
 CC domain. The enzyme could be used in the treatment of hypertrophic scars,
 CC keloids, and intervertebral disc disease. See also AAN91700. (Updated on
 CC 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX
 XX Sequence 631 AA;

Query Match 100.0%; Score 29; DB 1; Length 631;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6
 |||||
 Db 502 KAVFFA 507

RESULT 58
 AAR07969
 ID AAR07969 standard; protein; 631 AA.

XX AAR07969;
 AC
 DT 25-MAR-2003 (revised)
 DT 17-DEC-2001 (revised)
 DT 16-JAN-1991 (first entry)
 XX
 XX Complete type IV collagenase.

XX Type IV collagenase; peptide fragments; metalloproteinase detection;
 KW antibodies; metalloproteinase inhibition; angiogenesis; arthritis;
 KW tumour growth; metastasis; granulomatous inflammatory conditions;
 KW sarcoidosis.

XX Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..18
 FT Peptide /label= 1
 FT Peptide 19..33
 FT Peptide /label= 2
 FT Peptide 26..42
 FT Peptide /label= 3
 FT Protein 34..50
 FT Peptide /label= 4
 FT Peptide 51..66
 FT Peptide /label= 5

FT Peptide 67..89
 FT Peptide /label= 7
 FT Peptide 67..80
 FT Peptide /label= 6
 FT Peptide 69..75
 FT Peptide /label= 8
 FT Peptide 75..94
 FT Peptide /label= 9
 FT Peptide 141..150
 FT Peptide /label= 10
 FT Peptide 299..307
 FT Peptide /label= 11
 FT Peptide 308..318
 FT Peptide /label= 12
 FT Peptide 344..368
 FT Peptide /label= 13
 FT Peptide 371..386
 FT Peptide /label= 14
 FT Peptide 372..375
 FT Peptide /label= 15
 FT Peptide 472..491
 FT Peptide /label= 16

USN7317407-N.

21-AUG-1990.

01-MAR-1989; 89US-00317407.

01-MAR-1989; 89US-00317407.

(USSH) US NAT CANCER INST.

(USDC) US SEC OF COMMERCE.

Liotta LA, Stetlerste W, Krutzsch H;

WPI; 1990-290093/38.

New type-IV collagenase peptide fragments - used for metallo-proteinase
 detection and inhibition and for producing antibodies for enzyme
 detection.

Disclosure; Fig 1; -pp; English.

Type IV procollagenase was purified from human A2058 melanoma cells. The
 complete amino acid sequence was determined (see also Hoyhtya, M. et al,
 (1988) FEBS Letters 233, 109-113). Based on this sequence, peptides were
 synthesised (see features) having homology with a histidine contg. domain
 at residues 371-386, a cysteine contg. domain at residues 200-370, the 80
 residue amino terminus or a region 159 residues from the carboxy
 terminus. These regions correspond to the domain of the enzyme involved
 in enzyme activation and interaction of the enzyme with the substrate.
 The peptides are useful in metalloproteinase detection and inhibition.
 They can be used in the treatment of inappropriate angiogenesis,
 arthritis, tumour growth, invasion and metastasis and granulomatous
 inflammatory conditions such as sarcoidosis. The peptides can be used to
 produce antibodies. Peptide 6, at concn. of 0.1 mM inhibited 80% of the
 enzyme activity. See also US7494796-A and WO9010228. (Note: Revised entry
 submitted to correct the patent number format of US Government-owned NTIS
 applications to prevent clashes with ongoing US granted patent numbers.
 For further information please visit the Derwent web site at
 www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
 correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

Sequence 631 AA;

Query Match 100.0%; Score 29; DB 2; Length 631;

Best Local Similarity 100.0%; Pred. No. 6.8e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KAVFFA 6

|||||
 Db 502 KAVFFA 507

DE	XX	Human mature matrix metalloprotease-2 (MMP-2) protein sequence.
XX	XX	Matrix metalloprotease-2; MMP-2; alpha-v-beta-5 antagonist; treatment;
XX	XX	vitronectin receptor; inhibition; angiogenesis; integrin; tumour growth;
XX	XX	restenosis; neovascularisation.
OS	XX	Homo sapiens.
XX	XX	WO9745447-A1.
XX	XX	04-DEC-1997.
XX	XX	30-MAY-1997; 97WO-US009099.
XX	XX	31-MAY-1996; 96US-0015869P.
XX	XX	31-MAY-1996; 96US-0018733P.
XX	XX	(SCRI) SCRIPPS RES INST.
XX	XX	Brooks P, Cheresh DA, Friedlander M;
XX	XX	WPI; 1998-041758/04.
XX	XX	Packaging material containing polypeptide antagonist of alphav, beta5
XX	XX	integrin - used for inhibition of angiogenesis, and for treating tumours,
XX	XX	inflammation, eye diseases etc.
XX	XX	Disclosure; Fig 16; 117pp; English.
XX	XX	The present sequence represents the mature protein of human matrix
XX	XX	metalloprotease-2 (MMP-2). Fragments of this protein (AAW41228-33) are
XX	XX	able to act as alpha-v-beta-5 antagonists. Alpha-v-beta-5 is a
XX	XX	vitronectin receptor. Inhibitors of alpha-v-beta-5 can inhibit
XX	XX	angiogenesis. The specification describes a novel labelled package that
XX	XX	contains an inhibitor of angiogenesis i.e. an alpha-v-beta-5 antagonising
XX	XX	polypeptide that binds to integrin alpha-v-beta-5 and includes a part of
XX	XX	the C-terminal domain of MMP. The antagonists are used to inhibit
XX	XX	angiogenesis in inflamed tissue, in solid tumours or metastases, and in a
XX	XX	wide range of ocular disorders (e.g. diabetic or other forms of
XX	XX	retinopathy, neovascular glaucoma, or corneal transplants). They are
XX	XX	particularly used to induce regression or to inhibit growth of tumours.
XX	XX	The alpha-v-beta-5 antagonists can also be used to treat restenosis
XX	XX	caused by migration of smooth muscle cells following angioplasty and to
XX	XX	reduce blood supply to selected tissues. The antagonists particularly
XX	XX	inhibit neovascularisation where this is induced by cytokines, e.g.
XX	XX	transforming growth factor alpha, epidermal growth factor or especially
XX	XX	vascular endothelial growth factor
XX	XX	Sequence 631 AA;
XX	XX	Query Match 100.0%; Score 29; DB 2; Length 631;
XX	XX	Best Local Similarity 100.0%; Pred. No. 6.8e+02;
XX	XX	Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX	XX	Qy 1 KAVFFA 6
XX	XX	Db 502 KAVFFA 507
XX	XX	RESULT 61
XX	XX	ADM48668
XX	XX	ID ADM48668 standard; protein; 631 AA.
XX	XX	AC ADM48668;
XX	XX	XX
XX	XX	DT 03-JUN-2004 (first entry)
XX	XX	Human matrix metalloproteinase-2 (MMP-2) protein.
XX	XX	Cancer; metastasis; matrix metalloproteinase-2; MMP-2; vaccine;
XX	XX	immune response; gene therapy; cytostatic; enzyme; human.
XX	XX	Homo sapiens.
XX	XX	OS

XX US2003139345-A1.
 XX 24-JUL-2003.
 XX 23-JAN-2003; 2003US-00350258.
 XX 23-JAN-2002; 2002US-0351317P.
 XX (NETK/) NETKE S.
 XX (NIED/) NIEDZWIECKI A.
 XX (RATH/) RATH M.
 XX Netke S, Niedzwiecki A, Rath M;
 XX WPI; 2003-897356/82.
 XX
 XX New synthetic oligopeptide, useful for blocking or treating cancer
 XX invasion and metastases in a human patient, particularly as a vaccine for
 XX treating or preventing diagnosing brain cancer, lung cancer, skin cancer
 XX or breast cancer.
 XX
 XX Example 1; Fig 1; 11pp; English.
 XX
 XX The present invention relates to novel synthetic oligopeptides effective
 XX in blocking cancer invasion and metastasis. The invention relates to
 XX matrix metalloproteinase-2 (MMP-2) peptides. The synthetic oligopeptides
 XX are useful as pharmaceutical compositions for blocking or treating cancer
 XX invasion and metastases in a human patient. In particular, they are
 XX useful for treating brain cancer, lung cancer, skin cancer or breast
 XX cancer. The oligopeptides are also useful as vaccines for preventing
 XX these cancers, enhancing immune response or raising antibodies for assays
 XX used to diagnose diseases involving matrix metalloproteinases or clinical
 XX monitoring of the progression or regression of disease. They are also
 XX useful in gene therapy. The present sequence is the human MMP-2 protein.
 XX
 XX Sequence 631 AA;
 XX
 XX Query Match 100.0%; Score 29; DB 7; Length 631;
 XX Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 KAVFFFA 6
 XX |||||
 XX 502 KAVFFFA 507
 XX
 XX
 XX RESULT 62
 XX ADT05996
 XX ID ADT05996 standard; protein; 631 AA.
 XX AC ADT05996;
 XX 30-DEC-2004 (first entry)
 XX
 XX Human mature matrix metalloprotease (MMP-2).
 XX
 XX Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
 XX vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 XX inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 XX restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 XX cytosstatic; antiinflammatory; antiarthritic; antirheumatic;
 XX ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 XX peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase; human;
 XX enzyme.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX Region 410..631
 XX /note= "Corresponds to SEQ ID NO:17"
 XX Domain 439..631
 XX /label = Hemopexin_domain

FT FT Region /note = Corresponds to SEQ ID NO:18
 FT FT 439..546
 FT FT /note= "Corresponds to SEQ ID NO:20"
 FT FT 439..512
 FT FT /note= "Corresponds to SEQ ID NO:19"
 FT FT 510..631
 FT FT /note= "Corresponds to SEQ ID NO:21"
 FT FT 543..631
 FT FT /note= "Corresponds to SEQ ID NO:22"
 XX
 XX WO2004087057-A2.
 XX
 XX 14-OCT-2004.
 XX
 XX 26-MAR-2004; 2004WO-US009321.
 XX
 XX 28-MAR-2003; 2003US-00402212.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Brooks PC, Chereesh DA;
 XX
 XX WPI; 2004-737508/72.
 XX
 XX Administration of composition comprising organic peptidomimetic alpha-v
 XX beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 XX angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
 XX
 XX Example 2; Fig 7A-C; 184pp; English.
 XX
 XX The invention relates to a method of inhibiting angiogenesis in a tissue
 XX by the administration of a composition comprising an organic
 XX peptidomimetic antagonist of integrin alpha-V beta-3 (vitronectin
 XX receptor). The integrin alpha-V beta-3 antagonist and compositions
 XX containing it are useful for inhibiting angiogenesis in a variety of
 XX medical conditions. The antagonist may be used to induce the regression
 XX of solid tumours or solid tumour metastases; to inhibit the growth of
 XX solid tumours undergoing neovascularisation; to treat inflamed tissue in
 XX which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 XX treat neovascularisation in retinal tissue (e.g., in diabetic
 XX retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 XX cell migration (such as that which occurs following angioplasty); and to
 XX reduce the blood supply to a tissue required to support new growth of the
 XX tissue. The present sequence represents human mature matrix
 XX metalloprotease 2 (MMP-2, gelatinase) used in an example of the
 XX invention.
 XX
 XX Sequence 631 AA;
 XX
 XX Query Match 100.0%; Score 29; DB 8; Length 631;
 XX Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 XX Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 KAVFFFA 6
 XX |||||
 XX 502 KAVFFFA 507
 XX
 XX
 XX RESULT 63
 XX ADT05997
 XX ID ADT05997 standard; protein; 633 AA.
 XX AC ADT05997;
 XX 30-DEC-2004 (first entry)
 XX
 XX Mouse mature matrix metalloprotease (MMP-2).
 XX
 XX Angiogenesis inhibitor; integrin alpha-V beta-3 antagonist;
 XX vitronectin receptor antagonist; neovascularisation; cancer; tumour;
 XX inflammation; rheumatoid arthritis; retina; diabetic retinopathy;
 XX restenosis; smooth muscle cell migration; angioplasty; antiangiogenic;
 XX cytosstatic; antiinflammatory; antiarthritic; antirheumatic;

KW ophthalmological; antidiabetic; vasotropic; muscular-gen.;
 KW peptidomimetic; matrix metalloprotease 2; MMP-2; gelatinase; mouse;
 KW murine; enzyme.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 441..633
 FT /label = Hemopexin_domain
 XX
 XX WO2004087057-A2.
 XX
 XX 14-OCT-2004.
 XX
 XX 26-MAR-2004; 2004WO-US009321.
 XX
 XX 28-MAR-2003; 2003US-00402212.
 XX
 XX (SCRI) SCHRIPS RES INST.
 XX
 XX Brooks PC, Cheresah DA;
 XX
 XX WPI; 2004-737508/72.
 XX
 XX Administration of composition comprising organic peptidomimetic alpha-v
 FT beta-3 antagonist to e.g. inhibit angiogenesis (inflamed tissue
 PT angiogenesis, retinal angiogenesis and tumor angiogenesis) in a tissue.
 XX
 XX Example 2; Fig 7A-C; 184pp; English.
 XX
 CC The invention relates to a method of inhibiting angiogenesis in a tissue
 CC by the administration of a composition comprising an organic
 CC peptidomimetic antagonist of integrin alpha-v beta-3 (vitronectin
 CC receptor). The integrin alpha-v beta-3 antagonist and compositions
 CC containing it are useful for inhibiting angiogenesis in a variety of
 CC medical conditions. The antagonist may be used to induce the regression
 CC of solid tumours or solid tumour metastases; to inhibit the growth of
 CC solid tumours undergoing neovascularisation; to treat inflamed tissue in
 CC which neovascularisation is occurring (e.g., in rheumatoid arthritis); to
 CC treat neovascularisation in retinal tissue (e.g., in diabetic
 CC retinopathy); to treat restenosis in a tissue by inhibiting smooth muscle
 CC cell migration (such as that which occurs following angioplasty); and to
 CC reduce the blood supply to a tissue required to support new growth of the
 CC tissue. The present sequence represents mouse mature matrix
 CC metalloprotease 2 (MMP-2, gelatinase) used in an example of the
 CC invention.
 XX
 XX Sequence 633 AA;
 SQ
 Query Match 100.0%; Score 29; DB 8; Length 633;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db 504 KAVFFA 509
 |||||
 RESULT 64
 AAB20490
 ID AAB20490 standard; protein; 644 AA.
 XX
 XX AAB20490;
 AC
 XX 21-JUN-2001 (first entry)
 DT
 XX Human matrix metalloproteinase-2 (MMP-2).
 DE
 XX Matrix metalloproteinase-2; MMP-2; human; pain; analgesic;
 KW nerve tissue damage; stroke; haemorrhage; reperfusion injury;
 KW cerebral ischaemia; cerebral infarction; narcotic tolerance;
 KW narcotic withdrawal.
 XX

OS Homo sapiens.
 XX WO200126671-A1.
 FN
 XX 19-APR-2001.
 PD
 XX 11-OCT-2000; 2000WO-US027949.
 PF
 XX 12-OCT-1999; 99US-0158787P.
 PR
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Romanic Arnold A, Barone FC, Bingham S;
 FI
 XX WPI; 2001-290654/30.
 DR
 XX N-PSDB; NAF30807.
 DR
 XX Polypeptide for the treatment of pain and the reduction of tissue damage
 FT comprises an inhibitor of human matrix metalloproteinase.
 PT
 XX Claim 1; Fig 2; 61pp; English.
 PS
 XX The present sequence is that of human matrix metalloproteinase-2 (MMP-2),
 CC previously known as 72 kDa Gelatinase and Gelatinase A. MMP-2 is capable
 CC of degrading the extracellular matrix components of the basement
 CC membrane. The invention relates to methods for treating pain in a patient
 CC by administering a dual inhibitor of MMP-2 and MMP-9 (see AAB20491). The
 CC administration of an inhibitor of MMP-2 is useful for treating nerve
 CC tissue damage (claimed), where the patient is suffering from a disease or
 CC disorder selected from stroke, haemorrhage, reperfusion injury, cerebral
 CC ischaemia and cerebral infarction (claimed). The method is useful for
 CC treating a disease, disorder or nerve tissue damage selected from
 CC enhanced or exaggerated sensitivity to acute pain, burn pain, atypical
 CC facial pain, neuropathic pain, back pain, complex regional pain syndrome
 CC I and II, arthritic pain, sports injury pain, pain related to virus
 CC infection, post-herpetic neuralgia, phantom limb pain, labour pain,
 CC cancer pain, post-chemotherapy pain, post-operative pain, post-stroke
 CC pain, physiological pain, inflammatory pain, acute inflammatory
 CC conditions/visceral pain, neuralgia, painful diabetic retinopathy,
 CC traumatic nerve injury, and tolerance to narcotics or withdrawal from
 CC narcotics (claimed). MMP-2 polypeptides can also be used to screen for
 CC agonist or antagonist (inhibitor) compounds
 XX
 SQ Sequence 644 AA;
 Query Match 100.0%; Score 29; DB 4; Length 644;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFA 6
 Db 515 KAVFFA 520
 |||||
 RESULT 65
 AAR06420
 ID AAR06420 standard; protein; 660 AA.
 XX
 XX AAR06420;
 AC
 XX 25-MAR-2003 (revised)
 DT 13-DEC-1990 (first entry)
 DT
 XX Type IV collagenase cDNA product.
 DE
 XX hypertrophic scars; keloids; intervertebral disc disease; ds.
 KW
 XX Homo sapiens.
 OS
 XX US4923818-A.
 FN
 XX 08-MAY-1990.
 PD

XX 15-MAY-1989; 89US-00352069.
 XX
 XX 15-MAY-1989; 89US-00352069.
 XX
 XX (UNIW) UNIV WASHINGTON.
 XX
 XX Goldberg GL, Eisen AZ;
 PI
 XX WPI; 1990-245482/32.
 XX
 XX N-PSDB; AAQ05620.
 XX
 XX Recombinant human type IV collagenase - used in treatment of hypertrophic
 PT scars, keloids and intervertebral disc disease.
 XX
 XX Claim 3; Fig 9; 23pp; English.
 XX
 XX cDNA clone enables production of type IV collagenase, useful in
 CC catalysing cleavage of extracellular matrix macromolecules, and in
 CC treatment of hypertrophic scars, keloids and intervertebral disc disease.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 660 AA;
 SQ
 Query Match 100.0%; Score 29; DB 2; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFFA 6
 Db 531 KAVFFFA 536
 |||||
 RESULT 66
 AAB84607
 ID AAB84607 standard; protein; 660 AA.
 XX
 XX AAB84607;
 XX
 XX 05-SEP-2001 (first entry)
 DT
 XX
 XX Amino acid sequence of matrix metalloproteinase gelatinase A.
 DE
 XX Growth factor; protein inhibitor; protease; damaged tissue;
 KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
 KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
 KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
 KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
 KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
 KW vascular endothelial growth factor; urokinase plasminogen activator;
 KW dermal ulcer; wound.
 XX
 XX Homo sapiens.
 OS
 XX WO200149309-A2.
 XX
 XX 12-JUL-2001.
 PD
 XX
 XX 21-DEC-2000; 2000WO-IB001935.
 PF
 XX
 XX 29-DEC-1999; 99GB-00030768.
 PR
 XX (PFIZ) PFIZER LTD.
 PA
 XX (PFIZ) PFIZER INC.
 PA
 XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
 PI
 XX WPI; 2001-418351/44.
 XX
 XX N-PSDB; AAH28222.
 DR
 XX
 XX Composition for the treatment of damaged tissue i.e. chronic wounds and
 PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
 PT factor.

XX Disclosure; Page 552; 572pp; English.
 XX
 XX The specification describes a pharmaceutical composition, comprising a
 CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
 CC inhibits the action of at least one specific adverse protein, i.e. a
 CC protease, that is upregulated in a damaged tissue such as a wound
 CC environment. Growth factors which are included in the composition of the
 CC invention are platelet-derived growth factor (PDGF), fibroblast growth
 CC factor (FGF), connective tissue derived growth factor (CTGF),
 CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta
 CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
 CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
 CC and chrysalin. Inhibitors which are included in the composition of the
 CC invention include inhibitors of urokinase-type plasminogen activator
 CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
 CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
 CC The present sequence represents a human MMP-2, and is used to produce the
 CC composition of the invention
 XX
 XX Sequence 660 AA;
 SQ
 Query Match 100.0%; Score 29; DB 4; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KAVFFFA 6
 Db 531 KAVFFFA 536
 |||||
 RESULT 67
 AAE10431
 ID AAE10431 standard; protein; 660 AA.
 XX
 XX AAE10431;
 AC
 XX
 XX 10-DEC-2001 (first entry)
 DT
 XX
 XX Human matrix metalloproteinase-2 (MMP-2) protein.
 DE
 XX
 XX Human; matrix metalloproteinase; MMP-2; hair growth; antisense therapy;
 KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.
 KW
 XX Homo sapiens.
 OS
 XX Location/Qualifiers
 FH Peptide 1..27
 FT /label= Signal_peptide
 FT 28..660
 FT /label= Mature_MMP_2_protein
 FT 100..106
 FT /label= Cysteine_switch_domain
 FT 171..195
 FT /note= "Zinc and calcium binding domain"
 XX
 XX WO200166766-A2.
 XX
 XX 13-SEP-2001.
 PD
 XX
 XX 06-MAR-2001; 2001WO-US007167.
 PF
 XX
 XX 06-MAR-2000; 2000US-0187196P.
 PR
 XX
 XX (DARW-) DARWIN MOLECULAR CORP.
 PA (SCHA/) SCHATZMAN R.
 XX
 XX Fajardo M, Wang K, Smith R, Moss P;
 PI
 XX WPI; 2001-582276/65.
 DR
 XX
 XX Novel isolated matrix metalloproteinase-25 nucleic acid molecule and
 PT proteins encoded by them whose inhibition is useful for modulation of

```

PT hair growth in mammals.
XX
XX
XX Example 2; Fig 3; 119pp; English.
XX
XX The present sequence is human matrix metalloproteinase (MMP)-2 protein
XX used in the exemplification of the inventions. MMP-25 DNA is located on
XX chromosome 11q22. Matrix metalloproteinases are a family of zinc
XX dependent endopeptidases that function extracellularly to degrade
XX proteins typically found in the extracellular matrix. MMP-25 is expressed
XX in skin cells of mammals, particularly in breast cells and hair
XX follicles. MMP-25 DNA is useful for identifying a nucleic acid molecule
XX encoding all or part of MMP by hybridising MMP-25 to a nucleic acid
XX sample and identifying a sequence that hybridises in the nucleic acid
XX sample. The identification step involves performing polymerase chain
XX reaction (PCR) to amplify the hybridising sequence. MMP-25 antibody is
XX useful for identifying type 25 MMP. MMP-25 protein inhibitors may be used
XX to modulate hair growth and breast cancer in a mammal
XX
XX Sequence 660 AA;
SQ
    Query Match          100.0%; Score 29; DB 4; Length 660;
    Best Local Similarity 100.0%; Pred. No. 7.1e+02;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 531 KAVFFPA 536
|||||

RESULT 68
ABB97413
ID ABB97413 standard; protein; 660 AA.
AC ABB97413;
XX
XX 08-JUL-2002 (first entry)
DT
DE Human matrix metalloproteinase 2 protein.
XX
XX Human; matrix metalloproteinase-2; MMP-2; enzyme; thrombolytic;
XX anticoagulant; cardiant; antiarteriosclerotic; cytostatic; osteopathic;
XX antiinflammatory; antibacterial; virucide; fungicide; antipsoriatic;
XX vulnery; cerebroprotective; antiangiinal; ophthalmological;
XX antirheumatic; antiarthritic; antitumor; vasotropic; nephrotropic;
XX alpha-v-beta-3 integrin receptor; thrombosis; tumour; osteoporosis;
XX infection; veterinary medicine; rheumatoid arthritis; Crohn's disease;
XX antimicrobial; antiseptic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 466..660
XX /label= PEX
XX Binding-site 489..497
XX /label= alpha-v-beta-3_integrin_receptor_binding_site
XX Binding-site 570..585
XX /label= alpha-v-beta-3_integrin_receptor_binding_site
XX Binding-site 588..597
XX /label= alpha-v-beta-3_integrin_receptor_binding_site
XX
XX WO200220566-A2.
XX
XX 14-MAR-2002.
XX
XX 28-AUG-2001; 2001WO-EP009899.
XX
XX 07-SEP-2000; 2000DE-01044325.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Jonczyk A, Diefenbach B, Groth U, Zischinsky G;
XX WPI; 2002-329868/36.
XX

```

```

XX New matrix metalloprotease-2 derivative peptides, are alpha-v-beta-3
XX integrin receptor inhibitors useful e.g. for treating thrombosis, cardiac
XX infarction, tumors, osteoporosis, inflammation or infections.
XX
XX Disclosure; Page 11; 35pp; German.
XX
XX The invention relates to peptides (ABB79414-ABB79426) derived from the C-
XX terminal fragment PKX of matrix metalloprotease-2 (MMP-2). Matrix MMP-2
XX derivatives of formula X-Y-Z (I) and their salts and solvates are
XX described. X = H, 1-10C alkanoyl or peptide fragment consisting of 1-20
XX naturally occurring amino acid residues; Y = peptide fragment selected
XX from the sequence region 466-660 of human Pro-MMP-2; and Z = OH, NH 2, NH
XX -1-10C alkyl N(1-10C alkyl) 2 or peptide fragment consisting of 1-20
XX naturally occurring amino acid residues. Primary amino groups are
XX optionally protected conventionally. The peptides and MMP-2 derivatives
XX are used for combating diseases involving interaction of ligands
XX (specifically MMP-2) with the alpha-v-beta-3 integrin receptor,
XX especially pathological processes supported or propagated by
XX angiogenesis, thrombosis, cardiac infarction, coronary heart disease,
XX arteriosclerosis, tumours, osteoporosis, fibrosis, inflammation,
XX infections, psoriasis or wound healing deficiency. More generally the
XX peptides and MMP-2 derivatives are useful in human and veterinary
XX medicine for the treatment and/or prophylaxis of thrombosis, myocardial
XX infarction, apoplexy, angina pectoris, tumour diseases, osteolytic
XX diseases (e.g. osteoporosis or hypercalcaemia), pathological angiogenic
XX diseases (e.g. inflammation), ophthalmological diseases (e.g. diabetic
XX retinopathy, macular degeneration, myopia, ocular histoplasmosis or
XX rubeotic glaucoma), rheumatoid arthritis, osteoarthritis, ulcerative
XX colitis, Crohn's disease, atherosclerosis, psoriasis, restenosis after
XX angioplasty, viral, bacterial or fungal infections, acute renal failure
XX or wound healing deficiency; as antimicrobial/antiseptic agents in
XX operations involving biomaterials, implants, catheters or cardiac
XX pacemakers; or as diagnostic agents or reagents. The present sequence is
XX that of the human MMP-2 protein
XX
XX Sequence 660 AA;
SQ
    Query Match          100.0%; Score 29; DB 5; Length 660;
    Best Local Similarity 100.0%; Pred. No. 7.1e+02;
    Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 531 KAVFFPA 536
|||||

RESULT 69
ABB90738
ID ABB90738 standard; protein; 660 AA.
XX
XX AC ABB90738;
XX
XX 30-MAY-2002 (first entry)
DT
DE Human Tumour Endothelial Marker polypeptide SEQ ID NO 208.
XX
XX Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic;
XX normal endothelial marker; pan-endothelial marker; immunostimulant;
XX antiangiogenic; tumour; neoangiogenesis; vascularised tumour;
XX polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
XX psoriasis.
XX
XX Homo sapiens.
XX
XX WO200210217-A2.
XX
XX 07-FEB-2002.
XX
XX 01-AUG-2001; 2001WO-US024031.
XX
XX 02-AUG-2000; 2000US-0222599P.
XX
XX 11-AUG-2000; 2000US-0224360P.
XX

```


PR 11-APR-2001; 2001US-0282850P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX St Croix B, Kinzler KW, Vogelstein B;
XX WPI; 2002-291856/33.
DR N-PSDB; ABL92092.
XX
PT An isolated molecule comprising an antibody variable region which
PT specifically binds to an extracellular domain of a tumor endothelial
PT marker (TEM) protein, useful for inhibiting tumor growth.
XX
XX Claim 54; Page 166-168; 331pp; English.
XX
XX The invention relates to an isolated molecule comprising an antibody
XX variable region which specifically binds to an extracellular domain of a
XX tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740,
XX ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM
XX proteins have cytostatic, immunostimulant and antiangiogenic activity.
XX They are useful for inhibiting tumour growth, neoangiogenesis in subjects
XX bearing a vascularised tumour, polycystic kidney disease, diabetic
XX retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
XX genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
XX are disclosed, as are marker oligonucleotide sequences: tumour
XX endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal
XX endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
XX (PEM) ABL91903-ABL91995
SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 531 KAVFFPA 536

RESULT 70
AAU84348
ID AAU84348 standard; protein; 660 AA.
XX
XX AAU84348;
XX
XX 08-MAY-2002 (first entry)
XX
XX Protein MMP2 differentially expressed in breast cancer tissue.
XX
XX Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
XX MAI; mitotic activity index; cytostatic.
XX
XX Homo sapiens.
XX
XX WO200210436-A2.
XX
XX 07-FEB-2002.
XX
XX 27-JUL-2001; 2001WO-US023642.
XX
XX 28-JUL-2000; 2000US-0222093P.
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX (BAAK/) BAAK J.
XX Baak J, Mutter GL;
XX
XX WPI; 2002-180084/23.
XX N-PSDB; ABK35568.
XX
XX Diagnosing breast cancer comprises determining expression of nucleic acid
PT molecules or expression products that are differentially expressed in

PT normal and malignant tissue.
XX Claim 37; Page 185-187; 219pp; English.
XX
XX The present invention relates to a method for diagnosing breast cancer in
XX a subject suspected of having endometrial cancer. The method comprises
XX determining the expression of a set of human genes or expression products
XX in an endometrial sample suspected of being cancerous. The human genes of
XX the invention are differentially expressed in breast tumours
XX characterised as high or low MAI (mitotic activity index). These sets of
XX genes can be used to discriminate between high and low MAI breast
XX tumours. The invention also provides DNA and protein microarrays for
XX analysing the expression of the human genes and their protein products.
XX The methods and arrays are useful for the diagnosis and prognosis of
XX endometrial cancer, selecting and monitoring treatment regimes, and
XX identification of compounds useful for the treatment of endometrial
XX cancer. AAU84311-AAU84361 represent the human proteins of the invention
XX that are differentially expressed in breast cancer tissue
SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 5; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFPA 6
Db 531 KAVFFPA 536

RESULT 71
ABU54445
ID ABU54445 standard; protein; 660 AA.
XX
XX ABU54445;
XX
XX 12-MAR-2003 (first entry)
XX
XX Human tumour endothelial marker TEM 7.
XX
XX Human; endothelial cell; EC; tumour endothelial cell; TEM; NEM;
XX Tumour endothelial marker; normal endothelial marker; PEM;
XX pan-endothelial marker; polycystic kidney disease; psoriasis;
XX diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis;
XX neoangiogenesis; immune response; cytostatic; antidiabetic;
XX ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
XX
XX Homo sapiens.
XX
XX WO200283874-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US008253.
XX
XX 11-APR-2001; 2001US-0282850P.
XX 06-FEB-2002; 2002US-0354262P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Carson-Walter E, St Croix B, Kinzler KW, Vogelstein B;
XX
XX WPI; 2003-093016/08.
XX N-PSDB; ABX72017.
XX
XX New purified human transmembrane protein, designated as tumor endothelial
XX marker (TEM) 3, useful for detecting, diagnosing or treating tumors, or
XX polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
XX psoriasis.
XX
XX Disclosure; Page 173-174; 374pp; English.
XX
XX The present invention relates to a novel method for the isolation of

CC endothelial cells (ECs), and the identification of genes expressed in
 CC normal and tumour ECs. Tumour endothelial marker (TEM), normal
 CC endothelial marker (NEM), and pan-endothelial marker (PEM) genes are
 CC identified in human ECs. The human EC marker proteins and the
 CC polynucleotide sequences encoding them are useful for detecting,
 CC diagnosing or treating tumours as well as polycystic kidney disease,
 CC diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also
 CC useful for inhibiting neoangiogenesis or tumour angiogenesis, for
 CC inducing an immune response to tumour endothelial cells in a patient, or
 CC for identifying candidate drugs for treating tumours. The present
 CC sequence represents a human TEM or NEM protein of the invention
 XX
 SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 DB 531 KAVFFA 536
 |||||

RESULT 72
 ABP97136
 ID ABP97136 standard; protein; 660 AA.
 AC
 XX
 DT 24-JUN-2003 (first entry)
 XX
 DE Human matrix metalloproteinase 2 protein SEQ ID NO:14.
 XX
 DE Human; matrix metalloproteinase; MMP; anticancer; wound healing;
 KW matrix metalloproteinase inhibitor; antitumour; antiangiogenic; cardiant;
 KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
 KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
 KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
 KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
 KW macular degeneration; diabetic retinopathy; cleavage region.
 XX
 OS Homo sapiens.
 XX
 PN WO2003018748-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 15-AUG-2002; 2002WO-US026319.
 XX
 PR 16-AUG-2001; 2001US-0312726P.
 PR 21-DEC-2001; 2001US-00032376.
 PR 21-MAY-2002; 2002US-00153185.
 XX
 PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
 XX
 PI Quirk S, Weart IF;
 DR WPI; 2003-381408/36.
 XX
 PT Anti-angiogenic composition comprising peptide inhibitor of matrix
 PT metalloproteinase, useful for decreasing the expression of vascular
 PT endothelial growth factor and treating cancers and tissue injuries.
 XX
 PS Example 1; Page 43-44; 103pp; English.
 XX
 CC The present invention describes an anti-angiogenic composition (I) for
 CC inhibiting expression of vascular endothelial growth factor (VEGF). (I)
 CC comprises an effective amount of a peptide inhibitor of matrix
 CC metalloproteinase (MMP), where the peptide can inhibit the expression of
 CC VEGF. (II) has cytostatic, vulnary, cardiant, cerebroprotective,
 CC antidiabetic, ophthalmological and dermatological activities. (I) can be
 CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be

CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (I) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents the human MMP-2 protein, which is used in the exemplification
 XX
 SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
 DB 531 KAVFFA 536
 |||||

RESULT 73
 AAO16608
 ID AAO16608 standard; protein; 660 AA.
 XX
 AC AAO16608;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE Human matrix metalloproteinase 2 (MMP2) gelatinase protein.
 XX
 KW Human; enzyme; crystalline polypeptide; matrix metalloproteinase 9; MMP9;
 KW gelatinase; metalloproteinase mediated disease; drug design; arthritis;
 KW three-dimensional structure; MMP9 inhibitor; tumour growth;
 KW cancer metastasis; osteoarthritis; atherosclerosis; restenosis;
 KW periodontitis; multiple sclerosis; glomerulonephritis; MMP9 modulator;
 KW graft-versus-host disease; non-insulin dependent diabetes; MMP2;
 KW matrix metalloproteinase 2.
 OS Homo sapiens.
 XX
 PN WO2003002729-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 24-JUN-2002; 2002WO-SE001266.
 XX
 PR 27-JUN-2001; 2001SE-00002298.
 XX
 PA (ASTR) ASTRAZENECA AB.
 XX
 PI Jepson H, Minshull C, Paupit R, Rowsell S;
 DR WPI; 2003-201502/19.
 XX
 PT Novel crystalline form of a polypeptide corresponding to the catalytic
 PT domain of matrix metalloproteinase 9 protein, useful for selecting or
 PT designing chemical modulators which are used for treating diabetes,
 PT cancer, arthritis.
 XX
 PS Disclosure; Fig 7; 227pp; English.
 XX
 CC The invention comprises a crystalline form of a polypeptide corresponding
 CC to the catalytic domain of matrix metalloproteinase 9 (MMP9) protein - a
 CC gelatinase. The crystalline polypeptide of the invention is useful for
 CC treating a metalloproteinase mediated disease or condition in a warm-
 CC blooded animal. The crystalline polypeptide is also useful for
 CC determining the three-dimensional structure of the MMP9 catalytic domain
 CC to high resolution. The three-dimensional structure of the MMP9 catalytic
 CC domain is useful for rational drug design, and the atomic coordinates of
 CC the catalytic domain of MMP9 are useful for selecting or designing
 CC chemical modulators (preferably inhibitors) of MMP9. The crystalline
 CC polypeptide of the invention is useful in the treatment of a
 CC metalloproteinase mediated disease or condition, such as: tumour growth;
 CC metastasis in cancer; arthritis; osteoarthritis; atherosclerosis;

CC restenosis; periodontitis; multiple sclerosis; glomerulonephritis; graft-versus-host disease; and non-insulin dependent diabetes. The present amino acid sequence represents a human matrix metalloproteinase 2 (MMP2) protein

XX
SQ Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

RESULT 74
ABG76322
ID ABG76322 standard; protein; 660 AA.
XX AC ABG76322;
XX
XX 10-MAY-2003 (first entry)
XX
XX Human matrix metalloproteinase-2 (MMP-2).
XX
XX Human; peptide inhibitor; matrix metalloproteinase-2; MMP-2; cleavage region; proenzyme form; cellular proliferation; fibroblast; keratinocyte; healthy skin development; wound healing; scarring; skin tone; wrinkle; anti-aging; vulnerary.

XX Homo sapiens.

XX WO2003016520-A1.

XX 27-FEB-2003.

XX 15-AUG-2002; 2002WO-US026198.

XX 16-AUG-2001; 2001US-0312726P.

XX 21-DEC-2001; 2001US-00032376.

XX 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Malik S, Villanueva JM;

XX WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix metalloproteinases, e.g. matrix metalloproteinase-2, useful for stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Example 1; Page 41-42; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have peptide sequences related to the cleavage regions of the proenzyme forms of the MMPs. The peptide inhibitors are useful for stimulating cellular proliferation of fibroblasts or keratinocytes, promoting healthy skin tone, development, treating wounds, preventing scarring, improving skin tone, reducing wrinkling and for stimulating the development of smooth, healthy skin. The peptide inhibitors are useful as anti-aging and wound healing compounds. The present sequence represents human MMP-2

XX Sequence 660 AA;

Query Match 100.0%; Score 29; DB 6; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||

Db 531 KAVFFA 536

RESULT 75
ADD18578
ID ADD18578 standard; protein; 660 AA.
XX AC ADD18578;
XX
XX 15-JAN-2004 (first entry)
XX
XX Human disease related protein SeqID9.

XX human; disease state; cytostatic; antiinflammatory; ophthalmological; antiarteriosclerotic; vulnerary; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transport; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing.

XX Homo sapiens.

XX WO2003018621-A2.

XX 06-MAR-2003.

XX 23-AUG-2002; 2002WO-GB003892.

XX 23-AUG-2001; 2001GB-00020558.

XX 05-OCT-2001; 2001GB-00024037.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;

XX WPI; 2003-290046/28.

XX N-PSDB; ADD18579.

XX New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or wound healing.

XX Claim 25; SEQ ID NO 9; 424pp; English.

XX This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, the ophthalmological, antiarteriosclerotic or vulnerary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition, such as tumorigenesis, angiogenesis, apoptosis, inflammation, erythropoiesis, or the biological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transportation, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischaemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of a disease related protein of the invention.

XX Sequence 660 AA;

Query Match 100.0%; Score 29; DB 7; Length 660;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KAVFFA 6
|||||
Db 531 KAVFFA 536

Search completed: December 29, 2005, 17:33:40
Job time : 82.7742 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:42 ; Search time 78.1936 Seconds
(without alignments)
54.137 Million cell updates/sec

Title: US-10-009-122-12
Perfect score: 31
Sequence: 1 KPVFFA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 300 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	47	2 Q8G99_FUGRU	Q8G99_fugu rubrip
2	31	100.0	229	2 Q6RS99_TRTTU	Q6RS99_triticum tu
3	31	100.0	241	2 Q7XYC3_WHEAT	Q7XYC3_triticum ae
4	31	100.0	331	2 Q6K5X9_ORYSA	Q6K5X9_oryza sativ
5	31	100.0	331	2 Q84N87_ORYSA	Q84N87_oryza sativ
6	31	100.0	335	2 Q6I5W9_ORYSA	Q6I5W9_oryza sativ
7	31	100.0	353	2 Q4HQ66_CAMUP	Q4HQ66_campylobact
8	31	100.0	519	2 Q5ATG9_EMENI	Q5ATG9_aspergillus
9	31	100.0	935	2 Q7XM01_ORYSA	Q7XM01_oryza sativ
10	31	100.0	3044	2 Q7QYR7_GIALA	Q7QYR7_giardia lam
11	30	96.8	224	2 Q84NG7_HORVU	Q84NG7_hordeum vul
12	30	96.8	395	2 Q98GC2_RHILO	Q98GC2_triticum l
13	30	96.8	397	2 Q2Y1Y6_RHIME	Q2Y1Y6_rhizobium m
14	30	96.8	2643	2 Q5A3W3_CANAL	Q5A3W3_candida alb
15	30	96.8	2643	2 Q5A3Q1_CANAL	Q5A3Q1_candida alb
16	28	90.3	23	2 Q4XRS5_PLACH	Q4XRS5_plasmodium
17	28	90.3	43	2 Q73M63_TREDE	Q73M63_treponea d
18	28	90.3	49	2 Q3KAX7_BACHD	Q3KAX7_bacillus ha
19	28	90.3	150	2 Q7R979_PLAYO	Q7R979_plasmodium
20	28	90.3	152	2 Q4J122_AZOVI	Q4J122_azotobacter
21	28	90.3	177	2 Q20070_CAEEL	Q20070_caenorhabdi
22	28	90.3	199	2 Q6LSA9_PHOPR	Q6LSA9_photobacter
23	28	90.3	225	2 Q6UJY8_TRTTU	Q6UJY8_triticum tu
24	28	90.3	226	2 Q8LKV8_AEGTA	Q8LKV8_aegilops ta
25	28	90.3	241	2 Q7R8V4_PLAYO	Q7R8V4_plasmodium
26	28	90.3	242	2 Q7RA05_PLAYO	Q7RA05_plasmodium
27	28	90.3	250	2 Q7RNP5_PLAYO	Q7RNP5_plasmodium
28	28	90.3	251	2 Q7PDC0_PLAYO	Q7PDC0_plasmodium
29	28	90.3	251	2 Q7RPS1_PLAYO	Q7RPS1_plasmodium
30	28	90.3	252	2 Q7RAS7_PLAYO	Q7RAS7_plasmodium
31	28	90.3	252	2 Q7RF37_PLAYO	Q7RF37_plasmodium

32	28	90.3	255	2	Q7RLK2_PLAYO	Q7RLK2_plasmodium
33	28	90.3	262	2	Q7RCL4_PLAYO	Q7RCL4_plasmodium
34	28	90.3	265	2	Q7RC37_PLAYO	Q7RC37_plasmodium
35	28	90.3	268	2	Q7RB86_PLAYO	Q7RB86_plasmodium
36	28	90.3	285	2	Q529U4_MAGGR	Q529U4_magnaporthe
37	28	90.3	293	2	Q94284_CAEEL	Q94284_caenorhabdi
38	28	90.3	294	2	Q7RBUI_PLAYO	Q7RBUI_plasmodium
39	28	90.3	300	2	Q5UWP7_HALMA	Q5UWP7_haloarcula
40	28	90.3	321	2	Q7RBJ3_PLAYO	Q7RBJ3_plasmodium
41	28	90.3	326	2	F74429_SYNY3	F74429_synochocyst
42	28	90.3	380	2	Q6KI05_MYCWO	Q6KI05_mycoplasma
43	28	90.3	388	2	Q4MSJ5_BACCE	Q4MSJ5_bacillus ce
44	28	90.3	388	2	Q6HLH8_BACHK	Q6HLH8_bacillus th
45	28	90.3	388	2	Q73BD3_BACCL	Q73BD3_bacillus ce
46	28	90.3	388	2	Q63E03_BACCC	Q63E03_bacillus ce
47	28	90.3	388	2	Q8IT98_BACAN	Q8IT98_bacillus an
48	28	90.3	391	2	Q8IG40_BACCR	Q8IG40_bacillus ce
49	28	90.3	398	2	Q5NEA9_FRATT	Q5NEA9_francisella
50	28	90.3	409	2	Q73V08_MYCPA	Q73V08_mycobacteri
51	28	90.3	421	2	Q722C3_CAEEL	Q722C3_caenorhabdi
52	28	90.3	422	2	Q9PGG2_UREPA	Q9PGG2_ureaplasma
53	28	90.3	430	2	Q8FW04_BRUSU	Q8FW04_brucella su
54	28	90.3	432	2	Q6Q8W8_9GAMM	Q6Q8W8_uncultured
55	28	90.3	436	2	Q8M9J3_9AQUA	Q8M9J3_ilex pubesc
56	28	90.3	452	2	Q44595_CAEEL	Q44595_caenorhabdi
57	28	90.3	456	2	Q6GVJ4_9BURK	Q6GVJ4_burkholderi
58	28	90.3	465	1	RBL_NEPAL	RBL_nepenthes a
59	28	90.3	472	2	Q9NSQ8_CAEEL	Q9NSQ8_caenorhabdi
60	28	90.3	480	2	Q625W2_CAEER	Q625W2_caenorhabdi
61	28	90.3	482	2	Q5JJ16_PYRKO	Q5JJ16_pyrococcus
62	28	90.3	488	2	Q966D7_CAEEL	Q966D7_caenorhabdi
63	28	90.3	492	2	Q621X3_CAEER	Q621X3_caenorhabdi
64	28	90.3	506	2	Q38860_ARATH	Q38860_arabidopsis
65	28	90.3	508	1	MURE_BORBU	MURE_borrelia bu
66	28	90.3	509	2	P93058_BRAJU	P93058_brassica ju
67	28	90.3	509	2	Q8LSC7_BACRM	Q8LSC7_brassica ca
68	28	90.3	509	2	Q8S384_BRAJU	Q8S384_brassica ju
69	28	90.3	517	2	Q80729_ARATH	Q80729_arabidopsis
70	28	90.3	529	2	Q6NI23_CORDI	Q6NI23_corynebacte
71	28	90.3	538	2	Q7PQZ0_ANOGA	Q7PQZ0_anopheles g
72	28	90.3	558	2	Q5TTR3_ANOGA	Q5TTR3_anopheles g
73	28	90.3	571	2	Q97KU8_CLOAB	Q97KU8_clostridium
74	28	90.3	584	2	Q4UGB4_THEAN	Q4UGB4_theileria a
75	28	90.3	615	2	Q7PSI2_ANOGA	Q7PSI2_anopheles g
76	28	90.3	664	2	Q966D8_CAEEL	Q966D8_caenorhabdi
77	28	90.3	746	2	Q9NSQ9_CAEEL	Q9NSQ9_caenorhabdi
78	28	90.3	802	2	Q7R8Y2_PLAYO	Q7R8Y2_plasmodium
79	28	90.3	853	2	Q7QTQ4_GIALA	Q7QTQ4_giardia lam
80	28	90.3	922	1	GYRA_AERSA	GYRA_aeromonas a
81	28	90.3	1072	2	Q94537_SCHPO	Q94537_schistosacch
82	28	90.3	1165	2	Q962L9_PLAVI	Q962L9_plasmodium
83	28	90.3	1285	2	Q9WXU3_THENA	Q9WXU3_thermotoga
84	28	90.3	1558	2	Q5RH87_BRARE	Q5RH87_brachydanio
85	27	87.1	31	2	Q4YNS6_PLABE	Q4YNS6_plasmodium
86	27	87.1	36	2	Q4XB83_PLACH	Q4XB83_plasmodium
87	27	87.1	38	2	Q32187_EUGGR	Q32187_euglena gra
88	27	87.1	46	2	Q867A4_TRAJA	Q867A4_tragus ja
89	27	87.1	60	2	Q4YKM8_PLABE	Q4YKM8_plasmodium
90	27	87.1	77	2	Q52R02_CHICK	Q52R02_gallus gall
91	27	87.1	90	2	Q4XC01_PLACH	Q4XC01_plasmodium
92	27	87.1	92	2	Q8MPY0_CAEEL	Q8MPY0_caenorhabdi
93	27	87.1	96	2	Q611Z3_CAEER	Q611Z3_caenorhabdi
94	27	87.1	99	2	Q4T7Q1_TETNG	Q4T7Q1_tetradon n
95	27	87.1	114	2	Q6ZB28_ORYSA	Q6ZB28_oryza sativ
96	27	87.1	117	2	Q74KX8_LACJO	Q74KX8_lactobacill
97	27	87.1	121	2	Q6R983_MAIZE	Q6R983_zea mays (m
98	27	87.1	128	2	Q4MQN4_BACCE	Q4MQN4_bacillus ce
99	27	87.1	128	2	Q6HNK6_BACHK	Q6HNK6_bacillus th
100	27	87.1	128	2	Q81116_BACCR	Q81116_bacillus ce
101	27	87.1	128	2	Q73DN7_BACCC	Q73DN7_bacillus ce
102	27	87.1	128	2	Q63G38_BACCC	Q63G38_bacillus ce
103	27	87.1	128	2	Q81V92_BACAN	Q81V92_bacillus an
104	27	87.1	134	2	Q7R7Y0_PLAYO	Q7R7Y0_plasmodium

105	27	87.1	134	2	Q4XU22_PLACH	Q4xu22 plasmodium	178	27	87.1	345	2	Q4Z9Y8_9VIRU	Q4z9y8 bacterioph
106	27	87.1	135	2	Q8MYN0_CABEL	Q8myrn0 caenorhabdi	179	27	87.1	345	2	Q8KZ48_9PROT	Q8kz48 uncultured
107	27	87.1	138	2	O51365_BORBU	O51365 borrelia bu	180	27	87.1	346	1	ACSF_GLOVI	Q7naf1 gloebacter
108	27	87.1	140	2	Q9G4E5_FASGI	Q9g4e5 fasciola gi	181	27	87.1	349	1	ACSF_GRATL	Q6b8u1 gracillaria
109	27	87.1	140	2	O814D1_CABEL	O814d1 caenorhabdi	182	27	87.1	349	1	ACSF_PORPU	P51277 porphyra pu
110	27	87.1	144	2	O81WA3_HUMAN	O81wa3 homo sapien	183	27	87.1	350	2	Q9Y370_HUMAN	Q9y370 homo sapien
111	27	87.1	144	2	Q6WGM2_EDEBA	Q6wgm2 bdellovibri	184	27	87.1	351	2	Q8TCX1_HUMAN	Q8tcx1 homo sapien
112	27	87.1	146	2	Q6MUK5_MYCMS	Q6muk5 mycoplasma	185	27	87.1	352	2	Q96J00_HUMAN	Q96j00 homo sapien
113	27	87.1	148	2	Q6ZUC5_HUMAN	Q6zuc5 homo sapien	186	27	87.1	352	2	O17576_CABEL	O17576 caenorhabdi
114	27	87.1	148	2	O97657_CANFA	O97657 canis famil	187	27	87.1	354	1	ACSF_SYACA	Q7u1r8 cyanidium c
115	27	87.1	148	2	O6QLX0_CANFA	O6qlx0 canis famil	188	27	87.1	356	1	ACSF_SYNXP	Q7u6y8 synechococc
116	27	87.1	151	2	Q4WKU9_ASPFU	Q4wku9 aspergillus	189	27	87.1	356	2	Q5NPT3_ZYMMO	O5npt3 zymomonas m
117	27	87.1	164	2	Q6KAU3_MOUSE	Q6kau3 mus musculus	190	27	87.1	358	1	ACSF3_SYNY3	P7584 synochocyst
118	27	87.1	171	1	RT25_MOUSE	Q6d125 mus musculus	191	27	87.1	358	1	ACSF3_ANASP	Q8y7z2 anaena sp
119	27	87.1	172	2	Q4QR80_RAT	Q4qr80 rattus norv	192	27	87.1	362	2	Q75AT8_ASHGO	Q75at8 ashba goss
120	27	87.1	172	2	Q4RJV4_TETNG	Q4rjv4 tetraodon n	193	27	87.1	362	2	Q7RGM5_PLAYO	Q7rgm5 plasmodium
121	27	87.1	173	1	RT25_HUMAN	P82663 homo sapien	194	27	87.1	365	1	ACSF_RHOPA	O6n9j7 rhodopseudo
122	27	87.1	176	2	O63507_9TREM	O63507 echinostoma	195	27	87.1	369	2	Q6ZMI8_BRARE	Q6zmi8 brachydanio
123	27	87.1	176	2	O63508_9TREM	O63508 echinostoma	196	27	87.1	370	2	Q40093_IPONI	Q40093 ipomoea nil
124	27	87.1	176	2	O63509_9TREM	O63509 echinostoma	197	27	87.1	370	2	Q8A715_BACTN	Q8a715 bacteroides
125	27	87.1	179	2	Q4Z0C8_PLABE	Q4z0c8 plasmodium	198	27	87.1	370	2	Q98QH7_MYCPU	Q98qh7 mycoplasma
126	27	87.1	185	1	LEP1_BACAM	P41026 bacillus am	199	27	87.1	371	2	Q84RD7_TOBAC	Q84rd7 nicotiana t
127	27	87.1	185	2	O51736_BORBU	O51736 borrelia bu	200	27	87.1	375	2	Q6FVI2_CANGA	O6fvi2 candida gla
128	27	87.1	193	1	LEP2_BACAM	P41025 bacillus am	201	27	87.1	376	2	Q95NI2_CAEEL	O95ni2 caenorhabdi
129	27	87.1	193	1	LEFT_BACSU	F71013 bacillus su	202	27	87.1	393	2	Q8LEF4_ARATH	Q8lee4 arabidopsis
130	27	87.1	194	2	O50XJ3_ENTHI	Q50xj3 entamoeba h	203	27	87.1	405	1	CRD1_EUPES	Q945b7 euphorbia e
131	27	87.1	194	2	Q5NT24_ENTHI	Q5nt24 entamoeba h	204	27	87.1	405	1	CTH1_CHLRE	Q6sjv8 gossypium h
132	27	87.1	201	2	O96B03_HUMAN	Q96b03 homo sapien	205	27	87.1	407	1	Q45653_CAEEL	Q45653 caenorhabdi
133	27	87.1	201	2	O6PDB2_HUMAN	O6pdb2 homo sapien	206	27	87.1	408	2	Q9SDJ2_ORYSA	Q9sdj2 oryza sativ
134	27	87.1	208	2	Q83455_ADEP3	Q83455 porcine ade	207	27	87.1	408	2	CRD1_ARATH	Q9ms91 a magnesium
135	27	87.1	211	2	Q7RNJ3_PLAYO	Q7rnj3 plasmodium	208	27	87.1	409	1	Q5LHM5_BACFN	Q5lhm5 bacteroides
136	27	87.1	227	2	Q6PWQ4_XENLA	Q6pwq4 xenopus lae	209	27	87.1	415	2	Q4YF9_BACFR	Q4y9f9 bacteroides
137	27	87.1	228	2	Q9LHM5_ARATH	Q9lhm5 arabidopsis	210	27	87.1	415	2	CRD1_HORVU	O6sfu4 hordeum vul
138	27	87.1	232	2	O8ZDV0_YERPE	Q8zdvo versinia pe	211	27	87.1	417	1	Q6NKY4_ARATH	O6nky4 arabidopsis
139	27	87.1	238	1	Y014_BEL2	P42549 bacterioph	212	27	87.1	423	2	Q601R3_MYCHY	Q601r3 mycoplasma
140	27	87.1	239	2	Q5HRC1_STABQ	Q5hrc1 staphylococ	213	27	87.1	431	2	Q98TF3_ORYLA	Q98tf3 oryza lat
141	27	87.1	239	2	Q8CTN5_STAEP	Q8ctn5 staphylococ	214	27	87.1	432	2	Q681Y3_ARATH	Q681y3 arabidopsis
142	27	87.1	244	2	Q5B4B1_EMENI	Q5b4b1 aspergillus	215	27	87.1	432	2	Q6XRC0_9BACT	Q6xrc0 uncultured
143	27	87.1	246	2	Q4N8X3_THEPA	Q4n8x3 theileria p	216	27	87.1	435	2	Q9C954_ARATH	Q9c954 arabidopsis
144	27	87.1	246	2	Q8PB21_ECOL6	Q8pb21 escherichia	217	27	87.1	436	2	Q51EE2_ENTHI	O5lee2 entamoeba h
145	27	87.1	247	2	O81B21_PLAF7	Q81b21 plasmodium	218	27	87.1	437	2	Q51EE2_ENTHI	O5lee2 entamoeba h
146	27	87.1	256	2	O5L209_GEOKA	Q5l209 geobacillus	219	27	87.1	438	1	ENGA_CLOPE	Q8xjk1 clostridium
147	27	87.1	258	2	Q9CIL0_NEUCR	Q9cil0 neurospora	220	27	87.1	459	2	Q9WZ33_THEMEA	Q9wt90 sus scrofa
148	27	87.1	262	2	Q9BGL3_SHEEP	Q9bgl3 ovis aries	221	27	87.1	467	2	Q8VUM4_STAHO	Q8vum4 staphylococ
149	27	87.1	262	2	Q6PWQ5_XENLA	Q6pwq5 xenopus lae	222	27	87.1	469	2	Q51FM2_ENTHI	Q51fm2 entamoeba h
150	27	87.1	262	2	Q9WZS5_THEMEA	Q9wzs5 thermotoga	223	27	87.1	472	2	Q4UDY3_THEAN	Q4udy3 theileria a
151	27	87.1	278	2	Q9U336_CAEEL	Q9u336 caenorhabdi	224	27	87.1	478	2	Q6UR08_ANOGA	Q6ur08 anopheles g
152	27	87.1	287	2	O72P77_LEPIC	Q72p77 leptospira	225	27	87.1	479	2	Q7QCC7_ANOGA	Q7qcc7 anopheles g
153	27	87.1	287	2	Q8F779_LEPIN	Q8f779 leptospira	226	27	87.1	488	2	Q8760_CABEL	Q8760 caenorhabdi
154	27	87.1	300	2	Q34521_FASHE	Q34521 fasciola he	227	27	87.1	499	2	P87212_9APHY	P87212 polyporacea
155	27	87.1	300	2	Q9B8Y4_FASHE	Q9b8y4 fasciola he	228	27	87.1	504	2	Q8NKF3_9AGAR	Q8nkf3 termitomyce
156	27	87.1	300	2	Q88XR9_LACPL	Q88xr9 lactobacill	229	27	87.1	522	2	Q6QNE9_CABEL	Q6qne9 caenorhabdi
157	27	87.1	301	2	O7XJ11_TRIRP	Q7xj11 trifolium r	230	27	87.1	522	2	Q9LPY0_ARATH	Q9lpy0 arabidopsis
158	27	87.1	301	2	Q7XJ16_WHEAT	Q7xj16 triticum ae	231	27	87.1	524	2	Q75819_ASHGO	Q75819 ashba goss
159	27	87.1	308	2	Q7XJ12_BRANA	Q7xj12 brassica na	232	27	87.1	527	1	IPT1_YEAST	P38954 saccharomyc
160	27	87.1	308	2	Q6G917_YERPS	Q6g917 yerinia ps	233	27	87.1	543	2	Q7QXS6_GIALA	Q7qxs6 giardia lam
161	27	87.1	309	2	Q5LIS8_SILPO	Q5lls8 silicibacte	234	27	87.1	546	2	Q98TF2_ORYLA	Q98tf2 oryza lat
162	27	87.1	310	1	Y160_BUCAP	Q8k9x4 buchnera ap	235	27	87.1	553	2	Q4SKD2_TETNG	Q4skd2 tetraodon n
163	27	87.1	321	1	YCF35_CYAPA	P48279 cyanophora	236	27	87.1	560	2	Q4S0T5_TETNG	Q4s0t5 tetraodon n
164	27	87.1	324	2	Q6HKI3_BACHK	Q6hki3 bacillus th	237	27	87.1	574	2	Q7TJ02_BRARE	Q7tj02 brachydanio
165	27	87.1	325	2	Q81SA4_BACAN	Q81sa4 bacillus an	238	27	87.1	575	2	Q2USC3_XENLA	Q2usc3 xenopus lae
166	27	87.1	332	2	Q84RD6_CUGSA	Q84rd6 cucumis sat	239	27	87.1	576	2	Q6DCW8_XENLA	Q6dcw8 xenopus lae
167	27	87.1	333	2	O7XJ13_9ROSA	Q7xj13 rosa davuri	240	27	87.1	578	2	Q5BL52_XENTR	O5bl52 xenopus tro
168	27	87.1	333	2	O7XJ14_9ROSI	Q7xj14 salix babyi	241	27	87.1	580	1	MMP14_FIG	Mmp14 neisseria g
169	27	87.1	335	1	ACSF_CYAME	Q85fx6 cyanidiosch	242	27	87.1	581	2	O68921_NEIGO	O68921 neisseria g
170	27	87.1	335	2	Q5LE41_BACFN	Q5le41 bacteroides	243	27	87.1	581	2	Q5F8K1_NEIGI	Q5f8k1 neisseria g
171	27	87.1	335	2	Q9F749_BACFR	Q9f749 bacteroides	244	27	87.1	581	2	Q9J293_NEIMB	Q9j293 neisseria m
172	27	87.1	336	2	Q688Q2_ORYSA	Q688q2 oryza sativ	245	27	87.1	581	2	Q9JUB8_NEIMA	Q9jub8 neisseria m
173	27	87.1	339	2	Q9XDJ2_BACFR	Q9xdj2 bacteroides	246	27	87.1	582	1	MMP14_HUMAN	Mmp14 homo sapien
174	27	87.1	339	2	O5LGH6_BACFN	O5lgh6 bacteroides	247	27	87.1	582	1	MMP14_MOUSE	Mmp14 mus musculu
175	27	87.1	340	2	O5LIRA_BACFN	O5lira bacteroides	248	27	87.1	582	1	MMP14_RABIT	Mmp14 coryctolagus
176	27	87.1	340	2	Q64ZV1_BACFR	Q64zv1 bacteroides	249	27	87.1	582	1	MMP14_RAT	Mmp14 rattus norv
177	27	87.1	345	2	Q6Y7P5_9VIRU	Q6y7p5 staphylococ	250	27	87.1	582	2	Q6GSF3_HUMAN	Q6gsf3 homo sapien

251 27 87.1 582 2 Q9GLE4 BOVIN
252 27 87.1 582 2 Q9RES1_PONPY
253 27 87.1 582 2 Q9XSP0_CAPHI
254 27 87.1 582 2 Q99PG1_CRIGR
255 27 87.1 582 2 Q8BTX2 MOUSE
256 27 87.1 582 2 Q6DFU5 MOUSE
257 27 87.1 582 2 Q6IN06 RAT
258 27 87.1 585 2 Q7RDB0_PLAYO
259 27 87.1 585 2 Q4N9F3_THEPA
260 27 87.1 592 2 Q4RMY3_TETNG
261 27 87.1 599 2 Q752M5_ASHGO
262 27 87.1 607 2 Q76LU7_ORVLA
263 27 87.1 610 2 Q4W889_ORVLA
264 27 87.1 621 2 Q72J31_BRARE
265 27 87.1 626 2 Q98HT9_RHILO
266 27 87.1 689 1 SOIB2_MOUSE
267 27 87.1 695 2 Q419L8_GIBZE
268 27 87.1 698 2 Q5BD98_EMENI
269 27 87.1 721 2 O16363_CAEEL
270 27 87.1 732 2 Q4SKX7_TETNG
271 27 87.1 763 2 Q4Y7S4_PLACH
272 27 87.1 773 1 YOD3_CAEEL
273 27 87.1 780 2 Q6A1B3_ECHMU
274 27 87.1 789 2 Q5AGA4_CANAL
275 27 87.1 794 2 Q7RGA4_PLAYO
276 27 87.1 796 2 Q9LSC5_9ALPH
277 27 87.1 833 1 HMDH_AGRIP
278 27 87.1 846 2 Q4SL98_TETNG
279 27 87.1 856 1 HMDH_BLAG
280 27 87.1 923 2 Q73177_TREDE
281 27 87.1 1024 1 CAR12_HUMAN
282 27 87.1 1049 2 Q528F0_MAGGR
283 27 87.1 1068 2 Q55DX7_DICDI
284 27 87.1 1099 2 Q8IE72_PLAF7
285 27 87.1 1126 2 Q73ME8_TREDE
286 27 87.1 1144 2 Q86J82_DICDI
287 27 87.1 1145 2 Q5SA20_DICDI
288 27 87.1 1269 2 Q4YNH1_PLABE
289 27 87.1 1279 2 Q76IL3_BRARE
290 27 87.1 1469 2 Q4YZQ1_PLABE
291 27 87.1 1508 2 Q7RHF5_PLAYO
292 27 87.1 1563 2 Q61CM5_CAEER
293 27 87.1 1897 2 Q8IBK2_PLAF7
294 27 87.1 1917 2 Q4X570_PLACH
295 27 87.1 2118 2 Q7RR57_PLAYO
296 27 87.1 2921 2 Q5WNK5_CAEER
297 27 87.1 3978 2 Q97236_PLAF7
298 27 87.1 6739 2 Q7QYB8_GIALA
299 26 83.9 24 2 Q4X467_PLACH
300 26 83.9 27 2 Q4Z519_PLABE

ALIGNMENTS

RESULT 1
Q8QGY9_FUGRU
ID Q8QGY9_FUGRU PRELIMINARY; PRT; 47 AA.
AC Q8QGY9;
DT 01-JUN-2002 (TREMELrel. 21, Created)
DT 01-JUN-2002 (TREMELrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Guanine nucleotide binding protein (Fragment).
GN Name=Gnat2;
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97129408; PubMed=8973916;

RA Sarwal M.M., Sontag J.M., Hoang L., Brenner S., Wilkie T.M.;
RT "G protein alpha subunit multigene family in the Japanese puffer fish
RL Fugu rubripes: PCR from a compact vertebrate genome.";
RL Genome Res. 6:1207-1215(1996).
DR EMBL; L79897; AAL77630.1; -; Genomic_DNA.
DR HSP; P04695; 1TND.
DR GO; GO:0004871; P:signal transducer activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR001019; Gprotein_alpha.
DR Pfam; PF00503; G-alpha; 1.
FT NON_TER 1 1
FT NON_TER 47 47
SQ SEQUENCE 47 AA; 5255 MW; 9770A35D36E1FABC CRC64;

Query Match 100.0%; Score 31; DB 2; Length 47;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFPPA 6
DB 15 KVFPPA 20
|||||

RESULT 2

Q6RS99_TRITU PRELIMINARY; PRT; 229 AA.
ID Q6RS99;
AC Q6RS99;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Globulin.
OS Triticum turgidum (Poulard wheat) (Rivet wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4571;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15122014; DOI=10.1104/pp.103.038083;
RA Gu Y.Q., Coleman-Derr D., Kong X., Anderson O.D.;
RT "Rapid Genome Evolution Revealed by Comparative Sequence Analysis of
Orthologous Regions from Four Triticeae Genomes.";
RL Plant Physiol. 135:459-470(2004).
DR EMBL; AY494981; AAR95703.1; -; Genomic DNA.
DR GO; GO:0045733; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR Pfam; PF00234; Ttyp alpha amyl; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 229 AA; 25000 MW; 18E769DAB08E41E3 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 229;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFPPA 6
DB 3 KVFPPA 8
|||||

RESULT 3

Q7XYC3_WHEAT PRELIMINARY; PRT; 241 AA.
ID Q7XYC3;
AC Q7XYC3;
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)
DE 19 kDa globulin (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Triticum.

```

OX NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Seed;
RA Li J.R., Wang F., Li Q.Z., Zhang X.S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF475121; AAP80642.1; -; mRNA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp_alpha.amyl. 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
FT NON TER
SQ SEQUENCE 241 AA; 26139 MW; AAD8F2BB859DA016 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 241;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 15 KFVFFA 20

RESULT 4
Q6KX9 ORYSA
ID Q6KX9 ORYSA PRELIMINARY; PRT; 331 AA.
AC Q6KX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Transmembrane protein-like.
GN Name=O2055.H10.27-1; Synonyms=P0407A09.6-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005300; BAD19727.1; -; Genomic DNA.
DR EMBL; AP004747; BAD19452.1; -; Genomic DNA.
DR Gramene; Q6KX9; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
DR Transmembrane.
SQ SEQUENCE 331 AA; 36397 MW; EACAC4769463B9EA CRC64;

Query Match 100.0%; Score 31; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 80 KFVFFA 85

RESULT 5
Q84NE7 ORYSA
ID Q84NE7 ORYSA PRELIMINARY; PRT; 331 AA.
AC Q84NE7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transmembrane protein.

OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Lee R.H., Chen S.C.G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY030360; AAK50365.1; -; mRNA.
DR Gramene; Q84NE7; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
DR Transmembrane.
SQ SEQUENCE 331 AA; 36384 MW; 289C99F3D3F8229A CRC64;

Query Match 100.0%; Score 31; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 80 KFVFFA 85

RESULT 6
Q6I5W9 ORYSA
ID Q6I5W9 ORYSA PRELIMINARY; PRT; 335 AA.
AC Q6I5W9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transmembrane protein.
GN Name=QJ1076.H08.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC108498; AAT47018.1; -; Genomic DNA.
DR Gramene; Q6I5W9; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR004853; DUF250.
DR Pfam; PF03151; DUF250; 1.
DR Transmembrane.
SQ SEQUENCE 335 AA; 36826 MW; 5A0EF43F8578E46F CRC64;

Query Match 100.0%; Score 31; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
Db 80 KFVFFA 85

RESULT 7
Q4HQ66 CAMUP
ID Q4HQ66 CAMUP PRELIMINARY; PRT; 353 AA.
AC Q4HQ66;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

```


DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE GDP-fucose synthetase.
 GN Names-fcl; ORFNames=CUP1255;
 OS Campylobacter upsaliensis RM3195.
 CC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 CC Campylobacteraceae; Campylobacter.
 OX NCBI_TaxID=306264;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=RM3195;
 RA Fouts D.E.; Mongodin E.F.; Mandrell R.E.; Miller W.G.; Raeko D.A.;
 RA Jacques R.J.; Brinkac L.M.; DeBoy R.T.; Parker C.T.; Daugherty S.C.;
 RA Dodson R.J.; Durkin A.S.; Madupu R.R.; Sullivan S.A.; Shetty J.U.;
 RA Ayodeji M.A.; Shvartsbeyn A.A.; Schatz M.C.; Badger J.H.; Fraser C.M.;
 RA Nelson K.E.;
 RT "Major structural and novel potential virulence mechanisms from the
 RL genomes of multiple Campylobacter species.";
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAFJ01000007; HAL52977.1; -; Genomic DNA.
 SQ SEQUENCE 353 AA; 39798 MW; 59CC8A432D31EFAE CRC64;

Query Match 100.0%; Score 31; DB 2; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
 |||||
 DB 58 KFVFFA 63

RESULT 8
 QSATG9 EMENI
 ID QSATG9 EMENI PRELIMINARY; PRT; 519 AA.
 AC QSATG9;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AN8411.2;
 OS Aspergillus nidulans FGSC A4.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B.; Nusbaum C.; Abouelleil A.; Allen N.; Anderson S.;
 RA Arachchi H.M.; Barna N.; Bastien V.; Bloom T.; Boguslavskiy L.;
 RA Boukhgalter B.; Butler J.; Calvo S.E.; Camarata J.; Chang J.;
 RA Choepel Y.; Collamore A.; Cook A.; Cooke P.; Corum B.; DeArelano K.;
 RA Diaz J.S.; Dodge S.; Dooley K.; Dorris L.; Elkins T.; Engels R.;
 RA Erickson J.; Faro S.; Ferreira P.; FitzGerald M.; Gage B.; Galagan J.;
 RA Gardyna S.; Gnerre S.; Graham L.; Grand-Pierre N.; Hafez N.;
 RA Hagopian D.; Hagos B.; Hall J.; Horton L.; Hulme W.; Iliev I.;
 RA Jaffe D.; Johnson R.; Jones C.; Kamal M.; Kamat A.; Karatas A.;
 RA Kells C.; Landers T.; Levine R.; Lindblad-Toh K.; Liu G.; Lui A.;
 RA Ma L.-J.; Mabbitt R.; Maclean C.; Macdonald P.; Major J.; Manning J.;
 RA Matthews C.; Mauceli E.; McCarthy M.; Meldrim J.; Meneus L.;
 RA Mihova T.; Mienga V.; Murphy T.; Naylor J.; Nguyen C.; Nicol R.;
 RA Nielsen C.B.; Norbu C.; O'Connor T.; O'Donnell P.; O'Neill D.;
 RA Oliver J.; Peterson K.; Phunkhang P.; Pierre N.; Purcell S.;
 RA Rachupka A.; Ramasamy U.; Raymond C.; Retta R.; Rise C.; Rogov P.;
 RA Roman J.; Schauer S.; Schupbach R.; Seaman S.; Severy P.; Smirnov S.;
 RA Smith C.; Spencer S.; Stange-Thomann N.; Stojanovic N.; Stubbs M.;
 RA Talamas J.; Testaye S.; Theodore J.; Topham K.; Travers M.;
 RA Vasiliev H.; Venkataraman V.S.; Viel R.; Vo A.; Wang S.; Wilson B.;
 RA Wu X.; Wyman D.; Young G.; Zainoun J.; Zembek L.; Zimmer A.; Zody M.;
 RA Lander E.;
 RT "Genome Sequence of Aspergillus nidulans.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

CC -1- CATALYTIC ACTIVITY: Hydroxylation of N-alkanes at the terminal
 CC position.
 CC -1- CATALYTIC ACTIVITY: Obtusifoliol + 3 O(2) + 3 NADPH = 4-alpha-
 CC methyl-5-alpha-ergosta-8,14,24(28)-trien-3-beta-ol + formate + 3
 CC NADP(+) + 3 H(2)O.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC EMBL; AACD01000153; EAA67033.1; -; Genomic_DNA.
 DR GO; GO:0046872; F-metal ion binding; IEA.
 DR GO; GO:0004497; F-monoxygenase activity; IEA.
 DR GO; GO:0006118; F-electron transport; IEA.
 DR GO; GO:0008152; F-metabolism; IEA.
 DR GO; GO:0016126; P-sterol biosynthesis; IEA.
 DR InterPro; IPR001128; Cytochrome P450.
 DR InterPro; IPR002974; EP450 II_CYP52.
 DR InterPro; IPR002403; EP450IV.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PR01239; EP450IICYP52.
 DR PRINTS; PR00465; EP450IV.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN 1.
 KW Heme; Hypothetical protein; Iron; Lipid synthesis; Membrane;
 KW Metal-binding; Monoxygenase; Oxidoreductase; Steroid biosynthesis;
 KW Metal biosynthesis.
 SQ SEQUENCE 519 AA; 60440 MW; B367EE6EB6FPA287 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 519;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
 |||||
 DB 26 KFVFFA 31

RESULT 9
 Q7XM01 ORYSA
 ID Q7XM01 ORYSA PRELIMINARY; PRT; 935 AA.
 AC Q7XM01;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE OSJNBa008606.8 protein.
 GN Names=OSJNBa008606.8;
 OS Oryza sativa (japonica cultivar-group).
 CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=12447439; DOI=10.1038/nature01183;
 RA Peng Q.; Zhang Y.; Hao P.; Wang S.; Fu G.; Huang Y.; Li Y.; Zhu J.;
 RA Liu Y.; Hu X.; Jia P.; Zhang Y.; Zhao Q.; Ying K.; Yu S.; Tang Y.;
 RA Wang Q.; Zhang L.; Lu Y.; Mu J.; Lu Y.; Zhang L.S.; Yu Z.; Fan D.;
 RA Liu X.; Lu T.; Li C.; Wu Y.; Sun T.; Lei H.; Li T.; Hu H.; Guan J.;
 RA Wu M.; Zhang R.; Zhou B.; Chen Z.; Chen L.; Jin Z.; Wang R.; Yin H.;
 RA Cai Z.; Ren S.; Lv G.; Gu W.; Zhu G.; Tu Y.; Jia J.; Zhang Y.;
 RA Chen J.; Kang H.; Chen X.; Shao C.; Sun Y.; Hu Q.; Zhang X.; Zhang W.;
 RA Wang L.; Ding C.; Sheng H.; Gu J.; Chen S.; Ni L.; Zhu F.; Chen W.;
 RA Lan L.; Lai Y.; Cheng Z.; Gu M.; Jiang J.; Li J.; Hong G.; Xue Y.;
 RA Han B.;
 RT "Sequence and analysis of rice chromosome 4.";
 RL Nature 420:316-320(2002).
 RL EMBL; AL662981; CAB04860.2; -; Genomic_DNA.
 DR : Gramene; Q7XM01; -
 DR GO; GO:0006512; P-ubiquitin cycle; IEA.
 DR InterPro; IPR001810; P-box.
 DR Pfam; PF00646; P-box; 2.
 DR SMART; SM00256; FBOX; 2.
 DR PROSITE; PS50181; FBOX; 1.
 SQ SEQUENCE 935 AA; 103910 MW; 735DD287C6E1BC69 CRC64;

Query Match 100.0%; Score 31; DB 2; Length 935;

Best Local Similarity 100.0%; Pred. No. 3.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

QY 1 KVFVFA 6
|||
Db 74 KVFVFA 79

RESULT 10

ID Q7QVR7 GIALA PRELIMINARY; PRT; 3044 AA.
AC Q7QVR7;
DT 01-WAR-2004 (TRENBLrel. 26, Created)
DT 01-WAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-WAR-2004 (TRENBLrel. 26, Last annotation update)
DE GLP 70 49040 39906.
OS Giardia lamblia ATCC 50803.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.
OX NCBI_TaxID=184922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WB C6;
RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA Olsen G.J., Sogin M.L.;
RT "Draft sequence of the Giardia lamblia genome."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACB01000048; EAA40229.1; -; Genomic_DNA.
DR InterPro; IPR012351; Cytochrome_hlx.
KW Cytochrome.
SQ SEQUENCE 3044 AA; 347085 MW; 24F737600F128C6D CRC64;

Query Match 100.0%; Score 31; DB 2; Length 3044;
Best Local Similarity 100.0%; Pred. No. 9.6e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;

QY 1 KVFVFA 6
|||
Db 382 KVFVFA 387

RESULT 11

ID Q84NG7 HORVU PRELIMINARY; PRT; 224 AA.
AC Q84NG7;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Globulin.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triciteae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14663527; DOI=10.1139/g03-071;
RA Gu X.Q., Anderson O.D., Londeore C.F., Kong X., Chibbar R.N.,
RA Lazo G.R.;
RT "Structural organization of the barley D-hordein locus in comparison
RT with its orthologous regions of wheat genomes."
RL Genome 46:1084-1097(2003).
DR EMBL; AY268139; AAP31050.1; -; Genomic_DNA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp alpha amyl1. 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 224 AA; 24561 MW; 91A5BFF15C86394D CRC64;

Query Match 96.8%; Score 30; DB 2; Length 224;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 3 KVFVFA 8

RESULT 12

ID Q98GC2 RHIL0 PRELIMINARY; PRT; 395 AA.
AC Q98GC2;
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Putative peptidase.
CN OrderedLocusNames=ml13393;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL; BA000012; BAB50294.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004239; F:methionyl aminopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000994; Peptidase M24.
DR InterPro; IPR001714; Pept M24 MAP.
DR Pfam; PF00557; Peptidase M24_1.
DR PRINTS; PR00599; MAPEPTIDASE.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 395 AA; 43302 MW; E9ADDF4AADB1D472 CRC64;

Query Match 96.8%; Score 30; DB 2; Length 395;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 48 KVFVFA 53

RESULT 13

ID Q92YV6 RHIME PRELIMINARY; PRT; 397 AA.
AC Q92YV6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Putative proline dipeptidase.
CN OrderedLocusNames=RA0726; ORFNames=Sm1329;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1021;
RX MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,

Db 253 KFIFFA 250

RESULT 15
QSA3Q1 CANAL

ID	QSA3Q1 CANAL PRELIMINARY;	PRT;	2643 AA.
AC	QSA3Q1;		
DT	10-MAY-2005 (TrEMBLrel. 30, Created)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last sequence update)		
DT	10-MAY-2005 (TrEMBLrel. 30, Last annotation update)		
DE	Hypothetical protein IRA2.		
GN	Names=IRA2; ORFNames=CaO19.5219;		
OS	Candida albicans SC5314.		
OC	Rukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OC	Saccharomycetales; mitosporic Saccharomycetales; Candida.		
NCBI_TaxID=237561;			
OX	[1]		
RN	NUCLEOTIDE SEQUENCE.		
RP	STRAIN=SC5314;		
RC	PubMed=15123810; DOI=10.1073/pnas.0401648101;		
RX	James T., Pedersoli N.A., Chibana H., Dungan J., Kalman S.,		
RA	Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,		
RA	Davis R.W., Scherer S.;		
RT	"The diploid genome sequence of Candida albicans.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).		
RN	[2]		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=SC5314;		
RA	Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,		
RA	Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,		
RA	James T., Scherer S., Agabian N.;		
RT	"Annotation of the Genome of Candida albicans.";		
RL	Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; AACQ01000071; EAK97292.1; -; Genomic_DNA.		
DR	InterPro: IPR002114; HPR_Serp_S.		
DR	InterPro: IPR001936; RasGAP.		
DR	Pfam: PF00616; RasGAP; 1.		
DR	SMART: SM00323; RasGAP; 1.		
DR	PROSITE: PS00589; PTS_HPR_SER; UNKNOWN_1.		
DR	PROSITE: PS00509; RAS_GTPASE_ACTIV_1; 1.		
DR	PROSITE: PS00108; RAS_GTPASE_ACTIV_2; 1.		
KW	Hypothetical protein.		
SQ	SEQUENCE 2643 AA; 304839 MW; 3C1EAC60BD583AF CRC64;		

Query Match 96.8%; Score 30; DB 2; Length 2643;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFIFFA 6
||:|
||:|

Db 253 KFIFFA 258

RESULT 16
Q4XXR5 PLACH

ID	Q4XXR5 PLACH PRELIMINARY;	PRT;	23 AA.
AC	Q4XXR5;		
DT	13-SEP-2005 (TrEMBLrel. 31, Created)		
DT	13-SEP-2005 (TrEMBLrel. 31, Last sequence update)		
DT	13-SEP-2005 (TrEMBLrel. 31, Last annotation update)		
DE	Hypothetical protein (Fragment).		
GN	ORFNames=FC104709.00.0;		
OS	Plasmodium chabaudi.		
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.		
NCBI_TaxID=5825;			
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Hall N., Karras M., Raine J.D., Carlton J.M., Koolj T.W.A.,		
RA	Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,		
RA	James K., Rutherford K., Harris B., Harris D., Churcher C.,		
RA	Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,		
RA	Biwell S.H., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,		
RA	Janse C.J., Barrell B., Turner C.R., Waters A.P., Sinden R.S.;		

RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RL transcriptomic, and proteomic analyses.";
 CC Science 307:82-86(2005).

CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.

DR EMBL; CAJ01002391; CAH78296.1; -; Genomic_DNA.

FT NON TER 1

SQ SEQUENCE 23 AA; 3051 MW; ECFB64EBBCC09AA0 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 23;
 Best Local Similarity 83.3%; Pred. No. 74;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

Db |:||||

16 KVFVFA 21

RESULT 17

Q73M63 TREDE

ID Q73M63 TREDE PRELIMINARY; PRT; 43 AA.

AC Q73M63;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

GN OrderedLocustNames=I01646;

OS Treponema denticola.

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.

OX NCBI_TaxID=158;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 35405 / DSM 14222;

RX PubMed=15064399; DOI=10.1073/pnas.0307639101;

RA Seshadri R., Myers G.S.A., Tettelin H., Eisen J.A., Heidelberg J.F.,

RA Dodson R.J., Davidsen T.M., DeBoy R.T., Fouts D.E., Haft D.H.,

RA Selengut J., Ren O., Brinkac L.M., Madupu R., Kolonay J.F.,

RA Durkin S.A., Daugherty S.C., Shetty J., Shvartsbeyn A.,

RA Gebregeorgis E., Geer K., Tsengaye G., Malek J.A., Ayodeji B.,

RA Shatsman S., McLeod M.P., Smajs D., Howell J.K., Pal S., Amin A.,

RA Vashisth P., McNeill T.Z., Xiang Q., Sodergren E., Baca E.,

RA Weinstein G.M., Norris S.J., Fraser C.M., Paulsen I.T.;

RT "Comparison of the genome of the oral pathogen Treponema denticola

RT with other spirochete genomes.";

RL Proc. Natl. Acad. Sci. U.S.A. 101:5646-5651(2004).

DR EMBL; A5017251; AAS12163.1; -; Genomic_DNA.

DR TIGR; TDE1646; -.

KW Complete proteome.

SQ SEQUENCE 43 AA; 5202 MW; E1189303B62C9173 CRC64;

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 43;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

Db |||||:

20 KVFVFA 25

RESULT 18

Q9KAX7 BACHD

ID Q9KAX7 BACHD PRELIMINARY; PRT; 49 AA.

AC Q9KAX7;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE BH2159 protein.

GN OrderedLocustNames=BH2159;

OS Bacillus halodurans.

OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.

OX NCBI_TaxID=86665;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C-125 / JCM 9153;

RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;

RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,

RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,

RA Horikoshi K.;

RT "Complete genome sequence of the alkaliphilic bacterium Bacillus

RT halodurans and genomic sequence comparison with Bacillus subtilis.";

RL Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL; BA000004; BAB05878.1; -; Genomic_DNA.

DR FIR; G83919; G83919.

KW Complete proteome.

SQ SEQUENCE 49 AA; 5463 MW; D669731B66DCD0B1 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 49;

Best Local Similarity 83.3%; Pred. No. 1.4e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

Db |||||:

34 KVFVFA 39

RESULT 19

Q7R979 PLAYO

ID Q7R979 PLAYO PRELIMINARY; PRT; 150 AA.

AC Q7R979;

DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.

GN Name=PY06986;

OS Plasmodium yoelii yoelii.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OX NCBI_TaxID=73239;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=17XNL;

RX MEDLINE=2255706; PubMed=12368865; DOI=10.1038/nature01099;

RA Carlton J.M., Angioli S.V., Suh B.B., Kooij T.W., Perteu M.,

RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,

RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,

RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,

RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,

RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,

RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

RA Carucci D.J.;

RT "Genome sequence and comparative analysis of the model rodent malaria

RT parasite Plasmodium yoelii yoelii.";

RL Nature 419:512-519(2002).

CC -!- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; AABL01002464; EAA19320.1; -; Genomic_DNA.

DR InterPro; IPR006484; PYST-B.

DR TIGRFAMs; TIGR01597; PYST-B; 1.

KW Hypothetical protein.

SQ SEQUENCE 150 AA; 17794 MW; DA68536D398B37AC CRC64;

Query Match

Best Local Similarity 90.3%; Score 28; DB 2; Length 150;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

Db |||||:

7 KVFVFA 12

RESULT 20

QAJ122_AZOVI

```

ID Q4J122_AZOVI PRELIMINARY; PRT; 152 AA.
AC Q4J122;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Glyoxalase/bleomycin resistance protein/dioxygenase domain.
GN ORFNames=AVINDRAFT_6949;
OS Azotobacter vinelandii AVOP.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer P., Land W.;
RT "Annotation of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute;
RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAU03000001; EAM08399.1; -; Genomic_DNA.
KW Dioxygenase.
SQ SEQUENCE 152 AA; 16984 MW; 05A60BD5E879ED93 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 152;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 111 RFVFFA 116
:|||||

RESULT 21'
Q20070_CAEEL
ID Q20070_CAEEL PRELIMINARY; PRT; 177 AA.
AC Q20070;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Hypothetical protein F35H10.6.
GN ORFNames=F35H10.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;

```

```

RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018 (1998).
DR EMBL; U40934; AAA81680.1; -; Genomic_DNA.
DR PIR; T16280; T16280.
DR Ensembl; F35H10.6; Caenorhabditis elegans.
DR GO; GO:0016272; C:prefoldin complex; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0006457; F:protein folding; IEA.
DR InterPro; IPR004127; PFD_alpha_like.
DR Pfam; PF02996; Prefoldin; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 177 AA; 21142 MW; E8B71144250DB915 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 177;
Best Local Similarity 83.3%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 10 KVFVFA 15
:|||||

RESULT 22
Q6LSA9_PROPR
ID Q6LSA9_PROPR PRELIMINARY; PRT; 199 AA.
AC Q6LSA9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=PBPR1406;
OS Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=74109;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15746425; DOI=10.1126/science.1103341;
RA Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA Lauro F.M., Castaro A., Malacrida G., Simonati B., Cannata N.,
RA Romualdi C., Bartlett D.H., Valle G.;
RT "Life at depth: Photobacterium profundum genome sequence and
RT expression analysis.";
RL Science 307:1459-1461 (2005).
DR EMBL; CR378667; CAG19817.1; -; Genomic DNA.
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl_trans.
DR Pfam; PF00583; Acetyltransf_1; 1.
KW Complete proteome.
SQ SEQUENCE 199 AA; 22203 MW; AF44E115663FD3F6 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 199;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 47 KLFVFA 52
:|||||

RESULT 23
Q6UJY8_TRITU
ID Q6UJY8_TRITU PRELIMINARY; PRT; 225 AA.
AC Q6UJY8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Globulin.
OS Triticum turgidum (Poulard wheat) (Rivet wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

```

```

OC Triticeae; Triticum.
OX NCBI_TaxID=4571;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed:15159634; DOI=10.1023/B:PLAN.0000028768.21587.dc;
RA Kong X.-Y., Gu Y.-Q., You F.M., Dubcovsky J., Anderson O.D.;
RT "Dynamics of the evolution of orthologous and paralogous portions of a
RT complex locus region in two genomes of allopolyploid wheat.";
RL Plant Mol. Biol. 54:55-69(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Kong X.-Y., Gu Y.-Q., Anderson O.D.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY368673; AAQ93632.1; -; Genomic DNA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp_alpha_amyl; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 225 AA; 24502 MW; 45F4D19403BCDCC2 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 225;
Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db :|||||
3 RFVFFA 8

RESULT 24
OBLKV8_AECTA
ID OBLKV8_AECTA PRELIMINARY; PRT; 226 AA.
AC OBLKV8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Seed globulin.
GN Name=Glo-2;
OS Aegilops tauschii (Tausch's goatgrass) (Aegilops squarrosa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Aegilops.
OX NCBI_TaxID=37682;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22478028; PubMed=12590343;
RA Anderson O.D., Rausch C., Mouillet O., Lagudah E.S.;
RT "The wheat D-genome HMW-glutenin locus: BAC sequencing, gene
RT distribution, and retrotransposon clusters.";
RL Funct. Integr. Genomics 3:56-68(2003).
DR EMBL; AF497474; AAM77580.1; -; Genomic DNA.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001419; Glutenin.
DR Pfam; PF00234; Tryp_alpha_amyl; 1.
DR PRINTS; PR00210; GLUTENIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 226 AA; 24515 MW; 95397EB3C63D50AD CRC64;

Query Match 90.3%; Score 28; DB 2; Length 226;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db :|||||
3 RFVFFA 8

RESULT 25
Q7R8Y4_PLAYO
ID Q7R8Y4_PLAYO PRELIMINARY; PRT; 241 AA.

```

```

AC Q7R8Y4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY07086;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBSJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002524; EAA19443.1; -; Genomic DNA.
DR InterPro; IPR006484; PYST B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 241 AA; 28789 MW; BE9AD8A3E5924873 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 241;
Best Local Similarity 83.3%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db :|||||
7 KFVFFS 12

RESULT 26
Q7RA05_PLAYO
ID Q7RA05_PLAYO PRELIMINARY; PRT; 242 AA.
AC Q7RA05;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06703;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).

```



```

DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 251 AA; 30054 MW; 3D6A80EE6DFE9275 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 251;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db      |||||:
       7 KVFVFS 12

RESULT 30
Q7RA57 PLAYO
ID Q7RA57 PLAYO PRELIMINARY; PRT; 252 AA.
AC Q7RA57;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06647;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01001507; EAA16812.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 29750 MW; 86406549DB86516D CRC64;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01002275; EAA18895.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 29750 MW; 86406549DB86516D CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 252;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db      |||||:
       7 KVFVFS 12

RESULT 31
Q7RF37 PLAYO
ID Q7RF37 PLAYO PRELIMINARY; PRT; 252 AA.
AC Q7RF37;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY04873;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01001507; EAA16812.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 252 AA; 29757 MW; 64EB5B4C1F49786D CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 252;
  Best Local Similarity 83.3%; Pred. No. 5.4e+02;
  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db      |||||:
       7 KVFVFS 12

RESULT 32
Q7RLK2 PLAYO
ID Q7RLK2 PLAYO PRELIMINARY; PRT; 255 AA.
AC Q7RLK2;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY02539;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perte M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01000695; EAA21989.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 255 AA; 30283 MW; 51F1FD33FED980B3 CRC64;

  Query Match          90.3%; Score 28; DB 2; Length 255;

```


Best Local Similarity 83.3%; Pred. No. 5.5e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
| | | | |
Db 7 KVFVFFS 12

RESULT 33

Q7RC37 PLAYO
ID Q7RC37 PLAYO PRELIMINARY; PRT; 262 AA.
AC Q7RC37;
DT 01-MAR-2004 (TREMUREL. 26, Created)
DT 01-MAR-2004 (TREMUREL. 26, Last sequence update)
DT 01-MAR-2004 (TREMUREL. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY05947;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Sedegah M., Shoaibi A., Cummings L.M.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL: AABL01001873; EAA17841.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMS; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 262 AA; 7A520F097ABF0573 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 262;
Best Local Similarity 83.3%; Pred. No. 5.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
| | | | |
Db 7 KVFVFFS 12

RESULT 34

Q7RC37 PLAYO
ID Q7RC37 PLAYO PRELIMINARY; PRT; 265 AA.
AC Q7RC37;
DT 01-MAR-2004 (TREMUREL. 26, Created)
DT 01-MAR-2004 (TREMUREL. 26, Last sequence update)
DT 01-MAR-2004 (TREMUREL. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY05947;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Sedegah M., Shoaibi A., Cummings L.M.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL: AABL01001955; EAA18074.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMS; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 265 AA; 31511 MW; 7CD7DBBCC3A26FF CRC64;

Query Match 90.3%; Score 28; DB 2; Length 265;
Best Local Similarity 83.3%; Pred. No. 5.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
| | | | |
Db 7 KVFVFFS 12

RESULT 35

Q7RB86 PLAYO
ID Q7RB86 PLAYO PRELIMINARY; PRT; 268 AA.
AC Q7RB86;
DT 01-MAR-2004 (TREMUREL. 26, Created)
DT 01-MAR-2004 (TREMUREL. 26, Last sequence update)
DT 01-MAR-2004 (TREMUREL. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY06262;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Sedegah M., Shoaibi A., Cummings L.M.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL: AABL01002095; EAA18444.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMS; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
FT NON_TER 268 268
SQ SEQUENCE 268 AA; 32060 MW; D273B20E61AA181C CRC64;

Query Match 90.3%; Score 28; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 5.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6
| | | | |
Db 7 KVFVFFS 12

Query Match 90.3%; Score 28; DB 2; Length 268;
Best Local Similarity 83.3%; Pred. No. 5.7e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 KVFVFFA 6

```
Db          |||||:
            7 KVFVFS 12

RESULT 36
Q529U4 MAGGR
ID Q529U4_MAGGR PRELIMINARY; PRT; 285 AA.
AC Q529U4;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=MG02290.4;
OS Magnaporthe grisea 70-15.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthae.
OX NCBI_TaxID=242507;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA Ait-zahra H., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA Borowsky M., Boukgalter B., Brunch A., Butler J., Calixte N.,
RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA Collymore A., Conscience T., Cook A., Cooke P., Corum B., Cuomo C.,
RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA Jaffe D., Jones C., Kamal M., Kamat A., Kamysseelis M., Karlsson E.,
RA Kellis C., Kieu A., Kiener P., Kodira C., Kulbokas E., Labutti K.,
RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA Lui A., Ma L.J., Mabitt R., Macdonald J., Maclean C., Major J.,
RA Manning J., Marabella R., Maru K., Matthews C., Maucelli E.,
RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
RA Mesirov J., Mihalev A., Mihova T., Mikelsen T., Mlenga V., Moru K.,
RA Mozes J., Mulrain L., Munson G., Naylor J., News C., Nguyen C.,
RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pigani B.,
RA Purcell S., Rachupka T., Ramasamy U., Raneau R., Ray V., Raymond C.,
RA Retta R., Richardson S., Riese C., Rodriguez J., Rogers J., Rogov P.,
RA Rutnan M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA Towey S., Tsanla T., Tsomo N., Vallee D., Vassiliev H.,
RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wanchuk T.,
RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA Zimmer A., Zody M., Lander E.;
RT "The genome sequence of Magnaporthe grisea";
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=70-15;
RA Zhu H., Blackmon B.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
```

```
DR EMBL; AACU01000444; EAA54305.1; -; Genomic_DNA.
DR InterPro; IPR012351; Cytokine_4_hlx.
DR InterPro; IPR007568; RTA1.
DR Pfam; PF04479; RTA1; 1.
KW Hypothetical protein.
SQ SEQUENCE 285 AA; 31531 MW; DCE48A5EB9E4D1BD CRC64;

Query Match          90.3%; Score 28; DB 2; Length 285;
Best Local Similarity 83.3%; Pred. NO. 6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   |||||
DB 6 KVFVFA 11

RESULT 37
Q94284 CAEEL
ID Q94284_CAEL PRELIMINARY; PRT; 293 AA.
AC Q94284;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein M02B7.4.
GN ORFNames=M02B7.4;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=93069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; U70851; AAB09129.1; -; Genomic_DNA.
DR PIR; T29899; T29899.
DR Ensembl; M02B7.4; Caenorhabditis elegans.
DR WormBase; WBGene00019725; M02B7.4.
DR WormPep; M02B7.4; CEL2326.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 293 AA; 33247 MW; 90CE020650E5065 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 293;
Best Local Similarity 83.3%; Pred. NO. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   |||||
DB 258 KVFVFS 263

RESULT 38
Q7RBUI PLAYO
ID Q7RBUI_PLAYO PRELIMINARY; PRT; 294 AA.
AC Q7RBUI;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06045;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Emdiolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
```

```

RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC ENBL; AABL01002005; EAA18193.1; -; Genomic_DNA.
DR InterPro; IPR006484; PIST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 294 AA; 34611 MW; 281A85D322236659 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 294;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 7 KVFVFS 12

RESULT 39
QSUWP7 HALMA PRELIMINARY; PRT; 300 AA.
AC QSUWP7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Sugar ABC transport system permease protein.
GN Name=malFG-9; OrderedLocustNames=rrnB0104;
OS Haloarcula marismortui (Halo bacterium marismortui).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloarcula.
OX NCBI_TaxID=2238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 43049;
RA Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA Date S.V., Marcotte E., Hood L., Ng W.V.;
RA "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
RT the Dead Sea.";
RL Genome Res. 14:2221-2234(2004).
CC -1- FUNCTION: Part of a binding-protein-dependent transport system.
CC Probably responsible for the translocation of the substrate across
CC the membrane (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the binding-protein-dependent transport
CC system permease family.
DR ENBL; AY596238; ANV48306.1; -; Genomic_DNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0016020; C: membrane; IEA.
DR GO; GO:0005215; P: transporter activity; IEA.
DR GO; GO:0006810; P: transport; IEA.
DR InterPro; IPR000515; BPD transp.
DR Pfam; PF00528; BPD_transp_1; 1.
DR PROSITE; PS0928; ABC_TM1; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 300 AA; 32975 MW; 9C230B44EF19CE5A CRC64;

Query Match 90.3%; Score 28; DB 2; Length 300;
Best Local Similarity 83.3%; Pred. No. 6.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6

```

```

DB 86 KMFVFA 91

RESULT 40
Q7RB33 PLAYO PRELIMINARY; PRT; 321 AA.
AC Q7RB33;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY06150;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22355706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Sun B.B., Koolf T.W., Perce M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Sengut J.D., Koo H.B.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC ENBL; AABL01002053; EAA18307.1; -; Genomic_DNA.
DR InterPro; IPR006484; PYST-B.
DR TIGRFAMs; TIGR01597; PYST-B; 1.
KW Hypothetical protein.
SQ SEQUENCE 321 AA; 38948 MW; E1127BA81EB58FDB CRC64;

Query Match 90.3%; Score 28; DB 2; Length 321;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 51 KVFVFS 56

RESULT 41
P74429 SYNY3 PRELIMINARY; PRT; 326 AA.
AC P74429;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ycf39 gene product.
GN Name=ycf39; OrderedLocustNames=slr0399;
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sugita M., Saito K., Okumura S.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RA "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT

```

```

RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; BA000022; BAA18529.1; -; Genomic DNA.
DR PIR; S76400; S76400.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0051287; F:NAD binding; IEA.
DR GO; GO:0009225; P:nucleotide-sugar metabolism; IEA.
DR InterPro; IPR001509; Epimerase_Dh.
DR Pfam; PF01370; Epimerase; 1.
KW Complete proteome.
SQ SEQUENCE 326 AA; 36519 MW; 99F522C1E980B943 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 326;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 104 KVFVFS 109

RESULT 42
Q6KI05 MYCMO
ID Q6KI05 MYCMO PRELIMINARY; PRT; 380 AA.
AC Q6KI05.
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Restriction-modification enzyme mpuUVIII s subunit (EC 3.1.21.3).
GN Name=hds; OrderedLocusNames=MMOB2850;
OS Mycoplasma mobile.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=163K / ATCC 43663;
RX PubMed=15289470; DOI=10.1101/gr.2674004;
RA Jaffe J.D., Stange-Thomann N., Smith C., DeCaprio D., Fisher S.,
RA Butler J., Calvo S., Elkins T., Fitzgerald M.G., Hafez N.,
RA Kodira C.D., Major J., Wang J., Wilkerson J., Nicol R., Nusbaum C.,
RA Birren B., Berg H.C., Church G.M.;
RT "The complete genome and proteome of Mycoplasma mobile.";
RL Genome Res. 14:1447-1461(2004).
DR EMBL; AE017338; AAT27771.1; -; Genomic DNA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0009035; F:Type I site-specific deoxyribonuclease acti. . .; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR InterPro; IPR000055; Rest mod DNA.
DR Pfam; PF01420; Methylase_S; 2.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 380 AA; 44463 MW; D42428E38774F9CE CRC64;

Query Match 90.3%; Score 28; DB 2; Length 380;
Best Local Similarity 83.3%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 294 KVFVFA 299

RESULT 43
Q4MSJ5 BACCE
ID Q4MSJ5 BACCE PRELIMINARY; PRT; 388 AA.
AC Q4MSJ5.
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE Basic membrane protein DclB.
GN Name=dltB; ORFNames=BCE_G9241_1384;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

```

```

OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Ralstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA00100009; EAL15142.1; -; Genomic DNA.
SQ SEQUENCE 388 AA; 45590 MW; E21AEA22BA0511CF CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 286 RRVFPA 291

RESULT 44
Q6HLH8 BACHK
ID Q6HLH8 BACHK PRELIMINARY; PRT; 388 AA.
AC Q6HLH8;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE D-alanyl transfer protein.
GN Name=dltB; OrderedLocusNames=BT9727_1258;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=97-27;
RA Bretin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DDJ databases.
DR EMBL; AE017355; AAT61956.1; -; Genomic DNA.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45999 MW; DFB6794B3247A66B CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 286 RRVFPA 291

RESULT 45
Q73BD3 BACCI
ID Q73BD3 BACCI PRELIMINARY; PRT; 388 AA.
AC Q73BD3;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE DltB protein.

```

```

GN Name=dltB; OrderedLocusNames=BCE1486;
OS Bacillus cereus (strain ATCC 10987);
OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AB017269; AAS40415.1; -; Genomic_DNA.
DR TIGR; BCE1486; -.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 74CBF3D745AE3EC6 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 286 RFVFFA 291

RESULT 46
Q63E03_BACZ
ID Q63E03_BACZ PRELIMINARY; PRT; 388 AA.
AC Q63E03;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE D-alanyl transfer protein.
GN Name=dltB;
OS Bacillus cereus (strain ZK).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=288681;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18989.1; -; Genomic_DNA.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 009F62D466DF6FC7 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 286 RFVFFA 291

RESULT 47
Q81T98_BACAN
ID Q81T98_BACAN PRELIMINARY; PRT; 388 AA.
AC Q81T98; G61H5; Q6KVC6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE DltB protein..

```

```

GN Name=dltB; OrderedLocusNames=BA1388, BAS1286, GBAA1388;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=1392;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Bailly L.W., Paulsen I.T.,
RA Nelson K.E., Tectelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Kolonay J.F., Okstad O.A., Helgason E., Ristone J., Wu M.,
RA Holzapfel E.K., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.B., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.P., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus anthracis Sterne.";
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017028; AAP25332.1; -; Genomic_DNA.
DR EMBL; AB017334; AAT30485.1; -; Genomic_DNA.
DR EMBL; AB017225; AAT53606.1; -; Genomic_DNA.
DR TIGR; BA1388; -.
DR TIGR; GBAA1388; -.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 45590 MW; 009F62D466DF6FC7 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 388;
Best Local Similarity 83.3%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 286 RFVFFA 291

RESULT 48
Q81G40_BACCR
ID Q81G40_BACCR PRELIMINARY; PRT; 391 AA.
AC Q81G40;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein dltB.
GN OrderedLocusNames=BC1371;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kapral V., Bhattacharya A., Renik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyripides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis."
RL Nature 423:87-91(2003).
DR EMBL; AE017002; AAP08353.1; -; Genomic_DNA.
DR InterPro; IPR004299; MBOAT_fam.
DR Pfam; PF03062; MBOAT; 1.
KW Complete proteome.
SQ SEQUENCE 391 AA; 46119 MW; E875D00033C91C54 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 391;
Best Local Similarity 83.3%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 289 RVVFFA 294

RESULT 49
Q5NEA9 FRATT PRELIMINARY; PRT; 398 AA.
AC Q5NEA9;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Aromatic amino acid transporter of the HAAAP family.
GN OrderedLocNames=FTW1732c;
OS Francisella tularensis (subsp. tularensis).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales;
OC Francisellaceae; Francisella.
OX NCBI_TaxID=119856;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCHU S4 / Schu 4;
RX PubMed=15640799; DOI=10.1038/ng1499;
RA Larsson P., Oyston P.C.E., Chain P., Chu M.C., Duffield M.,
RA Fuxelius H.-H., Garcia E., Haeiltoorp G., Johansson D., Isherwood K.E.,
RA Karp P.D., Larsson E., Liu Y., Michell S., Prior J., Prior R.,
RA Malfatti S., Sjoestedt A., Svensson K., Thompson N., Vergez L.,
RA Wagg J.K., Wren B.W., Lindler L.E., Andersson S.G.E., Forsman M.,
RA Titball R.W.;
RT "The complete genome sequence of Francisella tularensis, the causative
RT agent of tularemia."
RL Nat. Genet. 37:153-159(2005).
DR EMBL; AJ749949; CAG46365.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR002422; AA/rel_permease2.
DR InterPro; IPR002091; AAA_permease.
DR Pfam; PF03222; Tnp_TyT_perme.1.
DR PRINTS; PR00166; AROA/PERMEASE.
KW Complete proteome; Transmembrane.
SQ SEQUENCE 398 AA; 44437 MW; 1A93FFD1D8AAA438 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 398;
Best Local Similarity 83.3%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 152 KVLFFA 157

RESULT 50

```

```

Q73V08 MYCPA
ID Q73V08 MYCPA PRELIMINARY; PRT; 409 AA.
AC Q73V08;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Nuoh.
GN Name=nuoh; OrderedLocNames=MAP3208;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
OX NCBI_TaxID=1770;
RN [1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Anonsin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017238; AAS05756.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_ND1_1; 1.
DR PROSITE; PS00668; COMPLEX1_ND1_2; 1.
KW Complete proteome.
SQ SEQUENCE 409 AA; 44971 MW; 693518B9DDF94B11 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 409;
Best Local Similarity 83.3%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
:|||||
Db 67 KVFVFA 72

RESULT 51
Q7Z2C3 CAEEL
ID Q7Z2C3 CAEEL PRELIMINARY; PRT; 421 AA.
AC Q7Z2C3;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN ORFNames=y19D10A.8;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; AC006722; AAK68421.2; -; Genomic DNA.
DR Ensemble; Y19D10A.8; Caenorhabditis elegans.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS.1.
DR Pfam; PF07690; MFS.1; 1.
DR PROSITE; PS50850; MFS; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 421 AA; 46361 MW; 75B7CF15ABE2C432 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 421;

```

```
Best Local Similarity 83.3%; Pred. No. 8.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 291 RFVFFA 296

RESULT 52
Q9PG2 UREPA
ID Q9PG2 UREPA PRELIMINARY; PRT; 422 AA.
AC Q9PG2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Unique hypothetical.
GN OrderedLocusNames=U0329;
GS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
OX NCBI_TaxID=134821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 700970;
RX MEDLINE=20500219; PubMed=11048724; DOI=10.1038/35037619;
RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,
RA Cassell G.H.;
RT "The complete sequence of the mucosal pathogen Ureaplasma
RT urealyticum."
RL Nature 407:757-762(2000).
DR EMBL; AS002130; AAF30738.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 422 AA; 49219 MW; 8EA5B3F2F76C8E8 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 422;
Best Local Similarity 83.3%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 208 KYVFFA 213

RESULT 53
Q8FW04 BRUSU
ID Q8FW04 BRUSU PRELIMINARY; PRT; 430 AA.
AC Q8FW04;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Uracil-xanthine permease, putative.
GN OrderedLocusNames=BR00661;
GS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=1330 / Blovax 1;
RX MEDLINE=2247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.P.,
RA Read T.D., Dodson R.J., Unayam L.A., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kral M., Shetty J., Malek J.A.,
RA Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
RA Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts."
RT Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AB014292; AAN33850.1; -; Genomic DNA.
DR TIGR; BR00661; -;
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
```

```
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR004711; BenE.
DR Pfam; PF00860; Xant_ur_permease; 1.
DR ProDom; PD024853; BenE; 1.
KW Complete proteome.
SQ SEQUENCE 430 AA; 44661 MW; B69F2E03E9A28C39 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 430;
Best Local Similarity 83.3%; Pred. No. 8.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 424 RFVFFA 429

RESULT 54
Q6QW8 9GAMM
ID Q6QW8 9GAMM PRELIMINARY; PRT; 432 AA.
AC Q6QW8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Predicted preprotein translocase subunit SecY.
GN ORFNames=Red20E09_103;
GS uncultured marine gamma proteobacterium EBAC20E09.
OC Bacteria; Proteobacteria; Gammaproteobacteria; SAR86 cluster;
OC environmental samples.
OX NCBI_TaxID=266134;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15305915; DOI=10.1111/j.1462-2920.2004.00676.x;
RA Sabehi G., Beja O., Suzuki M.T., Preston C.M., DeLong E.F.;
RT "Different SAR86 subgroups harbour divergent proteorhodopsins."
RL Environ. Microbiol. 6:903-910(2004).
DR EMBL; AY525455; AAS73104.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015450; F:protein translocase activity; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR GO; GO:0006605; P:protein targeting; IEA.
DR GO; GO:0015031; P:protein transport; IEA.
DR InterPro; IPR002208; SecY.
DR Pfam; PF00344; SecY; 1.
DR PRINTS; PR00303; SECYTNLCASE.
DR TIGRfams; TIGR00967; 3a0501a007; 1.
DR PROSITE; PS00756; SECY_2; 1.
KW Protein transport; Translocation; Transmembrane; Transport.
SQ SEQUENCE 432 AA; 47276 MW; CC0F2DA782EB8F79 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 432;
Best Local Similarity 83.3%; Pred. No. 8.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
Db 15 RFVFFA 20

RESULT 55
Q8M9J3 9AQUA
ID Q8M9J3 9AQUA PRELIMINARY; PRT; 436 AA.
AC Q8M9J3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribulose-bisphosphate carboxylase (EC 4.1.1.39) (Fragment).
GN Name=rbcL;
GS Illex pubescens.
OX Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```


OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; campanulids; Aquifoliales; Aquifoliaceae; Ilex.
 OX NCBI_TaxID=185543;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Manen J.F.;
 RT "The complex history of the genus Ilex L. (Aquifoliaceae): evidence
 RT from the comparison of plastid and nuclear DNA sequences and from
 RT fossil data.";
 RL Plant Syst. Evol. 0:0-0(0).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Manen J.F.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Rubisco catalyzes two reactions: the carboxylation of D-
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC the pentose substrate in the photorespiration process (By
 CC similarity).
 CC -!- FUNCTION: Rubisco catalyzes two reactions: the carboxylation of D-
 CC ribulose 1,5-bisphosphate, the primary event in photosynthetic
 CC carbon dioxide fixation, as well as the oxidative fragmentation of
 CC the pentose substrate in the photorespiration process. Both
 CC reactions occur simultaneously and in competition at the same
 CC active site (By similarity).
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
 CC 2 3-phospho-D-glycerate.
 CC -!- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-
 CC phospho-D-glycerate + 2-phosphoglycolate.
 CC -!- SUBUNIT: 8 large chains + 8 small chains (By similarity).
 CC -!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
 CC -!- SIMILARITY: Belongs to the Rubisco large chain family.
 DR EMBL; AJ492722; CAD37439.1; -; Genomic_DNA.
 DR SMR; Q8W9J3; 9-436.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0009573; C:ribulose biphosphate carboxylase complex (. . .); IEA.
 DR GO; GO:0016829; F:lyase activity; IEA.
 DR GO; GO:0004497; F:monooxygenase activity; IEA.
 DR GO; GO:0016984; F:ribulose-bisphosphate carboxylase activity; IEA.
 DR GO; GO:0015977; P:carbon utilization by fixation of carbon di. . .; IEA.
 DR GO; GO:0009853; P:photorespiration; IEA.
 DR GO; GO:0015979; P:photosynthesis; IEA.
 DR InterPro; IPR000685; RuBisCO_large.
 DR Pfam; PF00016; RuBisCO_large; 1.
 DR Pfam; PF02788; RuBisCO_large; 1.
 KW Carbon dioxide fixation; Chloroplast; Lyase; Monooxygenase;
 KW Oxidoreductase; Photorespiration; Photosynthesis.
 FT NON_TER 436 436
 SQ SEQUENCE 436 AA; 48367 MW; E1A65FFCF93985A1 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 436;
 Best Local Similarity 83.3%; Pred. No. 8.6e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFPA 6
 Db 217 RVFFPA 222
 RESULT 56
 ID O44595 CAEBL PRELIMINARY; PRT; 452 AA.
 AC O44595;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DE Hypothetical protein F56A4.10.
 GN ORFNames=F56A4.10;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidea;
 OC Rhabditidae; Feloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=93069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology.";
 RL Science 282:2012-2018(1998).
 DR EMBL; AC006645; AAF39848.1; -; Genomic_DNA.
 DR PIR; C88969; C88969.
 DR Ensembl; F56A4.10; Caenorhabditis elegans.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR011701; MFS_1.
 DR Pfam; PF07690; MFS_1; 1.
 DR PROSITE; PS50850; MFS; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 452 AA; 49858 MW; F1BED2FBB60CAE59 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 452;
 Best Local Similarity 83.3%; Pred. No. 8.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFPA 6
 Db 291 RVFFPA 296
 RESULT 57
 Q6GVJ4_9BURK
 ID Q6GVJ4_9BURK PRELIMINARY; PRT; 456 AA.
 AC Q6GVJ4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Glycosyltransferase.
 GN Name=wbce;
 OS Burkholderia cenocepacia.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
 OX NCBI_TaxID=95486;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=K56-2;
 RX PubMed=15887196; DOI=10.1128/JB.187.4.1324-1333.2005;
 RA Ortega X., Hunt T.A., Louet S., Vinion-Dubiel A.D., Datta A.,
 RA Choudhury B., Goldberg J.B., Carlson R., Valvano M.A.;
 RT "Reconstitution of O-Specific Lipopolysaccharide Expression in
 RT Burkholderia cenocepacia Strain J2315, Which Is Associated with
 RT Transmissible Infections in Patients with Cystic Fibrosis.";
 RL J. Bacteriol. 187:1324-1333(2005).
 DR EMBL; AY633623; AAT48329.1; -; Genomic_DNA.
 DR GO; GO:0016740; P:transferase activity; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR InterPro; IPR001296; Glyco_trans_1.
 DR Pfam; PF00534; Glycos_transf_1; 1.
 KW Transferase.
 SQ SEQUENCE 456 AA; 50801 MW; ESB3648E1BE54A54 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 456;
 Best Local Similarity 83.3%; Pred. No. 8.9e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVFFPA 6
 Db 6 KFLFFPA 11
 RESULT 58
 RBL_NEPAL
 ID RBL_NEPAL
 AC P28434;
 STANDARD; PRT; 465 AA.

DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Ribulose biphosphate carboxylase large chain (EC 4.1.1.39) (RuBisCO
 DE large subunit) (Fragment).
 GN Namesbcd, alata (Winged pitcher plant).
 OS Chloroplast.
 OC Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Caryophyllales; Nymphaeaceae; Nymphaeaceae.
 OX NCBI_TaxID=4376;
 [1]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92397008; PubMed=1523408;
 RA Albert V.A., Williams S.E., Chase M.W.;
 RL "Carnivorous plants: phylogeny and structural evolution."; Science
 257:1491-1495 (1992).
 CC -1- FUNCTION: RuBisCO catalyzes two reactions: the carboxylation of D-
 ribulose 1,5-bisphosphate, the primary event in photosynthetic
 carbon dioxide fixation, as well as the oxidative fragmentation of
 the pentose substrate in the photorespiration process. Both
 reactions occur simultaneously and in competition at the same
 active site.
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + CO(2) + H(2)O =
 2 3-phospho-D-glycerate + 2 H(+).
 CC -1- CATALYTIC ACTIVITY: D-ribulose 1,5-bisphosphate + O(2) = 3-
 phospho-D-glycerate + 2-phosphoglycolate.
 CC -1- COPACTOR: Binds 1 magnesium ion per subunit (By similarity).
 CC -1- SUBUNIT: Heterohexameric of 8 large chains and 8 small chains;
 disulfide-linked. The disulfide link is formed within the large
 subunit homodimers (By similarity).
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- DOMAIN: The basic functional RuBisCO is composed of a large chain
 homodimer in a "head-to-tail" conformation. In form I RuBisCO this
 homodimer is arranged in a barrel-like tetramer with the small
 subunits forming a tetrameric "cap" on each end of the "barrel"
 (By similarity).
 CC -1- PTM: The disulfide bond which can form in the large chain dimeric
 partners within the hexadecamer appears to be associated with
 oxidative stress and protein turnover (By similarity).
 CC -1- SIMILARITY: Belongs to the RuBisCO large chain family. Type I
 subfamily.

 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

 DR EMBL; L01936; AAA84502.2; -; Genomic DNA.
 DR HSSP; P00875; LAUS.
 DR SMR; P28434; 1-465.
 DR HAWAP; MF_01338; -; 1.
 DR InterPro; IPR000685; RuBisCO_large.
 DR Pfam; PF00016; RuBisCO_large; 1.
 DR Pfam; PF02788; RuBisCO_large; 1.
 DR PROSITE; PS00157; RUBISCO_LARGE; 1.
 KW Calvin cycle; Carbon dioxide fixation; Chloroplast; Lyase; Magnesium;
 KW Metal-binding; Methylation; Monooxygenase; Oxidoreductase;
 KW Photorespiration; Photosynthesis.
 FT ACT SITE 165 165 Proton acceptor (By similarity).
 FT ACT SITE 284 284 Proton acceptor (By similarity).
 FT METAL 191 191 Magnesium (via carboxylate group) (By
 similarity).
 FT METAL 193 193 Magnesium (By similarity).
 FT METAL 194 194 Magnesium (By similarity).
 FT BINDING 113 113 Substrate (in homodimeric partner) (By
 similarity).
 FT BINDING 163 163 Substrate; C1 phosphate group (By
 similarity).
 FT BINDING 167 167 Substrate (By similarity).
 FT BINDING 285 285 Substrate; C5 phosphate group (By
 similarity).

FT BINDING 317 317 Substrate; C5 phosphate group (By
 similarity).
 FT BINDING 369 369 Substrate; C5 phosphate group (By
 similarity).
 FT SITE 324 324 Transition state stabilizer (By
 similarity).
 FT MOD_RES 4 4 N6,N6,N6-trimethyllysine (By similarity).
 FT MOD_RES 191 191 N6-carboxyllysine (By similarity).
 FT DISULFID 237 237 Interchain (in linked form) (By
 similarity).
 FT NON_TER 1 1
 SQ SEQUENCE 465 AA; 51614 MW; 29B322894FE92451 CRC64;
 Query Match 90.3%; Score 28; DB 1; Length 465;
 Best Local Similarity 83.3%; Pred. No. 9.1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRVFFPA 6
 DB 207 RRVFFPA 212
 RESULT 59
 Q9NSQ8 CAEBL PRELIMINARY; PRT; 472 AA.
 ID Q9NSQ8 CAEBL PRELIMINARY; PRT; 472 AA.
 AC Q9NSQ8;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein F56A4.12.
 GN ORFNames=F56A4.12;
 OS Caenorhabditis elegans.
 OC Rukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG The C. elegans sequencing consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology"; Science 282:2012-2018 (1998).
 RL EMBL; AC006645; AAP39850.1; -; Genomic DNA.
 DR Ensembl; F56A4.12; Caenorhabditis elegans.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005215; P:transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR011701; MFS_1.
 DR Pfam; PF07690; MFS_1; 1.
 DR PROSITE; PS50850; MFS; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 472 AA; 52251 MW; C06DFDB6AAG755AE CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 472;
 Best Local Similarity 83.3%; Pred. No. 9.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KRVFFPA 6
 DB 340 RRVFFPA 345
 RESULT 60
 Q625W2 CAEBR PRELIMINARY; PRT; 480 AA.
 ID Q625W2 CAEBR PRELIMINARY; PRT; 480 AA.
 AC Q625W2;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein CBG01115.

```
GN Name=CBG01115;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC The C.briggsae Sequencing Consortium;
RG Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; CAAC01000007; CAE59039.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS0850; MFS; 1.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 53324 MW; BDC735BE20A6CC51 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 480;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 343 REVFFA 348

RESULT 61
Q5JU16_PYRKO
ID Q5JU16_PYRKO PRELIMINARY; PRT; 482 AA.
AC Q5JU16;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical membrane protein, conserved.
GN OrderedLocusNames=TKI1728;
OS Pyrococcus kodakaraensis (Thermococcus kodakaraensis).
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=69014;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KOD1;
RX PubMed=15710748; DOI=10.1101/gr.3003105;
RA Fukui T., Atomi H., Kanai T., Matsumi R., Fujiwara S., Imanaka T.;
RT "Complete genome sequence of the hyperthermophilic archaeon
RT Thermococcus kodakaraensis KOD1 and comparison with Pyrococcus
RT genomes.";
RL Genome Res. 15:352-363(2005).
DR EMBL; AP006878; BAD85917.1; -; Genomic DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 482 AA; 54068 MW; 097052D348C3BB4D CRC64;

Query Match 90.3%; Score 28; DB 2; Length 482;
Best Local Similarity 83.3%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 336 REVFFA 341

RESULT 62
Q966D7_CAEEL
ID Q966D7_CAEEL PRELIMINARY; PRT; 488 AA.
AC Q966D7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Y19D10A.11;

OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2;
RG MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AC006722; AAK68411.2; -; Genomic DNA.
DR Ensembl; Y19D10A.11; Caenorhabditis elegans.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR011701; MFS_1.
DR Pfam; PF07690; MFS_1; 1.
DR PROSITE; PS0850; MFS; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 488 AA; 54121 MW; A145401A124DB716 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 488;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 356 REVFFA 361

RESULT 63
Q621X3_CAEER
ID Q621X3_CAEER PRELIMINARY; PRT; 492 AA.
AC Q621X3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG02310 (Fragment).
GN Name=CBG02310;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAC01000012; CAE59030.1; -; Genomic DNA.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 2.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 492
SQ SEQUENCE 492 AA; 57471 MW; 4F1D61BB64DC5CFB CRC64;

Query Match 90.3%; Score 28; DB 2; Length 492;
Best Local Similarity 83.3%; Pred. No. 9.5e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 188 REVFFA 193

RESULT 64
```

```

Q38860 ARATH
ID Q38860 ARATH PRELIMINARY; PRT; 506 AA.
AC Q38860;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-PBB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fatty acid elongase 1.
GN Names:fael; Synonyms=AT4g34520, T4L20.100;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=9252821; PubMed=7734965; DOI=10.1105/tpc.7.3.309;
RA James D.W. Jr., Lim E., Keller J., Plooy I., Ralston E., Dooner H.K.;
RT "Directed tagging of the Arabidopsis FATTY ACID ELONGATION1 (FAE1)
RT gene with the maize transposon activator.";
RL Plant Cell 7:309-319(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Terry N., Ardiles W., Buyssehaert C., Daseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Giesen J., Van Montagu M., Jesse T., Heijnen L., Vos P.,
RA Hohelsel J., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Terry N., Ardiles W., Buyssehaert C., Daseville R., De Clerck R.,
RA De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarroel R.,
RA Giesen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U29142; AAA70154.1; -; Genomic DNA.
DR EMBL; AL023094; CAA18831.1; -; Genomic DNA.
DR EMBL; AL161585; CAB80169.1; -; Genomic DNA.
DR PIR; T05272; T05272.
DR GO; GO:0008415; F-acyltransferase activity; IEA.
DR GO; GO:0016740; F-transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 506 AA; 56263 MW; 4516D08F8E453D18 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 9.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
   |||||
Db 356 KFLFFA 361

RESULT 65
MURE BORBU
ID MURE BORBU STANDARD; PRT; 508 AA.
AC O51219;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase
DE (EC 6.3.2.13) (UDP-N-acetylmuramyl-tripeptide synthetase) (Meso-
DE diaminopimelate-adding enzyme) (UDP-MurNAC-tripeptide synthetase).
GN Name=mure; OrderedLocName=BB0201;
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;

Q38860 ARATH PRELIMINARY; PRT; 506 AA.
AC Q38860;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-PBB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fatty acid elongase 1.
GN Names:fael; Synonyms=AT4g34520, T4L20.100;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsiis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WS;
RX MEDLINE=9252821; PubMed=7734965; DOI=10.1105/tpc.7.3.309;
RA James D.W. Jr., Lim E., Keller J., Plooy I., Ralston E., Dooner H.K.;
RT "Directed tagging of the Arabidopsis FATTY ACID ELONGATION1 (FAE1)
RT gene with the maize transposon activator.";
RL Plant Cell 7:309-319(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Bevan M., Terry N., Ardiles W., Buyssehaert C., Daseville R.,
RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
RA Villarroel R., Giesen J., Van Montagu M., Jesse T., Heijnen L., Vos P.,
RA Hohelsel J., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Terry N., Ardiles W., Buyssehaert C., Daseville R., De Clerck R.,
RA De Keyser A., Neyt P., Rouze P., Van Den Daele H., Villarroel R.,
RA Giesen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; U29142; AAA70154.1; -; Genomic DNA.
DR EMBL; AL023094; CAA18831.1; -; Genomic DNA.
DR EMBL; AL161585; CAB80169.1; -; Genomic DNA.
DR PIR; T05272; T05272.
DR GO; GO:0008415; F-acyltransferase activity; IEA.
DR GO; GO:0016740; F-transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 506 AA; 56263 MW; 4516D08F8E453D18 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 506;
Best Local Similarity 83.3%; Pred. No. 9.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
   |||||
Db 356 KFLFFA 361

RESULT 66
P33058 BRAJU
ID P33058 BRAJU PRELIMINARY; PRT; 509 AA.
AC P33058;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fatty acid elongation 1.
GN Name=fael;
OS Brassica juncea (Leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Brassica.

```

```

OX NCBI_TaxID=3707;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RC TISSUE=Hypocotyl;
RA Venkateswari J., Kanrar S., Kirti P.B., Malathi V.G., Chopra V.L.;
RT "Molecular cloning and characterization of fatty acid elongation 1
RL (fae 1) gene of Brassica juncea cv. Pusa Bold.";
RL J. Plant Biochem. Biotechnol. 8:53-55(1999).
DR EMBL; Y11007; CAA71898.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56663 MW; B204DA5AB5887C5C CRC64;

Query Match          90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 359 KFLFFA 364
|||||

RESULT 67
Q8LSC7_BRAJ
ID Q8LSC7_BRAJ PRELIMINARY; PRT; 509 AA.
AC Q8LSC7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Fatty acid elongase.
OS Brassica campestris (field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yadav P., Bhat S., Chopra V.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF491878; AM33539.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56661 MW; 59ED8F07457CB6F5 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 358 KFLFFA 363
|||||

RESULT 68
Q8S384_BRAJ
ID Q8S384_BRAJ PRELIMINARY; PRT; 509 AA.
AC Q8S384;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Fatty acid elongase.
GN Name=Fael.2; Synonyms=fae 1.1;
OS Brassica juncea (leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yadav P., Bhat S., Chopra V.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

```

```

DR EMBL; AF491877; AM311648.1; -; Genomic DNA.
DR EMBL; AF491876; AM34043.1; -; Genomic DNA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 509 AA; 56616 MW; F6C553739AD86C23 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 509;
Best Local Similarity 83.3%; Pred. No. 9.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 358 KFLFFA 363
|||||

RESULT 69
O80729_ARATH
ID O80729_ARATH PRELIMINARY; PRT; 517 AA.
AC O80729;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Putative cytochrome P450 (At2G46950).
GN Name=At2G46950;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Renning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Ecker J.R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Kim C.J., Chen H., Cheuk R., Shinn P., Ecker J.R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR EMBL; AC004411; AAC34228.1; -; Genomic DNA.
DR EMBL; BT014808; AAT41791.1; -; mRNA.
DR EMBL; BT011625; AAS47631.1; -; mRNA.
DR PIR; T02192; T02192.
DR HSP; P14779; IJFZ.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR001128; Cytochrome_P450.
DR InterPro; IPR002401; EP450I.
DR Pfam; PF00067; p450; 1.
DR PRINTS; PR00463; EP450I.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW Heme; Iron; Metal-binding; Monooxygenase; Oxidoreductase;
KW Transmembrane.
SQ SEQUENCE 517 AA; 59021 MW; 3963BCEC988C19A2 CRC64;

Query Match          90.3%; Score 28; DB 2; Length 517;
Best Local Similarity 83.3%; Pred. No. 9.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 123 KVFVFS 128
|||||

```

```

RESULT 70
Q6N123 CORDI
ID Q6N123 CORDI PRELIMINARY; PRT; 529 AA.
AC Q6N123;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative peptide transport system secreted protein.
GN OrderedLocNames=DIP0956;
OS Corynebacterium diptheriae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1717;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Biotype gravis / NCTC 13129;
RX MEDLINE=22965443; PubMed=14602910; DOI=10.1093/nar/gkg874;
RA Cardeno-Tarraga A.-M., Efstratiou A., Dover L.G., Holden M.T.G.,
RA Fallan M.J., Bentley S.D., Besra G.S., Churcher C.M., James K.D.,
RA De Zoysa A., Chillingworth T., Cronin A., Dowd L., Feltwell T.,
RA Hamlin N., Holroyd S., Jagels K., Moule S., Quail M.A.,
RA Rabinowitz E., Rutherford K.M., Thomson N.R., Unwin L.,
RA Whitehead S., Barrell B.G., Parkhill J.;
RA "The complete genome sequence and analysis of Corynebacterium
RT diptheriae NCTC13129."
RL Nucleic Acids Res. 31:6516-6523(2003).
DR EMBL; BX248356; CAB49475.1; -; Genomic DNA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000914; SBP_bac_5.
DR Pfam; PF00496; SBP_bac_5; 1.
DR PROSITE; PS01040; SBP_BACTERIAL_5; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 529 AA; 57407 MW; 0E8BF5955BA6818A CRC64;

Query Match 90.3%; Score 28; DB 2; Length 529;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
DB 234 KPVFFA 239

RESULT 71
Q7PQ20 ANOGA
ID Q7PQ20 ANOGA PRELIMINARY; PRT; 538 AA.
AC Q7PQ20;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000001164 (Fragment).
GN ORFNames=ENSANG0000001003;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAB01008859; EAL40926.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003595; PTPc motif.
DR InterPro; IPR000980; SH2_
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00017; SH2; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR PRINTS; PR00401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 2.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC_motif; 1.
DR SMART; SM00252; SH2; 2.
DR PROSITE; PS00001; SH2; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00566; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
FT NON_TER 1 538
FT NON_TER 538 538
SQ SEQUENCE 538 AA; 62289 MW; 67D046AB3DBFAA78 CRC64;

Query Match 90.3%; Score 28; DB 2; Length 538;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
DB 503 KPVFFA 508

RESULT 72
Q5TTR3 ANOGA
ID Q5TTR3 ANOGA PRELIMINARY; PRT; 558 AA.
AC Q5TTR3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE ENSANGP00000029277 (Fragment).
GN ORFNames=ENSANG0000001003;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AAB01008859; EAL40926.1; -; Genomic DNA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003595; PTPc motif.
DR InterPro; IPR000980; SH2_
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.

```

DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PRO0700; PRTYPHPTASE.
 DR PRINTS; PRO0401; SH2DOMAIN.
 DR PRODOM; PD000093; SH2; 1.
 DR SMART; SM00194; PTPC; 1.
 DR SMART; SM00404; PTPC_motif; 1.
 DR SMART; SM00252; SH2; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
 DR PROSITE; PS50056; TYR PHOSPHATASE 2; 1.
 DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 558 558
 SQ SEQUENCE 558 AA; 63773 MW; 2EC76E5D5BAFE310 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 558;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEVFPA 6
 DB 519 KEVYFA 524
 RESULT 73
 Q97KU8 CLOAB PRELIMINARY; PRT; 571 AA.
 AC Q97KU8_1; 571 AA.
 DT 01-OCT-2001 (TRENBLrel. 18, Created)
 DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Diacylglycerol kinase/phosphodiesterase domain (GKDER) containing
 DE protein.
 GN OrderedLocusNames=CAC0818;
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RX DOI=10.1128/JB.183.16.4823-4838.2001;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,
 RA Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;
 RA "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum."
 RL J. Bacteriol. 183:4823-4838 (2001).
 DR EMBL; AE007597; RAK78794.1; -; Genomic_DNA.
 DR PIR; G97000; G97000.
 DR InterPro; IPR011623; 7TMR-DISM_7TM.
 DR InterPro; IPR000160; GGDDEF.
 DR Pfam; PF07695; 7TMR-DISM_7TM; 1.
 DR Pfam; PF00990; GGDDEF; 1.
 DR SMART; SM00267; DUF1; 1.
 DR TIGRfam; TIGR00254; GGDDEF; 1.
 DR PROSITE; PS50887; GGDDEF; 1.
 KW Complete proteome.
 SQ SEQUENCE 571 AA; 66225 MW; 64B51A5D9F5BD23F CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 571;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVFPA 6
 DB 314 KEVYFA 319

RESULT 74
 Q4UGB4 THEAN PRELIMINARY; PRT; 584 AA.
 AC Q4UGB4_1; 584 AA.
 DT 13-SEP-2005 (TRENBLrel. 31, Created)
 DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
 DE Seryl-trna synthetase, putative (EC 6.1.1.11).
 GN ORFNames=TA19195;
 OS Theileria annulata.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
 OC Theileria.
 OX NCBI_TaxID=5874;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ankara isolate clone C9;
 RA Pain A., Renauld H., Murphy L., Harris D.A., Quail M.A., Berriman M.,
 RA Hall N., Barrell B.G.;
 RT "The chromosome 1 sequence of Theileria annulata."
 RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR940347; CAI73875.1; -; Genomic_DNA.
 KW Aminoacyl-tRNA synthetase; Ligase.
 SQ SEQUENCE 584 AA; 66617 MW; 76FEB10EEF7C6691 CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 584;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEVFPA 6
 DB 13 RPFVFA 18
 RESULT 75
 Q7PS12 ANOGA PRELIMINARY; PRT; 615 AA.
 AC Q7PS12_1; 615 AA.
 DT 01-MAR-2004 (TRENBLrel. 26, Created)
 DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE ENSANGP0000017331.
 GN ORFNames=ENSANGG0000021622;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;
 OC Anophelinae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RT "Anopheles gambiae re-annotation."
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAAB01008846; EAA06305.3; -; Genomic_DNA.
 DR SMR; Q7PS12; 1-355.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0005856; C:cytoskeleton; IEA.
 DR GO; GO:0036020; C:membrane; IEA.
 DR GO; GO:0008092; F:cytoskeletal protein binding; IEA.
 DR InterPro; IPR000299; Band_4.1.
 DR InterPro; IPR011174; ERM.
 DR InterPro; IPR011259; ERM_C.
 DR InterPro; IPR000798; Ez/Rad/moesin.
 DR Pfam; PF00373; Band_41; 1.
 DR Pfam; PF00769; ERM; 1.

DR PIRSE; PIRSF002305; ERM; 1.
 DR PRINTS; PRO0661; ERMFAMILY.
 DR SMART; SM00295; B41; 1.
 DR PROSITE; PS00661; FERM 2; 1.
 DR PROSITE; PS00661; FERM 3; 1.
 DR PROSITE; PS00661; FERM 3; 1.
 SQ SEQUENCE 615 AA; 72579 MW; 804168798B4C5DDC CRC64;
 Query Match 90.3%; Score 28; DB 2; Length 615;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 Db 96 KVFVFS 101

Search completed: December 29, 2005, 17:47:28
 Job time : 79.1936 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:12:57 ; Search time 12.9677 Seconds
(without alignments)
44.518 Million cell updates/sec

Title: US-10-009-122-12

Perfect score: 31

Sequence: 1 KVFVFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

PIR 80:*

1: pirl:*

2: pirl:*

3: pirl:*

4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	96.8	397	2 F95352	probable proline d
2	28	90.3	49	2 G83919	hypothetical prote
3	28	90.3	177	2 T16280	hypothetical prote
4	28	90.3	293	2 T29899	hypothetical prote
5	28	90.3	326	2 S76400	hypothetical prote
6	28	90.3	422	2 E82904	hypothetical prote
7	28	90.3	452	2 C88969	protein F15E11.8 [
8	28	90.3	506	2 T05272	fatty acid elongas
9	28	90.3	508	2 A70125	UDP-N-acetylmuram
10	28	90.3	517	2 T02152	probable cytochrom
11	28	90.3	571	2 G97000	diguanylate cyclas
12	28	90.3	1072	2 T37742	serine threonine-p
13	28	90.3	1285	2 B72420	hypothetical prote
14	27	87.1	38	4 S07937	hypothetical prote
15	27	87.1	138	2 C70150	hypothetical prote
16	27	87.1	185	2 I40051	signal peptidase I
17	27	87.1	185	2 C70159	hypothetical prote
18	27	87.1	193	2 S45022	signal peptidase I
19	27	87.1	193	2 G69707	signal peptidase I
20	27	87.1	232	2 A80299	probable membrane
21	27	87.1	274	2 E72329	hypothetical prote
22	27	87.1	298	2 T29189	hypothetical prote
23	27	87.1	321	2 T06845	hypothetical prote
24	27	87.1	349	2 S73198	hypothetical prote
25	27	87.1	358	2 S74431	hypothetical prote
26	27	87.1	358	2 A82218	hypothetical prote
27	27	87.1	370	2 H90559	hypothetical prote
28	27	87.1	408	2 T23285	hypothetical prote
29	27	87.1	409	2 T47754	leucine zipper-con

30	27	87.1	436	2 E96635	hypothetical prote
31	27	87.1	459	2 B72361	conserved hypothet
32	27	87.1	488	2 T20124	hypothetical prote
33	27	87.1	522	2 H66248	protein T23J18.22
34	27	87.1	527	2 S49827	probable membrane
35	27	87.1	581	2 B81107	exodeoxyribonuclea
36	27	87.1	581	2 B81909	exodeoxyribonuclea
37	27	87.1	582	2 I38028	matrix metalloprot
38	27	87.1	582	2 I84471	matrix metalloprot
39	27	87.1	689	2 JC7286	liver-specific org
40	27	87.1	856	2 S30338	hydroxymethylgluta
41	27	87.1	857	2 S44883	ZC262.3 protein -
42	27	87.1	870	2 T31795	hypothetical prote
43	26	83.9	107	2 S56900	probable membrane
44	26	83.9	127	2 G87731	protein W10C8.3 [i
45	26	83.9	171	2 C81280	probable periplasm
46	26	83.9	183	2 T47707	hypothetical prote
47	26	83.9	188	2 A86806	transcription regu
48	26	83.9	203	2 S73449	MG028 homolog B01
49	26	83.9	216	2 G70437	soluble hyarogenas
50	26	83.9	218	2 F86844	hypothetical prote
51	26	83.9	243	2 T22101	hypothetical prote
52	26	83.9	255	2 B81693	conserved hypothet
53	26	83.9	265	2 T44414	hypothetical prote
54	26	83.9	289	2 B81857	probable acetyltra
55	26	83.9	289	2 D81085	HtrB/MsbB family p
56	26	83.9	294	2 A27692	sarcotoxin IIA pre
57	26	83.9	294	2 B36351	sarcotoxin II-2 -
58	26	83.9	297	2 S75656	hypothetical prote
59	26	83.9	323	2 D86216	protein T23G18.8 [
60	26	83.9	324	2 T24424	hypothetical prote
61	26	83.9	337	2 S08459	hypothetical prote
62	26	83.9	344	2 E90564	potassium channel
63	26	83.9	381	2 T34333	hypothetical prote
64	26	83.9	389	2 S68155	ubiquinol-cytochro
65	26	83.9	390	2 T22810	hypothetical prote
66	26	83.9	395	2 T00516	hypothetical prote
67	26	83.9	395	2 D81040	cytochrome c-type
68	26	83.9	395	2 B81986	probable membrane
69	26	83.9	397	2 T46710	multidrug resistan
70	26	83.9	397	2 AE1613	multidrug-efflux t
71	26	83.9	397	2 A11250	hypothetical prote
72	26	83.9	398	2 T44331	conserved hypothet
73	26	83.9	401	2 H69833	probable sugar upt
74	26	83.9	404	2 C95990	ubiquinol-cytochro
75	26	83.9	405	1 CBQFR	conserved hypothet
76	26	83.9	406	2 T43120	hypothetical prote
77	26	83.9	416	2 T23977	probable transmem
78	26	83.9	431	2 B81254	ubiquinol-cytochro
79	26	83.9	432	2 AD3311	probable transmem
80	26	83.9	436	2 A81443	probable MFS trans
81	26	83.9	438	2 H82974	MFS permease/proli
82	26	83.9	443	2 AB2841	probable mfs trans
83	26	83.9	443	2 D97618	probable transport
84	26	83.9	462	2 AF0057	hypothetical prote
85	26	83.9	483	2 T20895	cytochrome oxidase
86	26	83.9	486	2 S50644	proline/betaine tr
87	26	83.9	503	2 AC3296	probable chromatin
88	26	83.9	544	2 T40058	NADH2 dehydrogenas
89	26	83.9	664	2 T14132	probable membrane
90	26	83.9	749	2 S62171	chloride channel p
91	26	83.9	780	2 T02939	beta-adaptin-like
92	26	83.9	841	2 T48508	hypothetical prote
93	26	83.9	884	2 T25205	hypothetical prote
94	26	83.9	903	2 G82516	major merozoite su
95	26	83.9	1772	2 A45532	major merozoite su
96	26	83.9	1785	2 A45546	ribulose biphosph
97	26	83.9	2149	2 C96695	hypothetical prote
98	26	83.9	2948	2 T22664	beta-amyloloid prote
99	25	80.6	33	2 S23094	hypothetical prote
100	25	80.6	42	2 PN0512	hypothetical prote
101	25	80.6	50	2 A69055	Alzheimer's disease
102	25	80.6	57	2 A60045	

103	25	80.6	57	2	F60045	Alzheimer's diseases	176	25	80.6	711	2	C49219	toxin apxIII secre
104	25	80.6	57	2	D60045	Alzheimer's diseases	177	25	80.6	747	2	JH0773	Alzheimer's diseases
105	25	80.6	57	2	E60045	Alzheimer's diseases	178	25	80.6	764	2	T48446	hypothetical prote
106	25	80.6	57	2	G60045	Alzheimer's diseases	179	25	80.6	770	1	QRHUA4	Alzheimer's diseases
107	25	80.6	57	2	B60045	Alzheimer's diseases	180	25	80.6	771	2	AD3126	ATP-dependent DNA
108	25	80.6	78	2	E69969	hypothetical prote	181	25	80.6	771	2	E98161	probable ATP-depen
109	25	80.6	82	2	FQ0438	Alzheimer's diseases	182	25	80.6	841	2	A43254	protein-tyrosine-p
110	25	80.6	114	2	T33289	hypothetical prote	183	25	80.6	901	2	D70116	transcription elon
111	25	80.6	152	2	T06645	hypothetical prote	184	25	80.6	942	2	T20287	hypothetical prote
112	25	80.6	159	2	T30445	hypothetical prote	185	25	80.6	962	2	G86479	FlAD7_6 protein -
113	25	80.6	169	2	T15611	hypothetical prote	186	25	80.6	975	2	T22788	hypothetical prote
114	25	80.6	174	2	T15658	hypothetical prote	187	25	80.6	1016	2	S30236	genome polyprotein
115	25	80.6	177	2	T22603	hypothetical prote	188	25	80.6	1046	2	F71432	hypothetical prote
116	25	80.6	179	2	T17915	hypothetical prote	189	25	80.6	1436	2	S67655	probable membrane
117	25	80.6	191	2	A96765	hypothetical prote	190	25	80.6	1549	2	T13940	ankyrin - fruit fl
118	25	80.6	198	2	H84646	hypothetical prote	191	25	80.6	1683	2	S56811	probable membrane
119	25	80.6	210	2	F64609	conserved hypotet	192	25	80.6	1717	2	T50247	probable helicase
120	25	80.6	210	2	B71906	hypothetical prote	193	25	80.6	1848	2	S37771	ankyrin, erythrocy
121	25	80.6	220	2	T41562	hypothetical wtf p	194	25	80.6	1856	2	B35049	ankyrin 1, erythro
122	25	80.6	222	2	AE3114	hypothetical prote	195	25	80.6	1862	2	I49502	ankyrin - mouse
123	25	80.6	231	2	H85138	hypothetical prote	196	25	80.6	1880	2	A35049	ankyrin 1, erythro
124	25	80.6	237	2	AC1953	ruberythrin limpo	197	25	80.6	1881	1	SJHUK	ankyrin 1, erythro
125	25	80.6	242	2	AC2512	hypothetical prote	198	24	77.4	39	2	S00318	photosystem I chai
126	25	80.6	267	2	A40269	cyclin C - fruit f	199	24	77.4	47	2	G70191	hypothetical prote
127	25	80.6	270	2	H98172	amino acid ABC tra	200	24	77.4	51	2	T07326	hypothetical prote
128	25	80.6	273	2	B85896	probable dimethyl	201	24	77.4	71	2	T26661	hypothetical prote
129	25	80.6	277	2	F91051	probable dimethyl	202	24	77.4	71	2	T26663	hypothetical prote
130	25	80.6	277	2	F75187	sugar abc transpor	203	24	77.4	72	2	T26662	hypothetical prote
131	25	80.6	277	2	D71220	probable sugar tra	204	24	77.4	84	2	S77771	probable ribonucle
132	25	80.6	286	2	H86664	outer membrane lip	205	24	77.4	93	2	A89057	protein K09H11.5 [
133	25	80.6	288	2	T37709	hypothetical prote	206	24	77.4	94	2	F90448	hypothetical prote
134	25	80.6	300	2	T26245	hypothetical prote	207	24	77.4	109	2	S57547	hypothetical prote
135	25	80.6	303	2	T25501	hypothetical prote	208	24	77.4	113	2	PN0091	pullulanase [EC 3.
136	25	80.6	327	2	A83766	hypothetical prote	209	24	77.4	126	2	C96930	glyoxalase I [glyo
137	25	80.6	339	2	A30754	hypothetical prote	210	24	77.4	134	2	G89382	response regulator
138	25	80.6	342	2	A48454	cathepsin B-like c	211	24	77.4	134	2	B83804	small multidrug ex
139	25	80.6	342	2	T09355	hypothetical prote	212	24	77.4	138	2	T25620	hypothetical prote
140	25	80.6	346	2	A83686	hypothetical prote	213	24	77.4	139	2	G69543	conserved hypotet
141	25	80.6	349	2	T26247	hypothetical prote	214	24	77.4	140	2	H81959	patch repair prote
142	25	80.6	352	2	T48903	wax synthase limpo	215	24	77.4	143	2	S20937	photosystem I chai
143	25	80.6	356	2	G72386	conserved hypotet	216	24	77.4	143	2	A88093	hypothetical prote
144	25	80.6	361	2	T34411	hypothetical prote	217	24	77.4	143	2	F85938	hypothetical prote
145	25	80.6	389	2	T20811	hypothetical prote	218	24	77.4	143	2	B65069	hypothetical prote
146	25	80.6	397	2	A96925	uncharacterized co	219	24	77.4	149	2	A13586	xanthine/uracil pe
147	25	80.6	404	2	F87753	protein C43E11.7 [220	24	77.4	156	2	T43957	hypothetical prote
148	25	80.6	406	2	C86904	transporter yxpd [221	24	77.4	161	2	F72861	AcOrf-93 protein -
149	25	80.6	421	2	A99309	membrane transport	222	24	77.4	161	2	T41833	AcWNPV orF93 - Bom
150	25	80.6	428	2	T48008	hypothetical prote	223	24	77.4	167	1	F1SP5	photosystem I chai
151	25	80.6	439	2	E70371	apolipoprotein N-a	224	24	77.4	171	2	C86367	protein F26F24.18
152	25	80.6	497	2	AD3514	D-serine/D-alanine	225	24	77.4	171	2	D86475	unknown protein, 3
153	25	80.6	501	2	C70420	NADH2 dehydrogenas	226	24	77.4	176	2	G90120	hypothetical prote
154	25	80.6	508	2	T05156	probable glucose t	227	24	77.4	177	2	S34499	hypothetical prote
155	25	80.6	516	2	S34525	hypothetical prote	228	24	77.4	177	2	AE1410	hypothetical prote
156	25	80.6	520	2	D90014	hypothetical prote	229	24	77.4	184	2	S23381	signal peptidase I
157	25	80.6	534	2	E82269	conserved hypotet	230	24	77.4	186	1	WMR219	19K globulin precu
158	25	80.6	543	2	S62012	probable membrane	231	24	77.4	186	2	JC4784	alpha-globulin pre
159	25	80.6	568	2	D90525	hypothetical prote	232	24	77.4	188	2	B85481	yaaH protein [simi
160	25	80.6	573	2	AB2401	hypothetical prote	233	24	77.4	188	2	B90630	yaaH protein [simi
161	25	80.6	582	2	F71052	hypothetical prote	234	24	77.4	188	2	E56688	protein yaaH - Esc
162	25	80.6	584	2	F75090	archaeosine trna-r	235	24	77.4	191	2	T09553	conserved hypotet
163	25	80.6	616	2	B90554	lipoprotein limpo	236	24	77.4	197	2	S42129	light-harvesting c
164	25	80.6	632	2	A25784	hypothetical 70K p	237	24	77.4	197	2	T33525	hypothetical prote
165	25	80.6	663	2	T26835	hypothetical prote	238	24	77.4	211	2	T05276	hypothetical prote
166	25	80.6	692	2	C87644	fatty oxidation co	239	24	77.4	211	2	T12013	cuticular protein
167	25	80.6	695	1	A43795	Alzheimer's diseases	240	24	77.4	217	2	T31830	hypothetical prote
168	25	80.6	695	2	A27485	Alzheimer's diseases	241	24	77.4	219	2	C85834	hypothetical prote
169	25	80.6	695	2	S00550	Alzheimer's diseases	242	24	77.4	219	2	A98989	hypothetical prote
170	25	80.6	703	2	H45456	NADH2 dehydrogenas	243	24	77.4	220	2	S62598	cuticular protein
171	25	80.6	707	1	LEEBBV	hemolysin secretio	244	24	77.4	220	2	C98800	conserved hypotet
172	25	80.6	707	1	LEECB	hemolysin secretio	245	24	77.4	231	2	T12012	cuticular protein
173	25	80.6	707	2	A61378	hemolysin I secret	246	24	77.4	236	2	A97233	uncharacterized co
174	25	80.6	707	2	D43599	leukotoxin express	247	24	77.4	239	2	S27789	hypothetical prote
175	25	80.6	708	2	C30169	leukotoxin express	248	24	77.4	250	2	F84977	deoxyribonuclease

QY 1 KVFVFA 6
 Db 10 KVFVFS 15

 RESULT 4
 T29899
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T29899
 R:Nelson, J.; Wohlmann, P.
 A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
 A:Reference number: Z20706
 A:Cross-references: UNIPROT:Q94284; UNIPARC:UPI0000078391; EMBL:U70851; PIDN:AAB09129.1;
 A:Experimental source: strain Bristol N2; clone M02B7
 C:Genetics:
 A:Gene: CESP-M02B7.4
 A:Map position: 4
 A:Intron: 42/3; 150/2; 198/1; 230/3; 276/3

 Query Match 90.3%; Score 28; DB 2; Length 293;
 Best Local Similarity 83.3%; Pred. No. 69;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KVFVFA 6
 Db 258 KVFVFS 263

 RESULT 5
 S76400
 C:Species: Synecocystis sp. (strain PCC 6803)
 A:Variety: PCC 6803
 C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C:Accession: S76400
 R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 3, 109-136, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
 S.
 A:Reference number: S74322; MUID:97061201; PMID:8905231
 A:Accession: S76400
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-336 <KAN>
 A:Cross-references: UNIPROT:P74429; UNIPARC:UPI00000C1025; EMBL:D90915; GB:AB001339; NID
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

 Query Match 90.3%; Score 28; DB 2; Length 326;
 Best Local Similarity 83.3%; Pred. No. 76;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KVFVFA 6
 Db 104 KVFVFS 109

 RESULT 6
 E82904
 C:Species: Ureaplasma urealyticum
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: E82904
 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 A:Submitted to GenBank, February 2000

A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
 A:Reference number: A82870
 A:Accession: E82904
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-422 <GLA>
 A:Cross-references: UNIPARC:UPI00000C1C1F; GB:AE002130; GB:AF222894; NID:G6899302; PIDN:
 A:Experimental source: serovar 3; biovar 1
 C:Genetics:
 A:Gene: UU329
 A:Genetic code: SGC3

 Query Match 90.3%; Score 28; DB 2; Length 422;
 Best Local Similarity 83.3%; Pred. No. 96;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KVFVFA 6
 Db 208 KVFVFA 213

 RESULT 7
 C88969
 C:Species: Caenorhabditis elegans
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
 C:Accession: C88969
 R:anonymous, The C. elegans Sequencing Consortium.
 A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
 A:Reference number: A75000; MUID:99069613; PMID:9851916
 A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_ele
 A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
 A:Accession: C88969
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-452 <STO>
 A:Cross-references: UNIPROT:O44595; UNIPARC:UPI0000075D10; GB:chr_V; PIDN:AAB94205.1; PI
 C:Genetics:
 A:Gene: P15B11.8
 A:Map position: 5

 Query Match 90.3%; Score 28; DB 2; Length 452;
 Best Local Similarity 83.3%; Pred. No. 1e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 QY 1 KVFVFA 6
 Db 291 RKFVFA 296

 RESULT 8
 T05272
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T05272
 R:Bevan, M.; Terry, N.; Ardiles, W.; Buysaert, C.; Dasseville, R.; De Clerck, R.; De
 ewes, H.W.; Mayer, K.F.X.; Schueller, C.
 A:Reference number: Z15406
 A:Submitted to the Protein Sequence Database, September 1998
 A:Accession: T05272
 A:Molecule type: DNA
 A:Residues: 1-506 <BEV>
 A:Cross-references: UNIPROT:Q38860; UNIPARC:UPI0000047264; EMBL:AL023094
 A:Experimental source: cultivar Columbia; BAC clone T4L20
 C:Genetics:
 A:Map position: 4
 A:Note: T4L20.100
 C:Superfamily: very-long-chain 3-ketoacyl-CoA synthase

 Query Match 90.3%; Score 28; DB 2; Length 506;

Best Local Similarity 83.3%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFFA 6
DB 356 KFLFFA 361

RESULT 9
A70125
UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase (murE) homolog - Lyme
C;Species: Borrelia burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 05-Oct-2004
R;Accession: A70125
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A;Reference number: A70100; MUID:98065943; PMID:9403685
A;Accession: A70125
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-508 <KLE>
A;Cross-references: UNIPROT:O51219; UNIPARC:UPI00000573B3; GB:AE001130; GB:AE000783; NID
A;Experimental source: strain B31
C;Superfamily: UDP-N-acetylmuramate-alanine ligase

Query Match 90.3%; Score 28; DB 2; Length 508;
Best Local Similarity 83.3%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFFA 6
DB 41 RFVFFA 46

RESULT 10
T02192
probable cytochrome P450 At2g46950 [imported] - Arabidopsis thaliana
N;Alternate names: cytochrome P450 homolog F14M4.22
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
R;Accession: T02192; C84909
R;Roundley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ro
submitted to the EMBL Data Library, September 1998
A;Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.
A;Reference number: Z14609
A;Accession: T02192
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-517 <ROU>
A;Cross-references: UNIPROT:O80729; UNIPARC:UPI00000A147A; EMBL:AC004411; NID:g35222932;
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Roundley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-517 <STO>
A;Cross-references: UNIPARC:UPI00000A147A; GB:AE002093; NID:g35222946; PIDN:AAC34228.1; G
C;Genetics:
A;Gene: At2g46950; F14M4.22
A;Map position: 2
A;Introns: 95/1; 169/3; 252/2; 374/3
C;Superfamily: human cytochrome P450 CYP4B1; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;321-485/Domain: cytochrome P450 homology <P45>

F;463/Binding site: heme iron (Cys) (axial ligand) #status predicted
Query Match 90.3%; Score 28; DB 2; Length 517;
Best Local Similarity 83.3%; Pred. No. 1.2e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFFA 6
DB 123 KVFVFFS 128

RESULT 11
G97000
diguanylate cyclase/phosphodiesterase domain (GGDEF) containing protein [imported] - Clo
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
R;Accession: G97000
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: G97000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-571 <KUR>
A;Cross-references: UNIPROT:Q97KU8; UNIPARC:UPI00000C9FBF; GB:AE001437; PIDN:AAK78794.1
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0818

Query Match 90.3%; Score 28; DB 2; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.3e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFFA 6
DB 314 KFMFFA 319

RESULT 12
T37742
serine threonine-protein kinase - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
R;Accession: T37742
R;Rieger, M.; Wood, V.; Rajandream, M.A.; Barrett, B.G.
submitted to the EMBL Data Library, January 1999
A;Reference number: Z21743
A;Accession: T37742
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1072 <RIE>
A;Cross-references: UNIPROT:O94537; UNIPARC:UPI0000069E8D; EMBL:AL035248; PIDN:CAA22846
A;Experimental source: strain 972h-; cosmid c167
C;Genetics:
A;Gene: spaci67.01; SPDB:SPAC167.01
A;Map position: 1
A;Introns: 1015/3

Query Match 90.3%; Score 28; DB 2; Length 1072;
Best Local Similarity 83.3%; Pred. No. 2.3e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFFA 6
DB 13 KVFVFFS 18

RESULT 13
B72420
hypothetical protein TM0088 - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C/Accession: B72420
 R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A/Reference number: A72200; MUID:99287316; PMID:10360571
 A/Accession: B72420
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-1285 <ARN>
 A/Cross-references: UNIPROT:Q9WXU3; UNIPARC:UPI00000D3A9B; GB:AE001695; GB:AE000512; NID
 A/Experimental source: strain MSB8
 C/Genetics:
 A/Gene: TW0088

Query Match 90.3%; Score 28; DB 2; Length 1285;
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 |||||
 Db 341 KVFVFA 346

RESULT 14
 S07937
 hypothetical protein atpH 5'-region - Euglena gracilis chloroplast (fragment)
 C/Species: chloroplast Euglena gracilis
 C/Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 09-Jul-2004
 C/Accession: S07937
 R/Passavant, C.W.; Hallick, R.B.
 Plant Mol. Biol. 4, 347-354, 1985
 A/Title: Location, nucleotide sequence and expression of the proton-translocating subuni
 A/Reference number: S07400
 A/Accession: S07937
 A/Molecule type: DNA
 A/Residues: 1-38 <PAS>
 A/Cross-references: UNIPROT:Q32187; UNIPARC:UPI00000956CE; EMBL:M16844; NID:g336867; PID
 C/Comment: This is the hypothetical translation of a sequence that was not reported as a
 C/Genetics:
 A/Gene: chloroplast
 C/Keywords: chloroplast

Query Match 87.1%; Score 27; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFF 5
 |||||
 Db 18 KVFVFF 22

RESULT 15
 C70150
 hypothetical protein BB0404 - Lyme disease spirochete
 C/Species: Borrelia burgdorferi (Lyme disease spirochete)
 C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C/Accession: C70150
 R/Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 i Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A/Authors: Smith, H.O.; Venter, J.C.
 A/Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
 A/Reference number: A70100; MUID:98065943; PMID:9403685
 A/Accession: C70150
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-138 <KLE>
 A/Cross-references: UNIPROT:O51365; UNIPARC:UPI000005747C; GB:AE001146; GB:AE000783; NID
 A/Experimental source: strain B31

Query Match 87.1%; Score 27; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFF 5
 |||||
 Db 7 KVFVFF 11

RESULT 18
 S45022

C/Superfamily: Borrelia burgdorferi hypothetical protein BB0404
 Query Match 87.1%; Score 27; DB 2; Length 138;
 Best Local Similarity 66.7%; Pred. No. 57;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFA 6
 |||||
 Db 40 KVFVFA 45

RESULT 16
 I40051
 signal peptidase I (EC 3.4.21.89) - Bacillus amyloliquefaciens
 N/Alternate names: leader peptidase
 C/Species: Bacillus amyloliquefaciens
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I40051; S38885
 R/Tomlinson, I.M.; Cook, G.P.; Carter, N.P.; Elawarapu, R.; Smith, S.; Walter, G.; Bulu
 Hum. Mol. Genet. 3, 853-860, 1994
 A/Title: Human immunoglobulin VH and D segments on chromosomes 15q11.2 and 16p11.2.
 A/Reference number: 137619; MUID:95038735; PMID:7951227
 A/Accession: I40051
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: DNA
 A/Residues: 1-185 <RES>
 C/Cross-references: UNIPROT:P41026; UNIPARC:UPI000012E452; EMBL:Z27458; NID:g429069; PID
 C/Genetics:
 A/Gene: sipa
 A/Start codon: TTG
 C/Superfamily: signal peptidase I sips
 C/Keywords: hydrolase; serine proteinase

Query Match 87.1%; Score 27; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFF 5
 |||||
 Db 172 KVFVFF 176

RESULT 17
 C70199
 hypothetical protein BB0796 - Lyme disease spirochete
 C/Species: Borrelia burgdorferi (Lyme disease spirochete)
 C/Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
 C/Accession: C70199
 R/Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 i Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
 Nature 390, 580-586, 1997
 A/Authors: Smith, H.O.; Venter, J.C.
 A/Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
 A/Reference number: A70100; MUID:98065943; PMID:9403685
 A/Accession: C70199
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-185 <KLE>
 A/Cross-references: UNIPROT:O51736; UNIPARC:UPI00000575FE; GB:AE001178; GB:AE000783; NID
 A/Experimental source: strain B31

Query Match 87.1%; Score 27; DB 2; Length 185;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVFVFF 5
 |||||
 Db 7 KVFVFF 11

RESULT 18
 S45022

signal peptidase I (EC 3.4.21.89) - Bacillus amyloliquefaciens

N;Alternate names: leader peptidase

C;Species: Bacillus amyloliquefaciens

C;Date: 06-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S59966; S45022

R;Hoang, V.; Hofemeister, J.

Biochim. Biophys. Acta 1269, 64-68, 1995

A;Title: Bacillus amyloliquefaciens possesses a second type I signal peptidase with exte

A;Reference number: S59965; MUID:96049527; PMID:7578273

A;Accession: S59966

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-193 <HO2>

A;Cross-references: UNIPROT:P41025; UNIPARC:UPI000012E454; EMBL:Z33640; NID:9562273; PID

C;Genetics:

A;Start codon: TTG

C;Superfamily: signal peptidase I sips

C;Keywords: hydrolase; serine proteinase; transmembrane protein

Query Match 87.1%; Score 27; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 78;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5

Db 180 KPVFF 184

RESULT 19

G69707 signal peptidase I sipT - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: G69707

R;Kunzt, P.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertet

C.; Bron, S.; Bouillett, S.; Bruchsi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Toato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yaeumoto, K.; Yata, K.; Yoshida, K

A;Winters, Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G69707

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-193 <KUN>

A;Cross-references: UNIPROT:P71013; UNIPARC:UPI000006032F; GB:Z99111; GB:AL009126; NID:9

A;Experimental source: strain 168

C;Genetics:

A;Gene: sipT

C;Superfamily: signal peptidase I sips

Query Match 87.1%; Score 27; DB 2; Length 193;

Best Local Similarity 100.0%; Pred. No. 78;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5

Db 180 KPVFF 184

RESULT 20

AH0299

probable membrane protein YPO2455 [imported] - Yersinia pestis (strain CO92)

C;Species: Yersinia pestis

C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C;Accession: AH0299

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,

Nature 413, 523-527, 2001

A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AH0299

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-232 <KUR>

A;Cross-references: UNIPROT:Q8ZDV0; UNIPARC:UPI000000CD3B; GB:AL590842; PIDN:CAC91260.1

C;Genetics:

A;Gene: YPO2455

Query Match 87.1%; Score 27; DB 2; Length 232;

Best Local Similarity 100.0%; Pred. No. 92;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5

Db 19 KPVFF 23

RESULT 21

E72329

hypothetical protein TM0818 - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: E72329

R;Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: E72329

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-274 <ARN>

A;Cross-references: UNIPROT:Q9WZS5; UNIPARC:UPI000000D3985; GB:AE001749; GB:AE000512; NI

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM0818

Query Match 87.1%; Score 27; DB 2; Length 274;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVFF 5

Db 260 KPVFF 264

RESULT 22

T29189

hypothetical protein C55C3.2 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T29189

R;Woessene, J.; Steillyes, L.

submitted to the EMBL Data Library, April 1996

A;Description: The sequence of C. elegans cosmid C55C3.

A;Reference number: Z20585

A;Accession: T29189

A;Status: preliminary; translated from GB/EMBL/DBDB

A;Molecule type: DNA

A;Residues: 1-298 <WOE>

A;Cross-references: UNIPROT:Q18868; UNIPARC:UPI0000074B15; EMBL:U53335; PIDN:AAA96172.1

A;Experimental source: strain Bristol N2; clone C55C3

C;Genetics:

A;Gene: C55C3.2

A:Map position: 4
A:introns: 35/1; 64/3; 212/3; 260/1

Query Match 87.1%; Score 27; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
|||||
DB 85 KVFVF 89

RESULT 23

T06845

hypothetical protein ycf39 - Cyanophora paradoxa cyanelle

C:Species: Cyanelle Cyanophora paradoxa

C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004

C:Accession: T06845

R:Stewart, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.

submitted to the EMBL Data Library, July 1995

A:Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.

A:Reference number: Z15840

A:Accession: T06845

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-321 <STI>

A:Cross-references: UNIPROT:P48279; UNIPARC:UPI000013A4A8; EMBL:U30821; NID:g1016083; PI

A:Experimental source: cv. strain Pringsheim LB555

C:Genetics:

A:Gene: ycf39

A:Genome: cyanelle

C:Keywords: cyanelle

Query Match 87.1%; Score 27; DB 2; Length 321;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||:
DB 104 KFIFFS 109

RESULT 24

S73198

hypothetical protein 349 - red alga (Porphyra purpurea) chloroplast

C:Species: chloroplast Porphyra purpurea

C>Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C:Accession: S73198

R:Keith, M.; Munholland, J.

Plant Mol. Biol. Rep. 13, 333-335, 1995

A:Title: Complete nucleotide sequence of the Porphyra purpurea chloroplast genome.

A:Reference number: S73108

A:Accession: S73198

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-349 <REI>

A:Cross-references: UNIPROT:P51277; UNIPARC:UPI000013A78F; EMBL:U38804; NID:g1276652; PI

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995

C:Genetics:

A:Genome: chloroplast

C:Superfamily: leucine zipper-containing protein AT103

C:Keywords: chloroplast

Query Match 87.1%; Score 27; DB 2; Length 349;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||:
DB 156 KFIFA 161

RESULT 25

S74431

hypothetical protein all1214 - Synecocystis sp. (strain PCC 6803)

C:Species: Synecocystis sp.

A:Variety: PCC 6803

C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S74431

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.,

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis

8.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S74431

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-358 <KAN>

A:Cross-references: UNIPROT:P72584; UNIPARC:UPI00000C0997; EMBL:D90899; GB:AB001339; NID

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: leucine zipper-containing protein AT103

Query Match 87.1%; Score 27; DB 2; Length 358;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||:
DB 165 KFIFA 170

RESULT 26

AE2218

hypothetical protein alr3300 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: AE2218

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2218

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-358 <KUR>

A:Cross-references: UNIPROT:O8VEZ2; UNIPARC:UPI00000CE73B; GB:BA0000019; PIDN:BAE74999.1;

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr3300

C:Superfamily: leucine zipper-containing protein AT103

Query Match 87.1%; Score 27; DB 2; Length 358;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||:
DB 165 KFIFA 170

RESULT 27

H90559

hypothetical protein MYPV 3840 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C:Species: Mycoplasma pulmonis

C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C:Accession: H90559

R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.,

Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A:Reference number: A99512; MUID:21267165; PMID:11353084

A:Accession: H90559

A>Status: preliminary

A:Molecule type: DNA

A;Residues: 1-370 <KUR>
A;Cross-references: UNIPROT:Q98QH7; UNIPARC:UPI00000C807C; GB:AL445566; PID:g14089798; P
A;Experimental source: strain UAB Crip
C;Genetics:
A;Gene: MYPU 3840
A;Genetic code: SGC3

Query Match 87.1%; Score 27; DB 2; Length 370;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
|::|||
Db 23 KYIFFA 28

RESULT 28

T23285
hypothetical protein K03D7.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23285
R;Matthews, L.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19721
A;Accession: T23285
A;Status: preliminary; translated from GB/EMBL/DDBY
A;Molecule type: DNA
A;Residues: 1-408 <WIL>
A;Cross-references: UNIPROT:O45653; UNIPARC:UPI00000610BB; EMBL:Z81562; PIDN:CAB04555.1;
A;Experimental source: clone K03D7
C;Genetics:
A;Gene: CESP:K03D7.8
A;Map position: 5
A;Introns: 117/3; 304/1

Query Match 87.1%; Score 27; DB 2; Length 408;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|::|||
Db 243 KFVFF 247

RESULT 29

T47754
leucine zipper-containing protein AT103 - Arabidopsis thaliana
N;Alternate names: FNIL34 protein homolog; protein F24I3.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47754; S71218
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24475
A;Accession: T47754
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <NYA>
A;Cross-references: UNIPROT:Q9MK4; UNIPARC:UPI00000A741A; EMBL:AL138655
A;Experimental source: cultivar Columbia; BAC clone F24I3
R;Zheng, C.C.; O'Neill, S.D.
submitted to the EMBL Data Library, October 1995
A;Description: Molecular analysis of a novel phytochrome-regulated Phorbis cDNA and its
A;Reference number: S71218
A;Accession: S71218
A;Molecule type: mRNA
A;Residues: 37-156, 'S', 158-409 <ZHE>
A;Cross-references: UNIPARC:UPI00000A9BBC; EMBL:U38232; NID:g10333194; PID:g10333195
C;Genetics:
A;Gene: AT103
A;Map position: 3
A;Introns: 158/3; 180/2; 289/3; 322/3

A;Note: F24I3.20
C;Superfamily: leucine zipper-containing protein AT103

Query Match 87.1%; Score 27; DB 2; Length 409;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
|::|||
Db 210 KFIFYA 215

RESULT 30

E96635
hypothetical protein T7P1.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E96635
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
C.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-436 <STO>
A;Cross-references: UNIPROT:Q9C954; UNIPARC:UPI00000483C7; GB:AE005173; NID:G6751689; P
C;Genetics:
A;Gene: T7P1.13
A;Map position: 1

Query Match 87.1%; Score 27; DB 2; Length 436;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFFA 6
|::|||
Db 185 KYIFFA 190

RESULT 31

B72361
conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: B72361
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.N.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: B72361
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-459 <ARN>
A;Cross-references: UNIPROT:Q9WZ33; UNIPARC:UPI00000C13F0; GB:AE001731; GB:AE0000512; N
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0563

Query Match 87.1%; Score 27; DB 2; Length 459;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5

```

Db          210 KFVFF 214
|||||
RESULT 32
T20124
hypothetical protein C50H2.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T20124
R:McMurray, A.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19226
A:Accession: T20124
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Reference number: Z19226
A:Accession: T20124
A:Molecule type: DNA
A:Residues: 1-488 <WIL>
A:Cross-references: UNIPROT:Q18760; UNIPARC:UPI000007F0DB; EMBL:Z73971; PIDN:CAA98250.1;
A:Experimental source: clone C50H2
C:Genetics:
A:Gene: CESP:C50H2.2
A:Map position: 5
A:Introns: 67/2; 107/3; 138/3; 180/3; 337/2; 391/3; 445/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C50H2.2

Query Match      87.1%; Score 27; DB 2; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
DB 203 KFVFF 207
|||||

RESULT 33
H86248
protein T23J18.22 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86248
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-522 <STO>
A:Cross-references: UNIPROT:Q9LPY0; UNIPARC:UPI00000A13DA; GB:AE005172; NID:G6554189; PI
C:Genetics:
A:Gene: T23J18.22
A:Map position: 1

Query Match      87.1%; Score 27; DB 2; Length 522;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
DB 257 KFVFF 261
|||||

RESULT 34
S49827
probable membrane protein YDR072c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D4405; hypothetical protein YD8554.05c

```

```

C:Species: Saccharomyces cerevisiae
C:Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: S49827; S48758; S55820; S67889; S67888
R:Richards, C.; Harris, D.E.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49823
A:Accession: S49827
A:Molecule type: DNA
A:Residues: 1-527 <RIC>
A:Cross-references: UNIPROT:P38954; UNIPARC:UPI000012D81A; EMBL:Z46796; NID:G577794; PIL
R:Coster, F.; Jonniaux, J.L.; Goffeau, A.
submitted to the EMBL Data Library, October 1994
A:Reference number: S48758
A:Accession: S48758
A:Molecule type: DNA
A:Residues: 1-524 <COS>
A:Cross-references: UNIPARC:UPI0000168B70; EMBL:X82086; NID:G558241; PID:G558243
R:Coster, F.; Jonniaux, J.L.; Goffeau, A.
Yeast 11, 673-679, 1995
A:Title: Analysis of a 32.8 kb segment of yeast chromosome IV reveals 21 open reading fr
A:Reference number: S55819; MUID:96093910; PMID:7483840
A:Accession: S55820
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-525 <COW>
A:Cross-references: UNIPARC:UPI000017B30A; EMBL:X82086
R:Foury, F.; Jonniaux, J.L.; Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67889
A:Accession: S67889
A:Molecule type: DNA
A:Residues: 1-524 <FOU>
A:Cross-references: UNIPARC:UPI0000168B70; EMBL:Z74368; MIPS:YDR072c
A:Experimental source: strain S288C
R:Bloecker, H.; Brandt, F.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67587
A:Accession: S67888
A:Molecule type: DNA
A:Residues: 417-527 <BLO>
A:Cross-references: UNIPARC:UPI000017B30B; EMBL:Z74368; MIPS:YDR072c
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:SYR4
A:Cross-references: SGD:S0002479; MIPS:YDR072c
A:Map position: 4R
C:Keywords: transmembrane protein
F:24-40/Domain: transmembrane #status predicted <TM1>
F:101-117/Domain: transmembrane #status predicted <TM2>
F:153-169/Domain: transmembrane #status predicted <TM3>
F:194-210/Domain: transmembrane #status predicted <TM4>
F:294-310/Domain: transmembrane #status predicted <TM5>
F:462-478/Domain: transmembrane #status predicted <TM6>

Query Match      87.1%; Score 27; DB 2; Length 527;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFVFF 6
DB 62 KPAPFA 67
|||||

RESULT 35
B81107
exodeoxyribonuclease V, alpha chain NMB1233 [imported] - Neisseria meningitidis (strain
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81107
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Masiagnani, V.; Pizza, M.
Science 287, 1809-1815, 2000

```

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V
A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A;Reference number: AB1000; MUID:20175755; PMID:10710307
A;Accession: B81107
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-581 <TET>
A;Cross-references: UNIPROT:Q9JZ93; UNIPARC:UPI000000C4671; GB:AE0020471; GB:AE002098; NID
A;Experimental source: serogroup B, strain MC58
C;Genetics:
C;Superfamily: exodeoxyribonuclease V 67K chain

Query Match 87.1%; Score 27; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
|||||
546 KFVFF 550

Db

RESULT 36
B81909
exodeoxyribonuclease V alpha subunit NMA1401 [imported] - *Neisseria meningitidis* (strain
C;Species: *Neisseria meningitidis*
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B81909
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R;Holroyd, S.; Jegels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
A;Reference number: AB1775; MUID:20222556; PMID:10761919
A;Accession: B81909
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-581 <PAR>
A;Cross-references: UNIPROT:Q9JUB9; UNIPARC:UPI000000C4AB0; GB:AL162755; GB:AL157959; NID
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: raeD; NMA1401
C;Superfamily: exodeoxyribonuclease V 67K chain

Query Match 87.1%; Score 27; DB 2; Length 581;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
|||||
546 KFVFF 550

Db

RESULT 37
I38028
matrix metalloproteinase 14 (EC 3.4.24.-) membrane type precursor - human
N;Alternate names: matrix metalloproteinase MMP14; membrane type matrix metalloproteinase
C;Species: *Homo sapiens* (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: I38028; G03274; I38046; S78011; S45341; S71384
R;Will, H.; Hinzmann, B.
Eur. J. Biochem. 231, 602-608, 1995
A;Title: cDNA sequence and mRNA tissue distribution of a novel human matrix metalloprote
A;Reference number: I38028; MUID:95377289; PMID:7649159
A;Accession: I38028
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-582 <WILL>
A;Cross-references: UNIPROT:P50281; UNIPARC:UPI00000048136; EMBL:Z48481; NID:G963053; PII
R;Luo, G.
submitted to the EMBL Data Library, November 1995
A;Reference number: H00963
A;Accession: G02274
A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA
A;Residues: 1-582 <LUO>
A;Cross-references: UNIPARC:UPI00000048136; EMBL:U41078; NID:g1127836; PIDN:AAA83770.1;
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset,
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995
A;Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal c
A;Reference number: I38046; MUID:95224014; PMID:7708715
A;Accession: I38046
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-7,'S',9-582 <OKA>
A;Cross-references: UNIPARC:UPI000003096F; EMBL:X83535; NID:g804993; PIDN:CAA58519.1; P
R;Seiki, M.
submitted to the EMBL Data Library, January 1994
A;Reference number: S78011
A;Accession: S78011
A;Molecule type: mRNA
A;Residues: 1-7,'S',9-337,'K',339-582 <SEI>
A;Cross-references: UNIPARC:UPI000003DC76; EMBL:D26512; NID:g793762; PIDN:BAA05519.1; P
R;Sato, H.; Takino, T.; Okada, Y.; Cao, J.; Shingawa, A.; Yamamoto, E.; Seiki, M.
Nature 370, 61-65, 1994
A;Title: A matrix metalloproteinase expressed on the surface of invasive tumour cells.
A;Reference number: S45341; MUID:94286011; PMID:8015608
A;Accession: S45341
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-7,'S',9-188,'R',190,'A',192-267,'K',269-272,'HY',275,'P',277-285,'KQ',288
A;Cross-references: UNIPARC:UPI0000157586; EMBL:D26512
R;Sato, H.; Kinoshita, T.; Takino, T.; Nakayama, K.; Seiki, M.
FEBS Lett. 393, 101-104, 1996
A;Title: Activation of a recombinant membrane type 1-matrix metalloproteinase (MT1-MMP)
A;Reference number: S71384; MUID:96397540; PMID:8804434
A;Accession: S71384
A;Molecule type: protein
A;Residues: 112-116 <SAW>
A;Cross-references: UNIPARC:UPI0000175D8E
C;Genetics:
A;Gene: GDB:MMP14; MT1-MMP
A;Cross-references: GDB:375731; OMIM:600754
A;Map position: 14q11-14q12
C;Superfamily: interstitial
C;Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
P;1-23/Domain: signal sequence #status predicted <SIG>
P;24-97/Domain: activation peptide #status predicted <PRO>
P;61-284/Domain: matrix metalloproteinase homology <MMP>
P;98-582/Product: matrix metalloproteinase 14 membrane type #status predicted <MAT>
P;285-313/Domain: hinge #status predicted <HNG>
P;314-508/Domain: hemopexin repeat homology <PXN>
P;539-562/Domain: transmembrane #status predicted <TM>
P;93,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
P;130/Binding site: carboxylate (Asn) (covalent) #status predicted
P;239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
P;240/Active site: Glu #status predicted
P;319-508/Disulfide bonds: #status predicted

Query Match 87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
|||||
378 KFVFF 382

Db

RESULT 38
I84471
matrix metalloproteinase (EC 3.4.24.-) membrane type precursor - rat
N;Alternate names: membrane-type metalloproteinase
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I84471; I61946
R;Okada, A.; Bellocq, J.P.; Rouyer, N.; Chenard, M.P.; Rio, M.C.; Chambon, P.; Basset,
Proc. Natl. Acad. Sci. U.S.A. 92, 2730-2734, 1995

A>Title: Membrane-type matrix metalloproteinase (MT-MMP) gene is expressed in stromal cells
A:Reference number: 138046; MUID:95224014; PMID:7708715
A:Accession: I84471
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-582 <RES>
A:Cross-references: UNIPROT:Q10739; UNIPARC:UPI0000030970; EMBL:X83537; NID:g805012; PID: A161946
A:Accession: I61946
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-67, 'M', '69-254', 'A', '256-582 <RES>
A:Cross-references: UNIPARC:UPI00001679D1; EMBL:X91785; NID:g1001926; PIDN:CAA62897.1; F: C:Genetics:
A:Gene: mt-mmp
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:1-33/Domain: signal sequence #status predicted <SIG>
F:24-97/Domain: activation peptide #status predicted <PRO>
F:61-284/Domain: matrix metalloproteinase homology <MPP>
F:313-508/Domain: hemopexin repeat homology <PXN>
F:93,239,243,249/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status predicted
F:239,243,249/Binding site: zinc, catalytic (His) (active) #status predicted
F:240/Active site: Glu #status predicted

Query Match 87.1%; Score 27; DB 2; Length 582;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|||
Db 378 KFVFF 382

RESULT 39
JC7286
liver-specific organic anion transporter-1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C:Accession: JC7286
R:Ogura, K.; Choudhuri, S.; Klaassen, C.D.
Biochem. Biophys. Res. Commun. 272, 563-570, 2000
A>Title: Full-length cDNA cloning and genomic organization of the mouse liver-specific organic anion transporter-1
A:Reference number: JC7286
A:Accession: JC7286
A:Molecule type: mRNA
A:Residues: 1-689 <OGU>
A:Cross-references: UNIPROT:Q9JUL3; UNIPARC:UPI0000023434; DDBJ:AB031959
C:Genetics:
A:Gene: lst-1
C:Keywords: glycolysis; transmembrane protein

Query Match 87.1%; Score 27; DB 2; Length 689;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|||
Db 404 KFVFF 408

RESULT 40
S30338
hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) - German cockroach
C:Species: Blattella germanica (German cockroach)
C:Date: 02-Dec-1993 #sequence_revision 03-Aug-1995 #text_change 27-Oct-2003
C:Accession: S30338
R:Martinez-Gonzalez, J.; Buesa, C.; Piulachs, M.D.; Belles, X.; Hegardt, F.G.
Eur. J. Biochem. 213, 233-241, 1993
A>Title: Molecular cloning, developmental pattern and tissue expression of 3-hydroxy-3-methylglutaryl-CoA reductase
A:Reference number: S30338; MUID:93238692; PMID:8477698
A:Accession: S30338
A:Molecule type: mRNA
A:Residues: 1-856 <MAR>

A:Cross-references: UNIPARC:UPI0000174EF6
C:Superfamily: hydroxymethylglutaryl-CoA (HMG-CoA) reductase
C:Keywords: coenzyme A; NADP; oxidoreductase

Query Match 87.1%; Score 27; DB 2; Length 856;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|||
Db 360 KFVFF 364

RESULT 41
S44883
ZC262.3 protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S44883
R:Anderson, K.
submitted to the EMBL Data Library, September 1993
A:Description: Sequence of the C. elegans cosmid ZC262.
A:Reference number: S44818
A:Accession: S44883
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-857 <AND>
A:Cross-references: UNIPROT:P34595; UNIPARC:UPI0000179325; EMBL:L23647; NID:g388612; PID: C:Genetics:
A:Introns: 72/2; 145/1; 191/1; 263/3; 297/1; 363/2; 403/2; 448/2; 523/2; 563/2; 613/2; 7
C:Superfamily: Caenorhabditis elegans ZC262.3 protein

Query Match 87.1%; Score 27; DB 2; Length 857;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|||
Db 87 KFVFF 91

RESULT 42
T31795
hypothetical protein R02F11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31795
R:Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid R02F11.
A:Reference number: Z21087
A:Accession: T31795
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-870 <DAV>
A:Cross-references: UNIPROT:O16363; UNIPARC:UPI000016423C; EMBL:AF016439; PIDN:AAB65898.
A:Experimental source: strain Bristol N2; clone R02F11
C:Genetics:
A:Gene: CESP:R02F11.2
A:Map position: 5
A:Introns: 44/2; 116/2; 164/3; 265/2; 335/2; 380/1; 419/3; 475/1; 582/2; 643/3; 6

Query Match 87.1%; Score 27; DB 2; Length 870;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 6
|||
Db 2 RFIFPA 7

RESULT 43
SS6900

probable membrane protein YJL119c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J0738
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S56900
R;Cziepluch, C.; Kordes, E.; Fajol, A.; Jauniaux, J.C.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56891
A;Accession: S56900
A;Molecule type: DNA
A;Residues: 1-107 <CZI>
A;Cross-references: UNIPROT:P47021; UNIPARC:UPI000013B5B8; EMBL:Z49394; NID:g1008309; P
C;Genetics:
A;Gene: MIPS:YJL119c
A;Cross-references: SGD:S0003655
A;Map position: 10L
C;Superfamily: Saccharomyces probable membrane protein YJL119c
C;Keywords: transmembrane protein

Query Match 83.9%; Score 26; DB 2; Length 107;
Best Local Similarity 83.3%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
|||
Db 102 KPFFFA 107

RESULT 44
G87731
protein W10C8.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: G87731
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/c_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G87731
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-127 <STO>
A;Cross-references: UNIPARC:UPI0000164023; GB:chr_I; PIDN:AAB97593.1; PID:g2804486; GSP
C;Genetics:
A;Gene: W10C8.3
A;Map position: 1

Query Match 83.9%; Score 26; DB 2; Length 127;
Best Local Similarity 80.0%; Pred. No. 89;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
|||
Db 83 KPFF 87

RESULT 45
C81280
probable periplasmic cytochrome C Cj1358c [imported] - Campylobacter jejuni (strain NCTC
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: C81280
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: C81280
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-171 <PAR>

Query Match 83.9%; Score 26; DB 2; Length 188;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
|||
Db 170 KPFF 174

RESULT-48

A;Cross-references: UNIPROT:Q9PMU1; UNIPARC:UPI00000C1EDC; GB:AL139078; GB:AL111168; NI
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1358c
C;Superfamily: denitrification system component NapC/NirT(membrane-bound tetraheme cyto
Query Match 83.9%; Score 26; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
|||
Db 24 FVFFA 28

RESULT 46
T47707
hypothetical protein F116.90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47707
R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24473
A;Accession: T47707
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-183 <BEN>
A;Cross-references: UNIPROT:Q9M054; UNIPARC:UPI00000A21B5; EMBL:AL161667
A;Experimental source: cultivar Columbia; BAC clone F116
C;Genetics:
A;Map position: 3
A;Introns: 70/3
A;Note: F116.90

Query Match 83.9%; Score 26; DB 2; Length 183;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
|||
Db 18 FVFFA 22

RESULT 47
A86806
transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86806
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarre, K.; Weissenbach, J.; Ehr
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: A86806
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-188 <STO>
A;Cross-references: UNIPROT:Q9CFL8; UNIPARC:UPI00000C6A3D; GB:AE005176; PID:g12724440;
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yohc

Query Match 83.9%; Score 26; DB 2; Length 188;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
|||
Db 170 KPFF 174

RESULT-48

S73449
 MG028 homolog B01_orf203 - Mycoplasma pneumoniae (strain ATCC 29342)
 C:Species: Mycoplasma pneumoniae
 A:Variety: ATCC 29342
 C:Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 05-Oct-2004
 C:Accession: S73449
 R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkle, E.; Li, B.C.; Herrmann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996
 A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
 A:Reference number: S73327; MUID:97105885; PMID:8948633
 A:Accession: S73449
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-203 <HIM>
 A:Cross-references: UNIPROT:P75083; UNIPARC:UPI000013912P; EMBL:AE000015; GB:U00089; NID
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C:Genetics:
 A:Genetic code: SGC3
 C:Superfamily: uncharacterized conserved protein

Query Match 83.9%; Score 26; DB 2; Length 203;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
 |||||
 DB 89 FVFFA 93

RESULT 49
 G70437
 soluble hydrogenase small subunit - Aquifex aeolicus
 C:Species: Aquifex aeolicus
 C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
 C:Accession: G70437
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'
 V.
 Nature 392, 353-358, 1998
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
 A:Reference number: A70300; MUID:98196666; PMID:9537320
 A:Accession: G70437
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-216 <AQF>
 A:Cross-references: UNIPROT:O67529; UNIPARC:UPI0000056670; GB:AE000746; NID:G2983925; PI
 A:Experimental source: strain VF5
 C:Genetics:
 A:Gene: hys
 C:Superfamily: serine-pyruvate/aspartate aminotransferase

Query Match 83.9%; Score 26; DB 2; Length 216;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
 |||||
 DB 61 FVFFA 65

RESULT 50
 F86844
 hypothetical protein ysbD [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
 C:Species: Lactococcus lactis subsp. lactis
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C:Accession: F86844
 R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
 Genome Res. 11, 731-755, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: F86844
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-218 <STO>

A:Cross-references: UNIPROT:Q9CES6; UNIPARC:UPI0000006AFC; GB:AE005176; PID:g12724779; I
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: ysbD
 C:Superfamily: dedA protein

Query Match 83.9%; Score 26; DB 2; Length 218;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 |||||
 DB 155 KFVFF 159

RESULT 51
 T22101
 hypothetical protein F42F12.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T22101
 R:Lloyd, C.
 submitted to the EMBL Data Library, November 1995
 A:Reference number: Z19514
 A:Accession: T22101
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-243 <WIL>
 A:Cross-references: UNIPROT:Q20344; UNIPARC:UPI000007AEF3; EMBL:Z68116; PIDN:CAA92173.1;
 A:Experimental source: clone F42F12
 C:Genetics:
 A:Gene: CESP:F42F12.3
 A:Map position: X
 A:Introns: 85/2; 138/1; 222/2
 C:Superfamily: Caenorhabditis elegans hypothetical protein ZK1251.3

Query Match 83.9%; Score 26; DB 2; Length 243;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
 |||||
 DB 18 FVFFA 22

RESULT 52
 B81693
 conserved hypothetical protein TC0525 [imported] - Chlamydia muridarum (strain Nigg)
 C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: B81693
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 , C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: B81693
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-255 <TEF>
 A:Cross-references: UNIPROT:Q9PKE0; UNIPARC:UPI0000057969; GB:AE002321; GB:AE002160; NID
 A:Experimental source: strain Nigg (MoPn)
 C:Genetics:
 A:Gene: TC0525
 C:Superfamily: Chlamydia trachomatis hypothetical protein CT254

Query Match 83.9%; Score 26; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
 |||||
 DB 68 FVFFA 72

D81085
HtrB/MsbB family protein NMB1418 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C:Accession: D81085
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Xu, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V. V.
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: D81085
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-289 <TE>
A:Cross-references: UNIPROT:Q9JYV2; UNIPARC:UPI00000C46R0; GB:AE002491; GB:AE002098; N1
A:Experimental source: serogroup B, strain MC58
C:Genetics:
C:Superfamily: lipid A biosynthesis (KDO)2-(lauroyl)-lipid IVA acyltransferase

Query Match 83.9%; Score 26; DB 2; Length 289;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
DB 2 KFIFF 6

RESULT 56
A27692
sarcotoxin IIA precursor - flesh fly (Sarcophaga peregrina)
C:Species: Sarcophaga peregrina
C>Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: A27692
R:Ando, K.; Natori, S.
Biochemistry 27, 1715-1721, 1988
A:Title: Molecular cloning, sequencing, and characterization of cDNA for sarcotoxin IIA
A:Reference number: A27692; MUID:88209545; PMID:2452654
A:Accession: A27692
A:Molecule type: mRNA
A:Residues: 1-294 <AND>
A:Cross-references: UNIPROT:P14657; UNIPARC:UPI0000135ECC; GB:M18873; NID:g161272; PID:
P:1-24/Domain: signal sequence #status predicted <SIG>
P:25-294/Product: sarcotoxin IIA #status predicted <MAT>

Query Match 83.9%; Score 26; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
DB 4 FVFFA 8

RESULT 57
B36351
sarcotoxin II-2 - flesh fly (Sarcophaga peregrina)
C:Species: Sarcophaga peregrina
C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C:Accession: B36351
R:Kanai, A.; Natori, S.
Mol. Cell. Biol. 10, 6114-6122, 1990
A:Title: Analysis of a gene cluster for sarcotoxin II, a group of antibacterial protein
A:Reference number: A36351; MUID:91061717; PMID:2247051
A:Accession: B36351
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-294 <KAN>
A:Cross-references: UNIPROT:P24489; UNIPARC:UPI0000135ECC; GB:D90153; NID:g217388; PID:


```

Query Match      83.9%; Score 26; DB 2; Length 294;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
DB      4 FVFFA 8

RESULT 58
S75656
hypothetical protein slr1980 - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75656
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75656
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-297 <KAN>
A:Cross-references: UNIPROT:P74131; UNIPARC:UPI00000C100A; EMBL:D90912; GB:AB001339; NID
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match      83.9%; Score 26; DB 2; Length 297;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVEF 5
DB     104 KFIF 108

RESULT 59
D86216
protein T23G18.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86216
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Dewar, K.;
ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D86216
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <STO>
A:Cross-references: UNIPROT:Q9SGD8; UNIPARC:UPI000009EE07; GB:AE005172; NID:G6579209; PI
C:Genetics:
A:Gene: T23G18.8
A:Map position: 1

Query Match      83.9%; Score 26; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVEFA 6
DB     99 FVFFA 103

```

```

RESULT 60
T24424
hypothetical protein T04A8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24424
R:Palmer, S.
submitted to the EMBL Data Library, August 1994
A:Reference number: Z19889
A:Accession: T24424
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-324 <WLL>
A:Cross-references: UNIPROT:P46568; UNIPARC:UPI000006112C; EMBL:Z35663; PIDN:CAA84725.1;
A:Experimental source: clone T04A8
C:Genetics:
A:Gene: CESP:T04A8.1
A:Map position: 3
A:Introns: 77/3; 150/3; 198/3; 259/3

Query Match      83.9%; Score 26; DB 2; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
DB     262 FVFFA 266

RESULT 61
S08459
hypothetical protein 2 - spiroplasma virus 1
C:Species: spiroplasma virus 1, SpV1
C>Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 02-Mar-2001
C:Accession: S08459; S08447
R:Renaudin, J.; Aulio, P.; Vignault, J.C.; Bove, J.M.
Nucleic Acids Res. 18, 1293, 1990
A:Title: Complete nucleotide sequence of the genome of Spiroplasma citri virus SpV1-R8A2
A:Reference number: S08447; MUID:90206799; PMID:2320423
A:Accession: S08459
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-337 <REN>
A:Cross-references: UNIPARC:UPI0000138546; EMBL:X51344
A:Accession: S08447
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 262-337 <RE2>
A:Cross-references: UNIPARC:UPI0000161E8D; EMBL:X51344; NID:g61993; PIDN:CAA35725.1; PID
C:Genetics:
A:Genetic code: SGC3

Query Match      83.9%; Score 26; DB 2; Length 337;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KFVFF 5
DB      3 KFIF 7

RESULT 62
E90564
potassium channel protein [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: E90564
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A99512; MUID:21267165; PMID:1133084
A:Accession: E90564
A:Status: preliminary

```


R.;lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A'Reference number: AB4420; MUID:20083487; PMID:10617197

A'Accession: C84621

A>Status: preliminary

A'Molecule type: DNA

A'Residuals: 1-395 <STO>

A'Cross-references: UNIPARC:UPI00000AAFDA; GB:AE002093; NID:g2642447; PIDN:AAB87115.1; C

C'Genetics:

A'Gene: At2g23160; T20D16.21

A'Map position: 2

A'Introns: 295/3

A'Note: T20D16.21

C'Superfamily: hypothetical protein containing F-box domain

Query Match 83.9%; Score 26; DB 2; Length 395;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVFP 5
||:|
245 KPIFF 249

Db

RESULT 67

DB1040

Cytochrome c-type biogenesis protein, probable NMB1803 [imported] - Neisseria meningitidis

C'Species: Neisseria meningitidis

C'Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C'Accession: DB1040

R'Tetrelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scharlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A'Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve

A'Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.

A'Reference number: AB1000; MUID:20175755; PMID:10710307

A'Accession: DB1040

A>Status: preliminary

A'Molecule type: DNA

A'Residuals: 1-395 <TET>

A'Cross-references: UNIPROT:Q9JY05; UNIPARC:UPI00000C47CE; GB:AE002530; GB:AE002098; NID

A'Experimental source: serogroup B, strain MCS8

C'Genetics:

A'Gene: NMB1803

Query Match 83.9%; Score 26; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||||
120 FVFFA 124

Db

RESULT 68

BB1986

probable membrane protein NMA0660 [imported] - Neisseria meningitidis (strain Z2491 sero

C'Species: Neisseria meningitidis

C'Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C'Accession: BB1986

R'Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel i Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A'Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A'Reference number: AB1775; MUID:20222556; PMID:10761919

A'Accession: BB1986

A>Status: preliminary

A'Molecule type: DNA

A'Residuals: 1-395 <PAR>

A'Cross-references: UNIPROT:Q9JVV9; UNIPARC:UPI00000C4A09; GB:AL162753; GB:AL157959; NID

A'Experimental source: serogroup A, strain Z2491

C'Genetics:

A'Gene: NMA0660

Query Match 83.9%; Score 26; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||||
120 FVFFA 124

Db

RESULT 69

T46710

multidrug resistance transporter [imported] - Listeria monocytogenes

C'Species: Listeria monocytogenes

C'Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004

C'Accession: T46710

R'Huillet, E.E.H.; Larpin, S.; Pardon, P.; Berche, P. FEMS Microbiol. Lett. 174, 265-272, 1999

A'Title: Identification of a new locus in Listeria monocytogenes involved in cellobiose-

A'Reference number: Z23136; MUID:99271176; PMID:10339818

A'Accession: T46710

A>Status: preliminary; translated from GB/EMBL/DBJ

A'Molecule type: DNA

A'Residuals: 1-397 <HUI>

A'Cross-references: UNIPROT:Q9X769; UNIPARC:UPI0000055470; EMBL:AJ009627; NID:g4914621;

C'Genetics:

A'Gene: lltB

Query Match 83.9%; Score 26; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||||
245 FVFFA 249

Db

RESULT 70

AE1613

multidrug-efflux transporter homolog lin1446 [imported] - Listeria innocua (strain Clip1

C'Species: Listeria innocua

C'Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C'Accession: AE1613

R'Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H. D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001

A'Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Madueno, E.; Maitournam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wenland, A'Title: Comparative genomics of Listeria species.

A'Reference number: AB1077; MUID:21537279; PMID:11679669

A'Accession: AE1613

A>Status: preliminary

A'Molecule type: DNA

A'Residuals: 1-397 <GLA>

A'Cross-references: UNIPROT:Q92B08; UNIPARC:UPI00000CC57B; GB:AL592022; PIDN:CAC96677.1;

A'Experimental source: strain Clip11262

C'Genetics:

A'Gene: lin1446

Query Match 83.9%; Score 26; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
||||
245 FVFFA 249

Db

RESULT 71
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli:
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero:
 akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A9580; MUID:98044033; PMID:9384377
 A:Accession: H69833
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-401 <KUN>
 A:Cross-references: UNIPROT:O07563; UNIPARC:UPI00000601AF; GB:Z99109; GB:AL009136; NID:
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yhjI

Query Match 83.9%; Score 26; DB 2; Length 397;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFPA 6
 |||||
 DB 245 FVFPA 249

RESULT 72
 T44331
 Hypothetical protein wblD [imported] - *Vibrio cholerae*
 C:Species: *Vibrio cholerae*
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C:Accession: T44331
 R:Yamasaki, S.; Shimizu, T.; Hoshino, K.; Ho, S.T.; Shimada, T.; Nair, G.B.; Takeda, Y.
 Gene 237, 321-332, 1999
 A:Title: The genes responsible for O-antigen synthesis of *Vibrio cholerae* O139 are close
 A:Reference number: 222749; MUID:99453293; PMID:10521656
 A:Accession: T44331
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-398 <YAM>
 A:Cross-references: UNIPROT:O87160; UNIPARC:UPI000005419; EMBL:AB012957; NID:G4115688;
 A:Experimental source: strain O22
 C:Genetics:
 A:Note: wblD

Query Match 83.9%; Score 26; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFPA 6
 |||||
 DB 263 FVFPA 267

RESULT 73
 H69833
 conserved hypothetical protein yhjI - *Bacillus subtilis*
 C:Species: *Bacillus subtilis*
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C:Accession: H69833
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte:
 C.; Bron, S.; Broutillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch:
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall:
 lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelli:
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero:
 akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpsstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A9580; MUID:98044033; PMID:9384377
 A:Accession: H69833
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-401 <KUN>
 A:Cross-references: UNIPROT:O07563; UNIPARC:UPI00000601AF; GB:Z99109; GB:AL009136; NID:
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: yhjI

Query Match 83.9%; Score 26; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFPA 6
 |||||
 DB 215 FVFPA 219

RESULT 74
 C95990
 probable sugar uptake ABC transporter permease protein ggub [imported] - *Sinorhizobium*
 C:Species: *Sinorhizobium meliloti*
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C:Accession: C95990
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, P.J.; Herna:
 proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing end
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: C95990
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-404 <KUR>
 A:Cross-references: UNIPROT:Q92UB4; UNIPARC:UPI00000CB7A2; GB:AL591985; PIDN:CAC49587.1
 A:Experimental source: strain 1021, megaplasmid pSymb
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
 heault, P.; Vandenbol, M.; Vorholter, P.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, J.
 A:Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: ggub
 A:Genome: plasmid
 C:Superfamily: 1-arabinose transport system permease arah

Query Match 83.9%; Score 26; DB 2; Length 404;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFPA 6
 |||||
 DB 223 FVFPA 227

RESULT 75
 CBQFR
 ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - *Rhodospirillum rubrum*
 C:Species: *Rhodospirillum rubrum*
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C:Accession: S12257; A38814
 R:Majewski, C.; Trebat, A.

Mol. Gen. Genet. 224, 373-382, 1990
A:Title: The pet Genes of Rhodospirillum rubrum: cloning and sequencing of the genes for
A:Reference number: S12255; MUID:91094774; PMID:2176269
A:Accession: S12257
A:Molecule type: DNA
A:Residues: 1-405 <MA1>
A:Cross-references: UNIPROT:P23134; UNIPARC:UPI0000128ACD; EMBL:X55387; NID:946382; PIDN
A>Note: the authors translated the codon AAT for residue 161 as Leu and CTG for residue
A:Accession: A38814
A:Molecule type: protein
A:Residues: 1-26, 'E' <MA2>
A:Cross-references: UNIPARC:UPI0000171D0F
C:Genetics:
A:Gene: petB
C:Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol
C:Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; oxidoreductase
F:1-405/Product: cytochrome b #status experimental <MAT>
F:22-354/Domain: cytochrome b homology <CBH>
F:22-222/Domain: cytochrome b6 homology <CB6>
F:47-63/Domain: transmembrane #status predicted <TM1>
F:92-110/Domain: transmembrane #status predicted <TM2>
F:130-146/Domain: transmembrane #status predicted <TM3>
F:191-213/Domain: transmembrane #status predicted <TM4>
F:236-354/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F:244-260/Domain: transmembrane #status predicted <TM5>
F:303-319/Domain: transmembrane #status predicted <TM6>
F:338-356/Domain: transmembrane #status predicted <TM7>
F:368-384/Domain: transmembrane #status predicted <TM8>
F:94,195/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F:108,209/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

Query Match 83.9%; Score 26; DB 1; Length 405;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 FVFFA 6
Db 257 FVFFA 261

Search completed: December 29, 2005, 17:49:18
Job time : 13.9677 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:49:38 ; Search time 3.29032 Seconds
(without alignments)
13.656 Million cell updates/sec

Title: US-10-009-122-12

Perfect score: 31

Sequence: 1 KVFPPA 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 57103 seqs, 7488799 residues

Total number of hits satisfying chosen parameters: 57103

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database : Published Applications AA_New.*
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.ppe.*
2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.ppe.*
3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.ppe.*
4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.ppe.*
5: /cgn2_6/ptodata/2/pubppaa/US03_NEW_PUB.ppe.*
6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.ppe.*
7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.ppe.*
8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.ppe.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	87.1	582	7	US-11-030-439-58
2	27	87.1	592	6	US-10-467-657-4888
3	27	87.1	738	7	US-11-147-047-48
4	27	87.1	1070	7	US-11-147-047-49
5	26	83.9	19	6	US-10-467-657-8712
6	26	83.9	220	6	US-10-467-657-3154
7	26	83.9	299	6	US-10-467-657-2190
8	26	83.9	395	6	US-10-467-657-1950
9	26	83.9	418	6	US-10-467-657-5788
10	25	80.6	19	6	US-10-923-605-5
11	25	80.6	19	6	US-10-934-818-5
12	25	80.6	40	7	US-11-016-706-36
13	25	80.6	40	7	US-11-098-674-12
14	25	80.6	42	6	US-10-923-605-1
15	25	80.6	42	6	US-10-934-818-1
16	25	80.6	42	7	US-11-016-706-37
17	25	80.6	43	6	US-10-934-818-6
18	25	80.6	43	6	US-10-250-581-1
19	25	80.6	43	6	US-10-250-581-1
20	25	80.6	184	6	US-10-467-657-7560
21	25	80.6	525	7	US-11-082-389-350
22	25	80.6	770	6	US-10-982-545-15
23	25	80.6	770	6	US-10-789-273-38
24	24	77.4	194	6	US-10-467-657-3978
25	24	77.4	229	6	US-10-793-626-62

26	24	77.4	443	6	US-10-793-626-1860	Sequence 1860, Ap
27	24	77.4	533	6	US-10-467-657-4566	Sequence 4566, Ap
28	24	77.4	657	7	US-11-080-991-48	Sequence 48, Appl
29	24	77.4	916	6	US-10-467-657-4242	Sequence 4242, Ap
30	24	77.4	4384	6	US-10-821-234-1120	Sequence 1120, Ap
31	23	74.2	49	6	US-10-467-657-1370	Sequence 1370, Ap
32	23	74.2	49	6	US-10-467-657-2308	Sequence 2308, Ap
33	23	74.2	49	6	US-10-467-657-5610	Sequence 5610, Ap
34	23	74.2	49	6	US-10-467-657-7516	Sequence 7516, Ap
35	23	74.2	49	6	US-10-467-657-8322	Sequence 8322, Ap
36	23	74.2	54	6	US-10-467-657-4324	Sequence 4324, Ap
37	23	74.2	56	6	US-10-467-657-8286	Sequence 8286, Ap
38	23	74.2	126	6	US-10-793-626-2766	Sequence 2766, Ap
39	23	74.2	209	6	US-10-793-626-304	Sequence 304, App
40	23	74.2	234	6	US-10-793-626-1034	Sequence 1034, Ap
41	23	74.2	288	6	US-10-467-657-4456	Sequence 4456, Ap
42	23	74.2	391	6	US-10-613-744-13	Sequence 13, Appl
43	23	74.2	410	6	US-10-467-657-4858	Sequence 4858, Ap
44	23	74.2	432	7	US-11-055-822-1096	Sequence 1096, Ap
45	23	74.2	432	7	US-11-113-424-186	Sequence 186, App
46	23	74.2	449	6	US-10-467-657-678	Sequence 678, App
47	23	74.2	534	7	US-11-082-389-348	Sequence 348, App
48	23	74.2	633	6	US-10-467-657-3440	Sequence 3440, Ap
49	23	74.2	633	6	US-10-467-657-4632	Sequence 4632, Ap
50	23	74.2	660	7	US-11-186-284-125	Sequence 125, App
51	23	74.2	708	6	US-10-821-234-917	Sequence 917, App
52	23	74.2	766	6	US-10-793-626-420	Sequence 420, App
53	23	74.2	1012	6	US-10-995-561-908	Sequence 908, App
54	23	74.2	2323	6	US-10-793-626-760	Sequence 760, App
55	23	71.0	30	6	US-10-467-657-8998	Sequence 8998, Ap
56	22	71.0	72	7	US-11-000-463-378	Sequence 378, App
57	22	71.0	72	7	US-11-000-463-850	Sequence 850, App
58	22	71.0	77	6	US-10-467-657-360	Sequence 360, App
59	22	71.0	79	6	US-10-467-657-2026	Sequence 2026, Ap
60	22	71.0	101	6	US-10-485-517-286	Sequence 286, App
61	22	71.0	101	6	US-10-467-657-6824	Sequence 6824, Appl
62	22	71.0	139	7	US-11-125-837-24	Sequence 24, Appl
63	22	71.0	149	6	US-10-467-657-6110	Sequence 6110, Ap
64	22	71.0	149	6	US-10-467-657-7550	Sequence 7550, Ap
65	22	71.0	154	6	US-10-467-657-6130	Sequence 6130, Ap
66	22	71.0	180	6	US-10-485-517-346	Sequence 346, App
67	22	71.0	187	6	US-10-980-388-65	Sequence 65, Appl
68	22	71.0	210	6	US-10-467-657-4386	Sequence 4386, Ap
69	22	71.0	222	6	US-10-467-657-3000	Sequence 3000, Ap
70	22	71.0	238	6	US-10-467-657-6248	Sequence 6248, Ap
71	22	71.0	240	7	US-11-054-515-1391	Sequence 1391, Appl
72	22	71.0	241	7	US-11-074-176-66	Sequence 66, Appl
73	22	71.0	250	6	US-10-793-626-1124	Sequence 1124, Ap
74	22	71.0	254	6	US-10-467-657-6144	Sequence 6144, Ap
75	22	71.0	288	6	US-10-467-657-1178	Sequence 1178, Ap
76	22	71.0	268	6	US-10-467-657-5704	Sequence 5704, Ap
77	22	71.0	277	6	US-10-667-295-85	Sequence 85, Appl
78	22	71.0	326	6	US-10-873-528-33	Sequence 33, Appl
79	22	71.0	328	6	US-10-848-375-1	Sequence 1, Appli
80	22	71.0	331	6	US-10-873-528-147	Sequence 147, App
81	22	71.0	341	6	US-10-858-730-124	Sequence 124, App
82	22	71.0	346	6	US-10-793-626-504	Sequence 504, App
83	22	71.0	347	6	US-10-821-234-1379	Sequence 1379, Ap
84	22	71.0	353	7	US-11-067-884-6	Sequence 6, Appli
85	22	71.0	353	6	US-10-467-657-2872	Sequence 2872, Ap
86	22	71.0	362	6	US-10-875-716-9	Sequence 9, Appli
87	22	71.0	365	7	US-11-055-822-400	Sequence 400, App
88	22	71.0	366	7	US-11-055-822-492	Sequence 492, App
89	22	71.0	366	7	US-10-793-626-490	Sequence 490, App
90	22	71.0	376	6	US-10-793-626-2260	Sequence 2260, Ap
91	22	71.0	383	6	US-10-793-626-2026	Sequence 2026, Ap
92	22	71.0	436	6	US-10-467-657-7578	Sequence 7578, Ap
93	22	71.0	445	6	US-10-821-234-1606	Sequence 1606, Ap
94	22	71.0	465	6	US-10-793-626-1676	Sequence 1676, Ap
95	22	71.0	481	6	US-10-995-561-959	Sequence 959, App
96	22	71.0	494	6	US-10-467-657-592	Sequence 592, App
97	22	71.0	505	6	US-10-873-528-120	Sequence 120, App
98	22	71.0	522	6	US-10-793-626-604	Sequence 604, App

99	22	71.0	528	6	US-10-864-758-7	Sequence 7, Appli	172	21	67.7	652	6	US-10-873-528-26	Sequence 26, Appl
100	22	71.0	541	7	US-11-000-463-238	Sequence 238, App	173	21	67.7	658	6	US-10-873-528-17	Sequence 17, Appl
101	22	71.0	566	6	US-10-467-657-8046	Sequence 8046, Ap	174	21	67.7	676	6	US-10-510-947-1	Sequence 1, Appli
102	22	71.0	578	6	US-11-083-800-2	Sequence 2, Appli	175	21	67.7	677	6	US-10-873-528-155	Sequence 155, App
103	22	71.0	607	7	US-11-080-991-88	Sequence 88, Appl	176	21	67.7	697	6	US-10-485-517-202	Sequence 202, App
104	22	71.0	709	6	US-10-131-828A-202	Sequence 202, App	177	21	67.7	756	6	US-10-467-657-8694	Sequence 8694, Ap
105	22	71.0	786	6	US-10-467-962B-103	Sequence 103, App	178	21	67.7	801	6	US-10-793-626-2020	Sequence 2020, Ap
106	22	71.0	790	6	US-10-131-826A-204	Sequence 204, App	179	21	67.7	837	7	US-11-094-519A-43	Sequence 43, Appl
107	22	71.0	943	6	US-10-821-234-1012	Sequence 1012, Ap	180	21	67.7	845	7	US-11-094-519A-42	Sequence 42, Appl
108	22	71.0	1062	6	US-10-821-234-1079	Sequence 1079, Ap	181	21	67.7	1052	6	US-10-467-657-3992	Sequence 3992, Ap
109	22	71.0	1070	7	US-11-000-463-721	Sequence 721, App	182	21	67.7	1076	6	US-10-467-657-5708	Sequence 5708, Ap
110	22	71.0	1194	7	US-11-000-463-249	Sequence 249, App	183	21	67.7	1170	7	US-11-080-026-2	Sequence 2, Appli
111	21	67.7	5	7	US-11-098-674-1	Sequence 1, Appli	184	21	67.7	1170	7	US-11-107-028-4	Sequence 4, Appli
112	21	67.7	39	6	US-10-467-657-4630	Sequence 4630, Ap	185	21	67.7	1751	7	US-11-103-957-45	Sequence 45, Appl
113	21	67.7	40	6	US-10-467-657-4616	Sequence 4616, Ap	186	20	64.5	16	7	US-11-089-764-65	Sequence 65, Appl
114	21	67.7	43	6	US-10-467-657-8642	Sequence 8642, Ap	187	20	64.5	16	7	US-11-089-764-66	Sequence 66, Appl
115	21	67.7	47	6	US-10-467-657-5436	Sequence 5436, Ap	188	20	64.5	23	7	US-11-085-812-16	Sequence 16, Appl
116	21	67.7	55	6	US-10-485-517-387	Sequence 387, App	189	20	64.5	23	7	US-11-085-812-14	Sequence 14, Appl
117	21	67.7	57	7	US-11-000-463-770	Sequence 770, App	190	20	64.5	28	6	US-10-250-581-17	Sequence 17, Appl
118	21	67.7	63	7	US-11-000-463-353	Sequence 353, App	191	20	64.5	28	6	US-10-250-581-14	Sequence 14, Appl
119	21	67.7	63	7	US-11-000-463-825	Sequence 825, App	192	20	64.5	28	6	US-10-250-581-17	Sequence 17, Appl
120	21	67.7	72	6	US-10-467-657-5578	Sequence 5578, Ap	193	20	64.5	40	6	US-10-250-581-15	Sequence 15, Appl
121	21	67.7	72	7	US-11-000-463-298	Sequence 298, App	194	20	64.5	40	6	US-10-250-581-18	Sequence 18, Appl
122	21	67.7	75	6	US-10-467-657-8472	Sequence 8472, Ap	195	20	64.5	40	6	US-10-250-581-15	Sequence 15, Appl
123	21	67.7	79	7	US-11-123-896-134	Sequence 134, App	196	20	64.5	42	6	US-10-250-581-16	Sequence 16, Appl
124	21	67.7	90	6	US-10-467-657-4374	Sequence 4374, Ap	197	20	64.5	42	6	US-10-250-581-16	Sequence 16, Appl
125	21	67.7	91	6	US-10-821-234-1238	Sequence 1238, Ap	198	20	64.5	42	6	US-10-250-581-19	Sequence 19, Appl
126	21	67.7	94	6	US-10-467-657-4730	Sequence 4730, Ap	199	20	64.5	42	6	US-10-250-581-16	Sequence 16, Appl
127	21	67.7	102	6	US-10-467-657-5604	Sequence 5604, Ap	200	20	64.5	42	6	US-10-250-581-19	Sequence 19, Appl
128	21	67.7	113	6	US-10-793-626-1848	Sequence 1848, Ap	201	20	64.5	44	6	US-10-467-657-1118	Sequence 1118, Ap
129	21	67.7	120	6	US-10-793-626-2376	Sequence 2376, Ap	202	20	64.5	45	6	US-10-467-657-8968	Sequence 8968, Ap
130	21	67.7	140	6	US-10-982-145-66	Sequence 66, Appl	203	20	64.5	50	6	US-10-467-657-7892	Sequence 7892, Ap
131	21	67.7	141	6	US-10-982-145-67	Sequence 67, Appl	204	20	64.5	54	6	US-10-467-657-2264	Sequence 2264, Ap
132	21	67.7	164	6	US-10-467-657-1450	Sequence 1450, Ap	205	20	64.5	54	6	US-10-467-657-4978	Sequence 4978, Ap
133	21	67.7	168	6	US-10-927-641-69	Sequence 69, Appl	206	20	64.5	56	6	US-10-467-657-1050	Sequence 1050, Ap
134	21	67.7	188	6	US-10-793-626-724	Sequence 724, App	207	20	64.5	66	6	US-10-467-657-766	Sequence 766, App
135	21	67.7	182	6	US-10-467-657-8302	Sequence 8302, Ap	208	20	64.5	79	7	US-11-080-991-10	Sequence 10, Appl
136	21	67.7	183	7	US-11-069-642-1325	Sequence 125, App	209	20	64.5	92	6	US-10-467-657-5952	Sequence 5952, Ap
137	21	67.7	198	6	US-10-467-657-5440	Sequence 5440, Ap	210	20	64.5	105	6	US-10-467-657-9209	Sequence 9209, Ap
138	21	67.7	220	6	US-10-793-626-1822	Sequence 1822, Ap	211	20	64.5	115	6	US-10-793-626-1554	Sequence 1554, Ap
139	21	67.7	227	6	US-10-793-626-2396	Sequence 2396, Ap	212	20	64.5	120	6	US-10-467-657-6982	Sequence 6982, Ap
140	21	67.7	233	6	US-10-793-626-2842	Sequence 2642, Ap	213	20	64.5	120	6	US-10-467-657-7938	Sequence 7938, Ap
141	21	67.7	235	7	US-11-188-473-2	Sequence 2, Appli	214	20	64.5	123	6	US-10-821-234-988	Sequence 988, App
142	21	67.7	246	7	US-11-092-140-111	Sequence 111, App	215	20	64.5	127	7	US-10-467-657-6978	Sequence 6978, Ap
143	21	67.7	247	7	US-11-103-957-69	Sequence 69, Appl	216	20	64.5	127	7	US-11-106-796-10	Sequence 10, Appl
144	21	67.7	248	7	US-11-076-164-9	Sequence 9, Appli	217	20	64.5	129	6	US-10-501-039-8	Sequence 8, Appli
145	21	67.7	269	6	US-10-467-657-330	Sequence 30, App	218	20	64.5	135	6	US-10-793-626-2284	Sequence 2284, Ap
146	21	67.7	286	6	US-10-793-626-2192	Sequence 2192, Ap	219	20	64.5	138	6	US-10-793-626-1254	Sequence 1254, Ap
147	21	67.7	294	7	US-11-055-822-480	Sequence 480, App	220	20	64.5	150	6	US-10-793-626-2324	Sequence 2324, Ap
148	21	67.7	294	7	US-11-055-822-880	Sequence 880, App	221	20	64.5	154	7	US-11-082-389-424	Sequence 424, App
149	21	67.7	294	6	US-10-454-437-384	Sequence 384, App	222	20	64.5	155	6	US-10-467-657-2420	Sequence 2420, Ap
150	21	67.7	298	7	US-11-055-822-478	Sequence 478, App	223	20	64.5	160	7	US-11-009-939-44	Sequence 44, Appl
151	21	67.7	298	7	US-11-055-822-478	Sequence 478, App	224	20	64.5	166	6	US-10-821-234-1293	Sequence 1293, Ap
152	21	67.7	301	6	US-10-793-626-206	Sequence 206, App	225	20	64.5	166	6	US-10-878-556A-20	Sequence 20, Appl
153	21	67.7	355	6	US-10-467-657-7996	Sequence 7996, Ap	226	20	64.5	174	6	US-10-793-626-1520	Sequence 1520, Ap
154	21	67.7	400	6	US-10-793-626-1056	Sequence 1056, Ap	227	20	64.5	183	7	US-10-467-657-6906	Sequence 6906, Ap
155	21	67.7	403	7	US-11-109-156-29	Sequence 29, Appl	228	20	64.5	188	7	US-11-100-183-27	Sequence 27, Appl
156	21	67.7	407	6	US-10-821-234-1389	Sequence 1389, Ap	229	20	64.5	190	6	US-10-467-657-3436	Sequence 3436, Ap
157	21	67.7	419	7	US-11-084-624-18	Sequence 18, Appl	230	20	64.5	193	6	US-10-793-626-1240	Sequence 1240, Ap
158	21	67.7	419	7	US-11-084-624-18	Sequence 18, Appl	231	20	64.5	196	6	US-10-131-826A-168	Sequence 168, App
159	21	67.7	452	6	US-10-793-626-3092	Sequence 3092, Ap	232	20	64.5	196	6	US-10-793-626-2584	Sequence 2584, Ap
160	21	67.7	464	6	US-10-689-742-164	Sequence 316, App	233	20	64.5	201	5	US-09-940-308-5	Sequence 5, Appli
161	21	67.7	490	7	US-11-074-176-316	Sequence 60, Appl	234	20	64.5	211	6	US-10-821-234-1372	Sequence 1372, Ap
162	21	67.7	495	7	US-11-074-176-60	Sequence 60, Appl	235	20	64.5	211	6	US-10-467-657-6932	Sequence 6932, Ap
163	21	67.7	502	6	US-10-821-234-1554	Sequence 1554, Ap	236	20	64.5	215	6	US-10-131-826A-4	Sequence 4, Appli
164	21	67.7	514	6	US-10-467-657-2664	Sequence 2664, Ap	237	20	64.5	215	6	US-10-131-826A-488	Sequence 488, App
165	21	67.7	514	7	US-11-103-037-3	Sequence 3, Appli	238	20	64.5	215	7	US-11-080-991-112	Sequence 112, App
166	21	67.7	515	6	US-10-630-203-6	Sequence 6, Appli	239	20	64.5	221	6	US-10-793-626-1992	Sequence 1992, Ap
167	21	67.7	521	6	US-10-793-626-532	Sequence 532, App	240	20	64.5	221	6	US-10-793-626-2420	Sequence 2420, Ap
168	21	67.7	526	6	US-10-606-302-5	Sequence 5, Appli	241	20	64.5	228	6	US-10-793-626-360	Sequence 360, App
169	21	67.7	526	6	US-10-606-302-7	Sequence 7, Appli	242	20	64.5	228	6	US-10-793-626-488	Sequence 488, App
170	21	67.7	528	6	US-10-793-626-1930	Sequence 1930, Ap	243	20	64.5	228	6	US-10-467-657-568	Sequence 568, App
171	21	67.7	537	6	US-10-467-657-6958	Sequence 6958, Ap	244	20	64.5	228	6	US-10-467-657-4838	Sequence 4838, Ap

245 20 64.5 233 6 US-10-821-234-1322
 246 20 64.5 234 6 US-10-793-626-192
 247 20 64.5 245 6 US-10-467-657-7884
 248 20 64.5 263 6 US-10-510-386-234
 249 20 64.5 275 7 US-11-110-977-4
 250 20 64.5 276 7 US-11-112-882-86
 251 20 64.5 277 6 US-10-454-437-8
 252 20 64.5 277 6 US-11-055-822-608
 253 20 64.5 281 6 US-10-821-234-1080
 254 20 64.5 288 6 US-10-467-657-1272
 255 20 64.5 291 7 US-11-102-883-22
 256 20 64.5 292 7 US-11-102-883-24
 257 20 64.5 294 6 US-10-467-657-7686
 258 20 64.5 294 7 US-11-112-882-85
 259 20 64.5 295 7 US-11-091-100-2
 260 20 64.5 298 7 US-11-085-812-4
 261 20 64.5 306 6 US-11-112-882-3
 262 20 64.5 304 6 US-10-467-657-7222
 263 20 64.5 311 6 US-10-793-626-2450
 264 20 64.5 319 6 US-10-131-826A-134
 265 20 64.5 321 6 US-10-467-657-2504
 266 20 64.5 323 6 US-10-467-657-556
 267 20 64.5 324 6 US-10-793-626-1262
 268 20 64.5 324 6 US-10-467-657-7692
 269 20 64.5 324 6 US-10-467-657-8440
 270 20 64.5 325 5 US-09-940-308-8
 271 20 64.5 325 6 US-10-454-437-142
 272 20 64.5 330 7 US-11-085-812-2
 273 20 64.5 335 6 US-10-467-657-3818
 274 20 64.5 337 6 US-10-875-716-2
 275 20 64.5 338 6 US-10-467-657-136
 276 20 64.5 338 6 US-10-467-657-6798
 277 20 64.5 338 6 US-10-878-556A-19
 278 20 64.5 344 6 US-10-131-826A-376
 279 20 64.5 347 6 US-10-467-657-2014
 280 20 64.5 350 6 US-10-485-517-288
 281 20 64.5 350 7 US-11-095-624-2
 282 20 64.5 350 7 US-11-095-624-3
 283 20 64.5 350 7 US-11-095-624-4
 284 20 64.5 351 7 US-11-095-624-5
 285 20 64.5 353 7 US-11-060-023-2
 286 20 64.5 353 7 US-11-060-023-4
 287 20 64.5 353 7 US-11-060-023-6
 288 20 64.5 353 7 US-11-060-023-8
 289 20 64.5 353 7 US-11-060-023-12
 290 20 64.5 353 7 US-11-060-023-14
 291 20 64.5 353 7 US-11-060-023-15
 292 20 64.5 353 7 US-11-060-023-16
 293 20 64.5 355 6 US-10-454-437-102
 294 20 64.5 356 7 US-11-055-822-972
 295 20 64.5 356 7 US-11-055-822-1052
 296 20 64.5 359 7 US-11-060-023-11
 297 20 64.5 359 7 US-11-060-023-13
 298 20 64.5 360 7 US-11-060-023-17
 299 20 64.5 378 7 US-11-080-091-3
 300 20 64.5 378 7 US-11-080-091-11

ALIGNMENTS

RESULT 1
 US-11-050-439-58
 ; Sequence 58, Application US/11090439
 ; Publication No. US20050268442A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Squillace, Rachel
 ; APPLICANT: Weiner, Michael P.
 ; TITLE OF INVENTION: Immortalized Human Tuberculous Sclerosis Null
 ; TITLE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
 ; FILE REFERENCE: 24318-502
 ; CURRENT APPLICATION NUMBER: US/11/090.439
 ; CURRENT FILING DATE: 2005-03-25

Sequence 1322, Ap
 Sequence 192, App
 Sequence 7884, Ap
 Sequence 234, App
 Sequence 4, Appl
 Sequence 86, Appl
 Sequence 8, Appl
 Sequence 608, App
 Sequence 1080, Ap
 Sequence 1272, Ap
 Sequence 22, Appl
 Sequence 24, Appl
 Sequence 7686, Ap
 Sequence 85, Appl
 Sequence 2, Appl
 Sequence 4, Appl
 Sequence 3, Appl
 Sequence 7222, Ap
 Sequence 2450, Ap
 Sequence 134, App
 Sequence 2504, Ap
 Sequence 556, App
 Sequence 1262, Ap
 Sequence 7692, Ap
 Sequence 8440, Ap
 Sequence 8, Appl
 Sequence 142, App
 Sequence 2, Appl
 Sequence 3818, Ap
 Sequence 2, Appl
 Sequence 136, App
 Sequence 6798, Ap
 Sequence 19, Appl
 Sequence 376, App
 Sequence 2014, Ap
 Sequence 288, App
 Sequence 2, Appl
 Sequence 3, Appl
 Sequence 4, Appl
 Sequence 5, Appl
 Sequence 2, Appl
 Sequence 4, Appl
 Sequence 6, Appl
 Sequence 8, Appl
 Sequence 12, Appl
 Sequence 14, Appl
 Sequence 15, Appl
 Sequence 16, Appl
 Sequence 102, App
 Sequence 972, App
 Sequence 1052, Ap
 Sequence 11, Appl
 Sequence 13, Appl
 Sequence 17, Appl
 Sequence 11, Appl

Query Match 87.1%; Score 27; DB 7; Length 582;
 Best Local Similarity 100.0%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 DB 378 KVFVF 382

RESULT 2
 US-10-467-657-4888
 ; Sequence 4888, Application US/10467657
 ; Publication No. US20050260581A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHIRON SPA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/467,657
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8
 ; PRIOR FILING DATE: 2001-02-12
 ; NUMBER OF SEQ ID NOS: 9218
 ; SOFTWARE: SeqWin99, version 1.04
 ; SEQ ID NO 4888
 ; LENGTH: 592
 ; TYPE: PRT
 ; ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-4888

Query Match 87.1%; Score 27; DB 6; Length 592;
 Best Local Similarity 100.0%; Pred. No. 75;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
 DB 557 KVFVF 561

RESULT 3
 US-11-147-047-48
 ; Sequence 48, Application US/11147047
 ; Publication No. US20050260686A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Agarwal, Pankaj
 ; APPLICANT: Murdock, Paul R.
 ; APPLICANT: Rizvi, Safia K.
 ; APPLICANT: Smith, Randall F.
 ; APPLICANT: Xiang, Zhaoying
 ; TITLE OF INVENTION: NOVEL COMPOUNDS
 ; FILE REFERENCE: GP50016
 ; CURRENT APPLICATION NUMBER: US/11/147,047
 ; CURRENT FILING DATE: 2005-06-07
 ; PRIOR APPLICATION NUMBER: US/10/221,097
 ; PRIOR FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: PCT/US01/07143
 ; PRIOR FILING DATE: 2001-03-05
 ; PRIOR APPLICATION NUMBER: 60/187,107
 ; PRIOR FILING DATE: 2000-03-06
 ; PRIOR APPLICATION NUMBER: 60/236,874

```
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-48
```

```
Query Match      87.1%; Score 27; DB 7; Length 738;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFF 5
Db      184 KVVFF 188
```

```
RESULT 4
US-11-147-047-49
; Sequence 49, Application US/11147047
; Publication No. US20050260668A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdock, Paul R.
; APPLICANT: Rizvi, Safia K.
; APPLICANT: Smith, Randall F.
; APPLICANT: Xiang, Zhaoqing
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50016
; CURRENT APPLICATION NUMBER: US/11/147,047
; CURRENT FILING DATE: 2005-06-07
; PRIOR APPLICATION NUMBER: US/10/221,097
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: PCT/US01/07143
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/187,107
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/236,874
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/188,916
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/237,846
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 1070
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-147-047-49
```

```
Query Match      87.1%; Score 27; DB 7; Length 1070;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFF 5
Db      244 KVVFF 248
```

```
RESULT 5
US-10-467-657-8712
; Sequence 8712, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
```

```
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8712
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8712
```

```
Query Match      83.9%; Score 26; DB 6; Length 19;
Best Local Similarity 80.0%; Pred. No. 5;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVVFF 5
Db      15 KVVFF 19
```

```
RESULT 6
US-10-467-657-3154
; Sequence 3154, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3154
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3154
```

```
Query Match      83.9%; Score 26; DB 6; Length 220;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 FVFFA 6
Db      204 FVFFA 208
```

```
RESULT 7
US-10-467-657-2190
; Sequence 2190, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
```


; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2190
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2190

Query Match 83.9%; Score 26; DB 6; Length 299;
Best Local Similarity 80.0%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPP 5
|:|
Db 12 KTFPP 16

RESULT 8
US-10-467-657-1950
; Sequence 1950, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1950
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1950

Query Match 83.9%; Score 26; DB 6; Length 395;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPP 6
|:|
Db 120 FVFPP 124

RESULT 9
US-10-467-657-5788
; Sequence 5788, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5788
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

US-10-467-657-5788

Query Match 83.9%; Score 26; DB 6; Length 418;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFPP 6
|:|
Db 337 FVFPP 341

RESULT 10
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-923-605-5

Query Match 80.6%; Score 25; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFPP 6
|:|
Db 4 KLVPP 9

RESULT 11
US-10-934-818-5
; Sequence 5, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Abeta13-28
; OTHER INFORMATION: peptide with carboxyl terminal Cys residue

```
; OTHER INFORMATION: inserted and two added Gly residues
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)_
; OTHER INFORMATION: Xaa = acetyl histidine
US-10-934-818-5

Query Match      80.6%; Score 25; DB 6; Length 19;
Best Local Similarity 83.3%; Pred. No. 8;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      4 KLVFFA 9

RESULT 12
US-11-016-706-36
; Sequence 36, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 36
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-36

Query Match      80.6%; Score 25; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      16 KLVFFA 21

RESULT 13
US-11-098-674-12
; Sequence 12, Application US/11098674
; Publication No. US20050267029A1
; GENERAL INFORMATION:
; APPLICANT: Ancsin, John B.
; APPLICANT: Elmova, Elena
; APPLICANT: Kisilevsky, Robert
; TITLE OF INVENTION: Compounds which Modulate Amyloidogenesis and Methods for Their
; FILE REFERENCE: PTQ-0066
; CURRENT APPLICATION NUMBER: US/11/098,674
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: US 60/559,122
; PRIOR FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 40
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-098-674-12

Query Match      80.6%; Score 25; DB 7; Length 40;
Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      16 KLVFFA 21

RESULT 14
US-10-923-605-1
; Sequence 1, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-923-605-1

Query Match      80.6%; Score 25; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
Db      16 KLVFFA 21

RESULT 15
US-10-934-818-1
; Sequence 1, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta42 beta-amyloid peptide
US-10-934-818-1

Query Match      80.6%; Score 25; DB 6; Length 42;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 KVFVFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 16

US-11-016-706-37
; Sequence 6, Application US/11016706
; Publication No. US20050244334A1
; GENERAL INFORMATION:
; APPLICANT: CASTILLO, GERARDO
; APPLICANT: LAKE, THOMAS P.
; APPLICANT: NGUYEN, BETH P.
; APPLICANT: SANDERS, VIRGINIA J.
; APPLICANT: SNOW, ALAN D.
; TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
; TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
; FILE REFERENCE: PROTEO.P03C13
; CURRENT APPLICATION NUMBER: US/11/016,706
; CURRENT FILING DATE: 2004-12-16
; PRIOR APPLICATION NUMBER: 09/962,955
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/938,275
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 08/947,057
; PRIOR FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 37
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-016-706-37

Query Match 80.6%; Score 25; DB 7; Length 42;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 KVFVFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 17

US-10-934-818-6
; Sequence 6, Application US/10934818
; Publication No. US20050255122A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 152703-472000US
; CURRENT APPLICATION NUMBER: US/10/934,818
; CURRENT FILING DATE: 2004-09-02
; PRIOR APPLICATION NUMBER: US 60/067,740
; PRIOR FILING DATE: 1997-12-02
; PRIOR APPLICATION NUMBER: US 60/080,970
; PRIOR FILING DATE: 1998-04-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human Abeta43 beta-amyloid peptide
US-10-934-818-6

Query Match 80.6%; Score 25; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 KVFVFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 18

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 80.6%; Score 25; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 KVFVFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 19

US-10-250-581-1
; Sequence 1, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 1
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-250-581-1

Query Match 80.6%; Score 25; DB 6; Length 43;
Best Local Similarity 83.3%; Pred. No. 17;
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 KVFVFA 6
| | | | |
Db 16 KLVFFA 21

RESULT 20

US-10-467-657-7560
; Sequence 7560, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11

; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7560
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7560

Query Match 80.6%; Score 25; DB 6; Length 184;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KEVFFFA 6
|||||
Db 91 KEVFLA 96

RESULT 21
US-11-082-389-350
; Sequence 350, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:

; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberer, Gregor

; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE

; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082,389
; CURRENT FILING DATE: 2005-03-16

; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23

; PRIOR APPLICATION NUMBER: US 60/141031

; PRIOR FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: US 60/143262

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: US 60/151281

; PRIOR FILING DATE: 1999-08-27

; PRIOR APPLICATION NUMBER: DE 19930487.4

; PRIOR FILING DATE: 1999-07-01

; PRIOR APPLICATION NUMBER: DE 19930489.0

; PRIOR FILING DATE: 1999-07-01

; PRIOR APPLICATION NUMBER: DE 19931549.3

; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19931550.7

; PRIOR FILING DATE: 1999-07-08

; PRIOR APPLICATION NUMBER: DE 19932134.5

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: DE 19941379.7

; PRIOR FILING DATE: 1999-08-31

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 446

; SEQ ID NO 350

; LENGTH: 525

; TYPE: PRT

; ORGANISM: Corynebacterium glutamicum

US-11-082-389-350

Query Match 80.6%; Score 25; DB 7; Length 525;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEVFFFA 6
|:|:|:
Db 230 KVFVFA 235

RESULT 22

US-10-982-545-15
; Sequence 15, Application US/10982545
; Publication No. US20050244890A1
; GENERAL INFORMATION:

; APPLICANT: Davies, Huw Alun

; APPLICANT: McGuire, James

; APPLICANT: Simonsen, Anja Hvild

; APPLICANT: Blennow, Kaj

; APPLICANT: Podust, Vladimir

; APPLICANT: CIPHERGEN Biosystems, Inc.

; TITLE OF INVENTION: Biomarkers for Alzheimer's Disease

; FILE REFERENCE: 016866-011550US

; CURRENT APPLICATION NUMBER: US/10/982,545

; CURRENT FILING DATE: 2004-11-06

; PRIOR APPLICATION NUMBER: US 60/518,360

; PRIOR FILING DATE: 2003-11-07

; PRIOR APPLICATION NUMBER: US 60/526,753

; PRIOR FILING DATE: 2003-12-02

; PRIOR APPLICATION NUMBER: US 60/546,423

; PRIOR FILING DATE: 2004-02-19

; PRIOR APPLICATION NUMBER: US 60/547,250

; PRIOR FILING DATE: 2004-02-23

; PRIOR APPLICATION NUMBER: US 60/558,896

; PRIOR FILING DATE: 2004-04-02

; PRIOR APPLICATION NUMBER: US 60/572,617

; PRIOR FILING DATE: 2004-05-18

; PRIOR APPLICATION NUMBER: US 60/586,503

; PRIOR FILING DATE: 2004-07-08

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 15

; LENGTH: 770

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Amyloid beta A4 precursor (APP, ABPP), isoform a, protease

; OTHER INFORMATION: nexin II (PN-II), cerebral vascular amyloid peptide (CVAP),

; OTHER INFORMATION: amyloid-beta protein, beta-amyloid peptide, A4 amyloid protein,

; OTHER INFORMATION: Alzheimer's disease amyloid protein

; NAME/KEY: SIGNAL

; LOCATION: (1)..(17)

; OTHER INFORMATION: signal peptide

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (1)..(40)

; OTHER INFORMATION: biomarker peptide 4320 Da (IMAC-Ni), A-beta 1-40

; OTHER INFORMATION: peptide fragment of Amyloid beta A4 precursor

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (18)..(687)

; OTHER INFORMATION: soluble APP-alpha

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (18)..(671)

; OTHER INFORMATION: soluble APP-beta

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (672)..(770)

; OTHER INFORMATION: C99

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (672)..(713)

; OTHER INFORMATION: beta-amyloid protein 42

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (672)..(711)

; OTHER INFORMATION: biomarker peptide 4330 Da, fragment of Amyloid

; OTHER INFORMATION: beta A4 precursor, beta-amyloid protein 40

; FEATURE:

; NAME/KEY: PEPTIDE

; LOCATION: (688)..(770)

; OTHER INFORMATION: C83

FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(713)
OTHER INFORMATION: P3(42)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (688)..(711)
OTHER INFORMATION: P3(40)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (712)..(770)
OTHER INFORMATION: gamma-CTF(59)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (714)..(770)
OTHER INFORMATION: gamma-CTF(57)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (721)..(770)
OTHER INFORMATION: gamma-CTF(50)
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (740)..(770)
OTHER INFORMATION: C31
US-10-982-545-15

Query Match 80.6%; Score 25; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 687 KLVFFA 692

RESULT 23
US-10-789-273-38
Sequence 38, Application US/10789273
Publication No. US20050249725A1
GENERAL INFORMATION:
APPLICANT: Basi, Gurliq
APPLICANT: Saldanha, Jose
APPLICANT: Yednock, Ted
TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
FILE REFERENCE: ELN-002CP
CURRENT APPLICATION NUMBER: US/10/789,273
CURRENT FILING DATE: 2004-02-27
PRIOR APPLICATION NUMBER: US/10/388,389
PRIOR FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 10/010,942
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: US 60/251,892
PRIOR FILING DATE: 2000-12-06
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 770
TYPE: PRT
ORGANISM: Homo sapiens
US-10-789-273-38

Query Match 80.6%; Score 25; DB 6; Length 770;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 687 KLVFFA 692

RESULT 24
US-10-467-657-3978

Sequence 3978, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3978
LENGTH: 194
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3978

Query Match 77.4%; Score 24; DB 6; Length 194;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 13 RFAFFA 18

RESULT 25
US-10-793-626-62
Sequence 62, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
LENGTH: 229
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: amino acid sequence
US-10-793-626-62

Query Match 77.4%; Score 24; DB 6; Length 229;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
DB 59 KVVYF 63

RESULT 26
US-10-793-626-1860
Sequence 1860, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04

```
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1860
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1860

Query Match      77.4%; Score 24; DB 6; Length 443;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
DB      168 KVFVF 172
      |:|

RESULT 27
US-10-467-657-4566
; Sequence 4566, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4566
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4566

Query Match      77.4%; Score 24; DB 6; Length 533;
Best Local Similarity 83.3%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KVFVFA 6
DB      165 KDFVFA 170
      |||

RESULT 28
US-11-080-991-48
; Sequence 48, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petteer Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080,991
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US/10/176,847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 657
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-48

Query Match      77.4%; Score 24; DB 7; Length 657;
Best Local Similarity 80.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVF 5
DB      90 KVFVF 94
      |:|

RESULT 29
US-10-467-657-4242
; Sequence 4242, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4242
; LENGTH: 916
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4242

Query Match      77.4%; Score 24; DB 6; Length 916;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KVFVFA 6
DB      655 QYVFA 660
      ::|||

RESULT 30
US-10-821-234-1120
; Sequence 1120, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt seq_genes Version 1.0
; SEQ ID NO 1120
; LENGTH: 4384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1120

Query Match      77.4%; Score 24; DB 6; Length 4384;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

Qy 1 KFVFFA 6
Db 1320 KFVFFA 1325

RESULT 31
US-10-467-657-1370
; Sequence 1370, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1370
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1370

Query Match 74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
Db 23 FVFFS 27

RESULT 32
US-10-467-657-2308
; Sequence 2308, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2308
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2308

Query Match 74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
Db 23 FVFFS 27

RESULT 33
US-10-467-657-5610
; Sequence 5610, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5610
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5610

Query Match 74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
Db 23 FVFFS 27

RESULT 34
US-10-467-657-7516
; Sequence 7516, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7516
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7516

Query Match 74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFFA 6
Db 23 FVFFS 27

RESULT 35
US-10-467-657-8322
; Sequence 8322, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

```

```
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8322
; LENGTH: 49
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8322

Query Match          74.2%; Score 23; DB 6; Length 49;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 23 FVFFS 27

RESULT 36
US-10-467-657-4324
; Sequence 4324, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4324
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4324

Query Match          74.2%; Score 23; DB 6; Length 54;
Best Local Similarity 80.0%; Pred. No. 53;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 44 FVFFS 48

RESULT 37
US-10-467-657-8286
; Sequence 8286, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
```

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 8286
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8286

Query Match          74.2%; Score 23; DB 6; Length 56;
Best Local Similarity 80.0%; Pred. No. 55;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 30 FVFFS 34

RESULT 38
US-10-793-626-2766
; Sequence 2766, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2766
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2766

Query Match          74.2%; Score 23; DB 6; Length 126;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
Db 10 YVFFA 14

RESULT 39
US-10-793-626-304
; Sequence 304, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 304
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-304

Query Match          74.2%; Score 23; DB 6; Length 209;
```


Best Local Similarity 60.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
:|:|
Db 145 RPIFF 149

RESULT 40

US-10-793-626-1034
; Sequence 1034, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P0348005
; PRIOR APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1034
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1034

Query Match 74.2%; Score 23; DB 6; Length 234;

Best Local Similarity 80.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|:|:|
Db 124 FMPFA 128

RESULT 41

US-10-467-657-4456
; Sequence 4456, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4456
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4456

Query Match 74.2%; Score 23; DB 6; Length 288;

Best Local Similarity 80.0%; Pred. No. 2.5e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
|:|:|
Db 61 KFAFF 65

RESULT 42

US-10-613-744-13
; Sequence 13, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-00290105
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-613-744-13

Query Match 74.2%; Score 23; DB 6; Length 391;

Best Local Similarity 60.0%; Pred. No. 3.3e+02;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
:|:|
Db 61 RPIFF 65

RESULT 43

US-10-467-657-4858
; Sequence 4858, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4858
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4858

Query Match 74.2%; Score 23; DB 6; Length 410;

Best Local Similarity 80.0%; Pred. No. 3.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFFA 6
|:|:|
Db 207 FLFFA 211

RESULT 44

US-11-055-822-1096

```
; Sequence 1096, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; METABOLIC PATHWAY PROTEINS
; FILE REFERENCE: BGI-121PCPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 1096
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-055-822-1096
```

```
Query Match 74.2%; Score 23; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 FVFFA 6
Db 329 FVIFA 333
```

```
RESULT 45
US-11-113-424-186
; Sequence 186, Application US/11113424
; Publication No. US20050260713A1
; GENERAL INFORMATION:
; APPLICANT: Gangolli et al.
; TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-225
; CURRENT APPLICATION NUMBER: US/11/113,424
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: 60/256,704
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/311,590
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/257,314
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/311,613
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/315,617
; PRIOR FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: 60/307,506
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/322,358
```

```
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/294,075
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/288,153
; PRIOR FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 190
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 186
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-11-113-424-186
```

```
Query Match 74.2%; Score 23; DB 7; Length 432;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 FVFFA 6
Db 399 FLFFA 403
```

```
RESULT 46
US-10-467-657-678
; Sequence 678, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 678
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-678
```

```
Query Match 74.2%; Score 23; DB 6; Length 449;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 2 FVFFA 6
Db 395 FVIFA 399
```

```
RESULT 47
US-11-082-389-348
; Sequence 348, Application US/11082389
; Publication No. US20050244935A1
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE
; TITLE OF INVENTION: INVOLVED IN TRANSPORT
; FILE REFERENCE: BGI-131PCPN
; CURRENT APPLICATION NUMBER: US/11/082,389
```

```

; CURRENT FILING DATE: 2005-03-16
; PRIOR APPLICATION NUMBER: US 09/603024
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 60/143262
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: US 60/151281
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930487.4
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19930489.0
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931549.3
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931550.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932134.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; REMAINING Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 446
; SEQ ID NO 348
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-11-082-389-348

Query Match          74.2%; Score 23; DB 7; Length 534;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 239 KFIY 243

RESULT 48
US-10-467-657-3440
; Sequence 3440, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3440
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3440

Query Match          74.2%; Score 23; DB 6; Length 633;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 367 KPAPF 371

RESULT 49
US-10-467-657-4632
; Sequence 4632, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4632
; LENGTH: 633
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4632

Query Match          74.2%; Score 23; DB 6; Length 633;
Best Local Similarity 80.0%; Pred. No. 5.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVF 5
Db 367 KPAPF 371

RESULT 50
US-11-186-284-125
; Sequence 125, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 125
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-125

Query Match          74.2%; Score 23; DB 7; Length 660;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVPA 6
Db 531 KAVEFA 536

```

```
/ TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ TITLE OF INVENTION: DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 908
/ LENGTH: 1012
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-995-561-908

Query Match      74.2%; Score 23; DB 6; Length 1012;
Best Local Similarity 80.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |:|||
Db      988 FLFFA 992

RESULT 54
US-10-793-626-760
/ Sequence 760, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 760
/ LENGTH: 2323
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-760

Query Match      74.2%; Score 23; DB 6; Length 2323;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |:|||
Db      1210 FMFFA 1214

RESULT 55
US-10-467-657-8998
/ Sequence 8998, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON Spa
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 8998
```

```
US-10-821-234-917
/ Sequence 917, Application US/10821234
/ Publication No. US20050255114A1
/ GENERAL INFORMATION:
/ APPLICANT: Labat, Ivan
/ APPLICANT: Stache-Crain, Birgit
/ APPLICANT: Andarmani, Susan
/ APPLICANT: Tang, Y. Tom
/ TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
/ FILE REFERENCE: 821A
/ CURRENT APPLICATION NUMBER: US/10/821,234
/ CURRENT FILING DATE: 2004-04-07
/ PRIOR APPLICATION NUMBER: US 60/462,047
/ PRIOR FILING DATE: 2003-04-07
/ NUMBER OF SEQ ID NOS: 1704
/ SOFTWARE: pc_SEQ_genes Version 1.0
/ SEQ ID NO 917
/ LENGTH: 708
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-821-234-917

Query Match      74.2%; Score 23; DB 6; Length 708;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KEVFFA 6
      |:|||
Db      579 KAVFFA 594

RESULT 52
US-10-793-626-420
/ Sequence 420, Application US/10793626
/ Publication No. US20050255478A1
/ GENERAL INFORMATION:
/ APPLICANT: KIMMERLY, WILLIAM JOHN
/ TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
/ FILE REFERENCE: PU3480US
/ CURRENT APPLICATION NUMBER: US/10/793,626
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: 60/164,258
/ PRIOR FILING DATE: 1999-11-09
/ NUMBER OF SEQ ID NOS: 4472
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 420
/ LENGTH: 766
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
/ OTHER INFORMATION: amino acid sequence
US-10-793-626-420

Query Match      74.2%; Score 23; DB 6; Length 766;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFFA 6
      |:|||
Db      357 FMFFA 361

RESULT 53
US-10-995-561-908
/ Sequence 908, Application US/10995561
/ Publication No. US2005027054A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
```

```
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8998

Query Match          71.0%; Score 22; DB 6; Length 30;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFF 5
Db      7 FVFF 10

RESULT 56
US-11-000-463-378
; Sequence 378, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 378
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-378

Query Match          71.0%; Score 22; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFF 5
Db      8 FVFF 11

RESULT 57
US-11-000-463-850
; Sequence 850, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
```

```
; APPLICANT: Chen, Rui-hong B.
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 850
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-850

Query Match          71.0%; Score 22; DB 7; Length 72;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFF 5
Db      8 FVFF 11

RESULT 58
US-10-467-657-360
; Sequence 360, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 360
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-360

Query Match          71.0%; Score 22; DB 6; Length 77;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 FVFF 5
Db      8 FVFF 11
```

Db 32 FVFF 35

RESULT 59
US-10-467-657-2026
; Sequence 2026, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2026
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2026

Query Match 71.0%; Score 22; DB 6; Length 79;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
:|:|
Db 10 QVFF 14

RESULT 60
US-10-485-517-286
; Sequence 286, Application US/10485517
; Publication No. US2005025629A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynex Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 286
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-286

Query Match 71.0%; Score 22; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5
|||
Db 83 FVFF 86

RESULT 61
US-10-467-657-6824
; Sequence 6824, Application US/10467657

; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6824
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6824

Query Match 71.0%; Score 22; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5
|||
Db 62 FVFF 65

RESULT 62
US-11-125-837-24
; Sequence 24, Application US/11125837
; Publication No. US20050266003A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Rwa
; APPLICANT: Chang, Chung Nan
; APPLICANT: Chen, Pei-Jiun
; APPLICANT: Huang, Chiu-Chen
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: 13062-011001
; CURRENT APPLICATION NUMBER: US/11/125,837
; CURRENT FILING DATE: 2005-05-10
; PRIOR APPLICATION NUMBER: US 60/569,892
; PRIOR FILING DATE: 2004-05-10
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-125-837-24

Query Match 71.0%; Score 22; DB 7; Length 139;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
|:|
Db 6 KVVFF 10

RESULT 63
US-10-467-657-6110
; Sequence 6110, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6110
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6110

Query Match 71.0%; Score 22; DB 6; Length 149;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6
: ||||
Db 88 EFPFFA 93

RESULT 64
US-10-467-657-7550
; Sequence 7550, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7550
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7550

Query Match 71.0%; Score 22; DB 6; Length 149;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6
: ||||
Db 88 EFPFFA 93

RESULT 65
US-10-467-657-6130
; Sequence 6130, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 6130
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6130

Query Match 71.0%; Score 22; DB 6; Length 154;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFFA 6
: ||||
Db 93 EFPFFA 98

RESULT 66
US-10-485-517-346
; Sequence 346, Application US/10485517
; Publication No. US20050256299A1
; GENERAL INFORMATION:
; APPLICANT: University of Sheffield
; APPLICANT: Biosynexus Incorporated
; APPLICANT: Foster, Simon
; APPLICANT: Mond, James
; TITLE OF INVENTION: Antigenic Polypeptides
; FILE REFERENCE: P100629WO
; CURRENT APPLICATION NUMBER: US/10/485,517
; CURRENT FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: GB 0118825.9
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: GB 0200349.9
; PRIOR FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 424
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 346
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-346

Query Match 71.0%; Score 22; DB 6; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FVFF 5
: ||||
Db 134 FVFF 137

RESULT 67
US-10-980-388-65
; Sequence 65, Application US/10980388
; Publication No. US20050255490A1
; GENERAL INFORMATION:
; APPLICANT: Vogell, Gabriel
; APPLICANT: Parodi, Luis A.
; APPLICANT: Hiebsch, Ronald R.
; APPLICANT: Lind, Peter
; APPLICANT: Kaytes, Paul S.
; APPLICANT: Ruff, Valerie
; APPLICANT: Ruff, Rita M.
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related App
; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303

```

; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 65
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-65

Query Match          71.0%; Score 22; DB 6; Length 187;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 179 RVVFA 184

RESULT 68
US-10-467-657-4386
; Sequence 4386, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4386
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4386

Query Match          71.0%; Score 22; DB 6; Length 210;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 72 FVFF 75

RESULT 69
US-10-467-657-3000
; Sequence 3000, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega

```

```

; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3000
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3000

Query Match          71.0%; Score 22; DB 6; Length 222;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 143 FVFF 146

RESULT 70
US-10-467-657-6248
; Sequence 6248, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6248
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6248

Query Match          71.0%; Score 22; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 218 FVFF 221

RESULT 71
US-11-054-515-1391
; Sequence 1391, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PFS23F3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14

```


; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1391
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1391

Query Match 71.0%; Score 22; DB 7; Length 240;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 56 RFVYVA 61

RESULT 72
US-11-074-176-66
; Sequence 66, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAuliffe, Olivia
; APPLICANT: Peril, Andrea Ascarate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Lactobacillus acidophilus
US-11-074-176-66

Query Match 71.0%; Score 22; DB 7; Length 241;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 229 KFDVFA 234

RESULT 73
US-10-793-626-1124
; Sequence 1124, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US

; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1124
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1124

Query Match 71.0%; Score 22; DB 6; Length 250;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 65 FVFF 68

RESULT 74
US-10-467-657-6144
; Sequence 6144, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 6144
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-6144

Query Match 71.0%; Score 22; DB 6; Length 254;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FVFF 5
Db 197 FVFF 200

RESULT 75
US-10-467-657-1178
; Sequence 1178, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12

```
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 1178
; LENGTH: 268
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1178

Query Match      71.0%; Score 22; DB 6; Length 268;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 FVFFA 6
      | |||
Db      25 FAFFA 29

Search completed: December 29, 2005, 18:50:19
Job time : 3.29032 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2005, 17:47:53 ; Search time 66.2903 Seconds
(without alignments)
37.818 Million cell updates/sec

Title: US-10-009-122-12

Perfect score: 31

Sequence: 1 KPVFFA 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 300 summaries

Database :

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	6	3	US-09-867-847-13
2	31	100.0	6	3	US-09-867-847-21
3	31	100.0	6	3	US-09-915-092-3
4	31	100.0	6	3	US-09-915-092-11
5	31	100.0	6	3	US-09-747-408-4
6	31	100.0	6	3	US-09-747-408-12
7	31	100.0	6	5	US-10-728-028-3
8	31	100.0	6	5	US-10-728-028-11
9	31	100.0	6	5	US-10-825-958-11
10	31	100.0	6	5	US-10-825-958-19
11	31	100.0	59	4	US-10-424-599-174685
12	31	100.0	64	4	US-10-424-599-164908
13	31	100.0	102	4	US-10-424-599-203722
14	31	100.0	175	4	US-10-437-963-118848
15	31	100.0	372	4	US-10-437-963-118846
16	31	100.0	373	4	US-10-437-963-138916
17	30	96.8	420	4	US-10-437-963-118773
18	30	90.3	54	4	US-10-424-599-266901
19	28	90.3	115	4	US-10-425-115-327241
20	28	90.3	126	4	US-10-425-115-290464
21	28	90.3	159	4	US-10-425-115-193086
22	28	90.3	240	4	US-10-767-701-37567
23	28	90.3	452	4	US-10-369-493-6279
24	28	90.3	490	5	US-10-994-726-438
25	28	90.3	506	3	US-09-877-476-2
26	28	90.3	506	3	US-09-877-476-28
27	28	90.3	506	3	US-09-877-476-30

28	90.3	506	3	US-09-877-476-36	Sequence 36, Appl
28	90.3	506	4	US-10-276-977-7	Sequence 7, Appl
28	90.3	506	4	US-10-758-524-2	Sequence 2, Appl
28	90.3	506	4	US-10-758-524-28	Sequence 28, Appl
28	90.3	506	4	US-10-758-524-30	Sequence 30, Appl
28	90.3	506	4	US-10-758-524-36	Sequence 36, Appl
28	90.3	508	4	US-10-282-122A-47052	Sequence 47052, A
28	90.3	508	5	US-10-994-726-437	Sequence 437, App
28	90.3	509	5	US-10-732-923-18725	Sequence 18725, A
28	90.3	509	5	US-10-732-923-18726	Sequence 18726, A
28	90.3	509	5	US-10-732-923-18737	Sequence 18737, A
28	90.3	571	4	US-10-282-122A-51929	Sequence 51929, A
28	90.3	1089	4	US-10-369-493-2154	Sequence 2154, Ap
27	87.1	34	4	US-10-425-115-236339	Sequence 236339, A
27	87.1	46	4	US-10-425-115-200545	Sequence 200545, A
27	87.1	47	4	US-10-424-599-232761	Sequence 232761, A
27	87.1	48	4	US-10-425-115-206883	Sequence 206883, A
27	87.1	56	4	US-10-437-963-176215	Sequence 176215, A
27	87.1	57	4	US-10-425-114-38807	Sequence 38807, A
27	87.1	62	3	US-09-764-877-1136	Sequence 1136, Ap
27	87.1	62	4	US-10-242-515-1136	Sequence 1136, Ap
27	87.1	63	4	US-10-424-599-146372	Sequence 146372, A
27	87.1	72	4	US-10-425-115-248149	Sequence 248149, A
27	87.1	73	4	US-10-425-115-229605	Sequence 229605, A
27	87.1	80	4	US-10-425-115-259222	Sequence 259222, A
27	87.1	81	4	US-10-425-115-215979	Sequence 215979, A
27	87.1	82	4	US-10-424-599-195261	Sequence 195261, A
27	87.1	82	5	US-10-450-763-44156	Sequence 44156, A
27	87.1	83	4	US-10-425-115-275005	Sequence 275005, A
27	87.1	88	4	US-10-424-599-259257	Sequence 259257, A
27	87.1	92	4	US-10-424-599-246138	Sequence 246138, A
27	87.1	96	4	US-10-424-599-207674	Sequence 207674, A
27	87.1	99	4	US-10-425-115-221194	Sequence 221194, A
27	87.1	103	4	US-10-424-599-182454	Sequence 182454, A
27	87.1	103	4	US-10-437-963-201763	Sequence 201763, A
27	87.1	104	3	US-09-823-153-4	Sequence 4, Appl
27	87.1	104	4	US-10-713-981-4	Sequence 4, Appl
27	87.1	106	4	US-10-425-115-215097	Sequence 215097, A
27	87.1	107	4	US-10-424-599-207673	Sequence 207673, A
27	87.1	107	4	US-10-437-963-146282	Sequence 146282, A
27	87.1	109	4	US-10-424-599-278159	Sequence 278159, A
27	87.1	109	4	US-10-425-115-208261	Sequence 208261, A
27	87.1	110	4	US-10-425-115-286779	Sequence 286779, A
27	87.1	115	3	US-09-864-408A-4214	Sequence 4214, Ap
27	87.1	116	4	US-10-425-115-256025	Sequence 256025, A
27	87.1	125	4	US-10-425-115-289631	Sequence 289631, A
27	87.1	131	4	US-10-424-599-208184	Sequence 208184, A
27	87.1	131	4	US-10-424-599-221174	Sequence 221174, A
27	87.1	146	5	US-10-450-763-56921	Sequence 56921, A
27	87.1	146	4	US-10-424-599-214877	Sequence 214877, A
27	87.1	153	4	US-10-424-599-243854	Sequence 243854, A
27	87.1	158	4	US-10-424-599-169140	Sequence 169140, A
27	87.1	173	4	US-10-408-765A-1782	Sequence 1782, Ap
27	87.1	173	5	US-10-220-335-207	Sequence 207, App
27	87.1	189	4	US-10-432-198-4	Sequence 4, Appl
27	87.1	189	4	US-10-432-198-5	Sequence 5, Appl
27	87.1	189	4	US-10-432-198-6	Sequence 6, Appl
27	87.1	189	4	US-10-432-198-7	Sequence 7, Appl
27	87.1	206	4	US-10-238-075-489	Sequence 489, App
27	87.1	211	4	US-10-425-115-359320	Sequence 359320, A
27	87.1	212	4	US-10-425-115-359323	Sequence 359323, A
27	87.1	212	4	US-10-424-599-211252	Sequence 211252, A
27	87.1	221	5	US-10-276-722A-7	Sequence 7, Appl
27	87.1	221	5	US-10-450-763-37353	Sequence 37353, A
27	87.1	240	5	US-10-450-763-53342	Sequence 53342, A
27	87.1	240	4	US-10-724-972A-7100	Sequence 7100, Ap
27	87.1	285	4	US-10-437-963-183912	Sequence 183912, A
27	87.1	285	4	US-10-425-115-246512	Sequence 246512, A
27	87.1	297	3	US-09-864-921-180	Sequence 180, App
27	87.1	332	5	US-10-766-682-180	Sequence 180, App
27	87.1	332	4	US-10-424-599-247557	Sequence 247557, A
27	87.1	335	4	US-10-425-115-359332	Sequence 359332, A
27	87.1	335	5	US-10-739-930-8473	Sequence 8473, Ap


```

247 26 83.9 426 3 US-09-738-626-6036
248 26 83.9 426 4 US-10-627-476-424
249 26 83.9 431 5 US-10-495-148-21
250 26 83.9 431 5 US-10-732-923-11170
251 26 83.9 437 5 US-10-501-282-5896
252 26 83.9 442 4 US-10-437-963-145134
253 26 83.9 444 4 US-10-369-493-9766
254 26 83.9 446 5 US-10-732-923-23883
255 26 83.9 459 4 US-10-369-493-18271
256 26 83.9 459 5 US-10-732-923-23570
257 26 83.9 465 4 US-10-424-599-254007
258 26 83.9 466 5 US-10-732-923-11191
259 26 83.9 470 4 US-10-437-963-155526
260 26 83.9 483 4 US-10-369-493-5486
261 26 83.9 483 4 US-10-369-493-5487
262 26 83.9 504 6 US-11-097-143-21684
263 26 83.9 518 4 US-10-032-585-7864
264 26 83.9 526 4 US-10-369-493-3924
265 26 83.9 536 4 US-10-424-599-21613
266 26 83.9 548 4 US-10-282-122A-63246
267 26 83.9 581 6 US-11-097-143-15831
268 26 83.9 618 5 US-10-450-763-56476
269 26 83.9 641 5 US-10-450-763-55856
270 26 83.9 661 4 US-10-425-115-330488
271 26 83.9 681 4 US-10-335-977-5995
272 26 83.9 690 4 US-10-425-114-61393
273 26 83.9 698 4 US-10-437-963-132561
274 26 83.9 712 4 US-10-335-977-5996
275 26 83.9 717 4 US-10-335-977-5997
276 26 83.9 749 4 US-10-369-493-22359
277 26 83.9 754 6 US-11-097-143-23787
278 26 83.9 860 6 US-11-097-143-21294
279 26 83.9 888 4 US-10-282-122A-63048
280 26 83.9 891 6 US-11-097-143-26673
281 26 83.9 919 5 US-10-200-545-95
282 26 83.9 960 4 US-10-437-963-129061
283 26 83.9 976 5 US-10-732-923-1219
284 26 83.9 994 4 US-10-437-963-129064
285 26 83.9 1082 4 US-10-282-122A-49664
286 26 80.6 6 3 US-09-867-847-7
287 25 80.6 6 3 US-09-867-847-11
288 25 80.6 6 3 US-09-867-847-19
289 25 80.6 6 3 US-09-867-847-20
290 25 80.6 6 3 US-09-972-475-9
291 25 80.6 6 3 US-09-915-092-1
292 25 80.6 6 3 US-09-915-092-9
293 25 80.6 6 3 US-09-915-092-10
294 25 80.6 6 3 US-09-915-092-28
295 25 80.6 6 3 US-09-956-625-25
296 25 80.6 6 3 US-09-747-408-1
297 25 80.6 6 3 US-09-747-408-3
298 25 80.6 6 3 US-09-747-408-10
299 25 80.6 6 3 US-09-747-408-11
300 25 80.6 6 4 US-10-463-729-9

```

ALIGNMENTS

```

RESULT 1
US-09-867-847-13
; Sequence 13, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20

```

```

; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-13

Query Match 100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
DB 1 KPVFFA 6

RESULT 2
US-09-867-847-21
; Sequence 21, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-09-867-847-21

Query Match 100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
DB 1 KPVFFA 6

RESULT 3
US-09-915-092-3
; Sequence 3, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xianqi
; APPLICANT: Chalfour, Robert

```

```
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-3
```

```
Query Match          100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVFA 6
        |||||
Db       1 KVFVFA 6
```

RESULT 4

```
US-09-915-092-11
; Sequence 11, Application US/09915092
; Publication No. US2002011571A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139
; CURRENT APPLICATION NUMBER: US/09/915,092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220,808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-092-11
```

```
Query Match          100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVFA 6
        |||||
Db       1 KVFVFA 6
```

RESULT 5

```
US-09-747-408-4
; Sequence 4, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-4
```

```
Query Match          100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVFA 6
        |||||
Db       1 KVFVFA 6
```

RESULT 6

```
US-09-747-408-12
; Sequence 12, Application US/09747408
; Publication No. US20030003141A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan M.
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: Compounds And Methods For Modulating
; FILE OF INVENTION: Cerebral Amyloid Angiopathy
; FILE REFERENCE: NBI-088
; CURRENT APPLICATION NUMBER: US/09/747,408
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,877
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-747-408-12
```

```
Query Match          100.0%; Score 31; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 KVFVFA 6
        |||||
Db       1 KVFVFA 6
```

RESULT 7

```
US-10-728-028-3
; Sequence 3, Application US/10728028
; Publication No. US20050048000A1
; GENERAL INFORMATION:
; APPLICANT: Gervais, Francine
; APPLICANT: Kong, Xiangqi
; APPLICANT: Chalifour, Robert
; APPLICANT: Migneault, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; FILE OF INVENTION: USES THEREOF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; CURRENT FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: 60/443291
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 09/915092
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: 60/220808
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-3

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 1 KVFVFA 6

RESULT 8

US-10-728-028-11
; Sequence 11, Application US/10728028
; Publication No. US20050048000A1

; GENERAL INFORMATION:
; APPLICANT: GERVAIS, Francine
; APPLICANT: KONG, Xianqi
; APPLICANT: CHALIFOUR, Robert
; APPLICANT: MIGNERULT, David
; TITLE OF INVENTION: AMYLOID TARGETING IMAGING AGENTS AND
; TITLE OF INVENTION: US2 THEROF
; FILE REFERENCE: NBI-139CP
; CURRENT APPLICATION NUMBER: US/10/728,028
; PRIOR FILING DATE: 2003-12-03
; PRIOR FILING DATE: 2003-01-29
; PRIOR FILING DATE: 2001-07-24
; PRIOR FILING DATE: 2000-07-25
; PRIOR FILING DATE: 2000-07-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-728-028-11

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 1 KVFVFA 6

RESULT 9

US-10-825-958-11
; Sequence 11, Application US/10825958
; Publication No. US20050090439A1

; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11

; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-10-825-958-11

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 1 KVFVFA 6

RESULT 10

US-10-825-958-19
; Sequence 19, Application US/10825958
; Publication No. US20050090439A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 50291/004002
; CURRENT APPLICATION NUMBER: US/10/825,958
; CURRENT FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (6)
; OTHER INFORMATION: AMIDATION
US-10-825-958-19

Query Match 100.0%; Score 31; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
Db 1 KVFVFA 6

RESULT 11

US-10-424-599-174685
; Sequence 174685, Application US/10424599
; Publication No. US20040031072A1

; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 174685
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_12875C.1.pep
US-10-424-599-174685

Query Match 100.0%; Score 31; DB 4; Length 59;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 11 KVFVFA 16

RESULT 12
US-10-424-599-164908
; Sequence 164908, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 164908
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_11992C.1.pep
US-10-424-599-164908

Query Match 100.0%; Score 31; DB 4; Length 64;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 34 KVFVFA 39

RESULT 13
US-10-424-599-203722
; Sequence 203722, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 203722
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_25988C.1.pep
US-10-424-599-203722

Query Match 100.0%; Score 31; DB 4; Length 102;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVFVFA 6
Db 5 KVFVFA 10

RESULT 14
US-10-437-963-118848
; Sequence 118848, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118848
; LENGTH: 175
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22120C.1.pep
US-10-437-963-118848

Query Match 100.0%; Score 31; DB 4; Length 175;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 80 KVFVFA 85

RESULT 15
US-10-437-963-118846
; Sequence 118846, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118846
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(372)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_22119C.1.pep
US-10-437-963-118846

Query Match 100.0%; Score 31; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 121 KVFVFA 126

RESULT 16

US-10-437-963-138916
; Sequence 138916, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 138916
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_4025C.1.pep
US-10-437-963-138916

Query Match 100.0%; Score 31; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 80 KVFVFA 85

RESULT 17

US-10-437-963-118773
; Sequence 118773, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 118773
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_22052C.1.pep

US-10-437-963-118773

Query Match 96.8%; Score 30; DB 4; Length 420;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 355 KVFVFA 360

RESULT 18

US-10-424-599-266901
; Sequence 266901, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 266901
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(54)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_83031C.1.pep
US-10-424-599-266901

Query Match 90.3%; Score 28; DB 4; Length 54;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
Db 18 KVFVFA 23

RESULT 19

US-10-425-115-327241
; Sequence 327241, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 327241
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_61513C.1.pep
US-10-425-115-327241

Query Match 90.3%; Score 28; DB 4; Length 115;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
|||||
Db 72 KVFVFS 77

RESULT 20

US-10-425-115-290464
; Sequence 290464, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 290464
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_27992C.1.pap
US-10-425-115-290464

Query Match 90.3%; Score 28; DB 4; Length 126;
Best Local Similarity 83.3%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVEFA 6
||:|
Db 99 KFVFFA 104

RESULT 21

US-10-425-115-193086
; Sequence 193086, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 193086
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(159)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_10767C.1.pap
US-10-425-115-193086

Query Match 90.3%; Score 28; DB 4; Length 159;
Best Local Similarity 83.3%; Pred. No. 5.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVEFA 6
:|||||
Db 89 RVVFFA 94

RESULT 22

US-10-767-701-37567
; Sequence 37567, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 37567
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C3123_1.pap
US-10-767-701-37567

Query Match 90.3%; Score 28; DB 4; Length 240;
Best Local Similarity 83.3%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
|||||
Db 155 KVFVFS 160

RESULT 23

US-10-369-493-6279
; Sequence 6279, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6279
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6279

Query Match 90.3%; Score 28; DB 4; Length 452;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFFA 6
:|||||
Db 291 RVVFFA 296

RESULT 24

US-10-994-726-438
; Sequence 438, Application US/10994726
; Publication No. US20050147999A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Lyme Disease Vaccines
; FILE REFERENCE: PB481D1

; CURRENT APPLICATION NUMBER: US/10/994,726
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: 09/830,230
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: PCT/US98/12718
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/057,483
; PRIOR FILING DATE: 1997-09-03
; PRIOR APPLICATION NUMBER: 60/053,344
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/053,377
; PRIOR FILING DATE: 1997-07-22
; PRIOR APPLICATION NUMBER: 60/050,359
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 438
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-994-726-438

Query Match 90.3%; Score 28; DB 5; Length 490;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 23 RVVFA 28
:|||||

RESULT 25
US-09-877-476-2
; Sequence 2, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-877-476-2

Query Match 90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 356 KFLFFA 361
:|||||

RESULT 26
US-09-877-476-28
; Sequence 28, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476

; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 176 amino acids from B. napus elongase KCS (SEQ ID NO:4) and 3' 330 amino acids from A. thaliana
; OTHER INFORMATION: FAE1 (SEQ ID NO:2); designated Bn176
US-09-877-476-28

Query Match 90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 356 KFLFFA 361
:|||||

RESULT 27
US-09-877-476-30
; Sequence 30, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' 399 amino acids from A. thaliana FAE1 (SEQ ID NO:2) and 3' 107 amino acids from B. napus
; OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399
; NAME/KEY: VARIANT
; LOCATION: (0)...(0)
; OTHER INFORMATION: Xaa = Pro or Gln
US-09-877-476-30

Query Match 90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
Db 356 KFLFFA 361
:|||||

RESULT 28
US-09-877-476-36
; Sequence 36, Application US/09877476
; Patent No. US20020049994A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108001
; CURRENT APPLICATION NUMBER: US/09/877,476

```

; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,326
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 506 amino acids from A. thaliana FAE1 (SEQ ID
; OTHER INFORMATION: NO:2) having a mutation at residue 92; designated
; OTHER INFORMATION: At K92R; hypothetical
US-09-877-476-36

Query Match          90.3%; Score 28; DB 3; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
      ||:|||
Db      356 KFLFFA 361

RESULT 29
US-10-276-977-7
; Sequence 7, Application US/10276977
; Publication No. US2004049806A1
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF BRITISH COLUMBIA
; APPLICANT: KUNST, LJERKA
; APPLICANT: SMITH, MARK A.
; APPLICANT: MOON, HANGSIK
; TITLE OF INVENTION: NUCLEIC ACID ENCODING A PLANT VERY LONG CHAIN
; TITLE OF INVENTION: FATTY ACID BIOSYNTHETIC ENZYME
; FILE REFERENCE: 56120-5004US
; CURRENT APPLICATION NUMBER: US/10/276,977
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: PCT/IB01/01140
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,789
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-276-977-7

Query Match          90.3%; Score 28; DB 4; Length 506;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVFA 6
      ||:|||
Db      356 KFLFFA 361

RESULT 30
US-10-758-524-2
; Sequence 2, Application US/10758524
; Publication No. US20040139498A1
; GENERAL INFORMATION:
; APPLICANT: Jaworski, Jan G.
; APPLICANT: Blacklock, Brenda J.
; TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
; TITLE OF INVENTION: SYNTHASE POLYPEPTIDES
; FILE REFERENCE: 07148-108002
; CURRENT APPLICATION NUMBER: US/10/758,524
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: 09/877,476
; PRIOR FILING DATE: 2001-06-08

```

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 30
 LENGTH: 506
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: 5' 399 amino acids from A. thaliana PAE1 (SEQ ID NO:2) and 3' 107 amino acids from B. napus
 OTHER INFORMATION: elongase KCS (SEQ ID NO:4); designated At399
 FEATURE:
 NAME/KEY: VARIANT
 LOCATION: (0)...(0)
 OTHER INFORMATION: Xaa = Pro or Gln
 US-10-758-524-30

Query Match 90.3%; Score 28; DB 4; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 33

US-10-758-524-36
 Sequence 36, Application US/10758524
 Publication No. US20040139498A1
 GENERAL INFORMATION:
 APPLICANT: Jaworski, Jan G.
 APPLICANT: Blacklock, Brenda J.
 TITLE OF INVENTION: FATTY ACID ELONGASE 3-KETOACYL COA
 FILE REFERENCE: 07148-108002
 CURRENT APPLICATION NUMBER: US/10758,524
 CURRENT FILING DATE: 2004-01-15
 PRIOR APPLICATION NUMBER: 09/877,476
 PRIOR FILING DATE: 2001-06-08
 PRIOR APPLICATION NUMBER: 60/210,326
 PRIOR FILING DATE: 2000-06-08
 NUMBER OF SEQ ID NOS: 56
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 36
 LENGTH: 506
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: 506 amino acids from A. thaliana PAE1 (SEQ ID NO:2) having a mutation at residue 92; designated
 OTHER INFORMATION: At K92R; hypothetical
 US-10-758-524-36

Query Match 90.3%; Score 28; DB 4; Length 506;
 Best Local Similarity 83.3%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
 ||:||||
 Db 356 KFLFFA 361

RESULT 34

US-10-282-122A-47052
 Sequence 47052, Application US/10282122A
 Publication No. US20040029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel

APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELIFRA.034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 47052
 LENGTH: 508
 TYPE: PRT
 ORGANISM: Borrelia burgdorferi
 US-10-282-122A-47052

Query Match 90.3%; Score 28; DB 4; Length 508;
 Best Local Similarity 83.3%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVFFA 6
 ||:||||
 Db 41 RLVFFA 46

RESULT 35

US-10-994-726-437
 Sequence 437, Application US/10994726
 Publication No. US20050147999A1
 GENERAL INFORMATION:
 APPLICANT: Ni et al.
 TITLE OF INVENTION: Lyme Disease Vaccines
 FILE REFERENCE: PB481D1
 CURRENT APPLICATION NUMBER: US/10/994,726
 CURRENT FILING DATE: 2004-11-23
 PRIOR APPLICATION NUMBER: 09/830,230
 PRIOR FILING DATE: 2001-04-24
 PRIOR APPLICATION NUMBER: PCT/US98/12718
 PRIOR FILING DATE: 1998-06-18
 PRIOR APPLICATION NUMBER: 60/057,483
 PRIOR FILING DATE: 1997-09-03
 PRIOR APPLICATION NUMBER: 60/053,344
 PRIOR FILING DATE: 1997-07-22
 PRIOR APPLICATION NUMBER: 60/053,377
 PRIOR FILING DATE: 1997-07-22
 PRIOR APPLICATION NUMBER: 60/050,359
 PRIOR FILING DATE: 1997-06-20
 NUMBER OF SEQ ID NOS: 756
 SOFTWARE: PatentIn Ver. 3.3
 SEQ ID NO 437
 LENGTH: 508

```
; TYPE: PRT
; ORGANISM: Borrelia burgdorferi
US-10-994-726-437

Query Match          90.3%; Score 28; DB 5; Length 508;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||||
Db 41 RVVFFA 46

RESULT 36
US-10-732-923-18725
; Sequence 18725, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18725
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica juncea
US-10-732-923-18725

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||||
Db 359 KFLFFA 364

RESULT 37
US-10-732-923-18726
; Sequence 18726, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18726
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica juncea
US-10-732-923-18726

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||||
Db 358 KFLFFA 363

RESULT 38
US-10-732-923-18737
; Sequence 18737, Application US/10732923
; Publication No. US20050108791A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 18737
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Brassica rapa
US-10-732-923-18737

Query Match          90.3%; Score 28; DB 5; Length 509;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
   :|||||
Db 358 KFLFFA 363

RESULT 39
US-10-282-122A-51929
; Sequence 51929, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51929
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-282-122A-51929
```

Query Match 90.3%; Score 28; DB 4; Length 571;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFF 6
Db 314 KFMFFA 319

RESULT 40
US-10-369-493-2154
; Sequence 2154, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2154
; LENGTH: 1089
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; NAME/KEY: unsure
; LOCATION: (1)..(1089)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2154

Query Match 90.3%; Score 28; DB 4; Length 1089;
Best Local Similarity 83.3%; Pred. No. 3.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFF 6
Db 13 KFPVFF 18

RESULT 41
US-10-425-115-236339
; Sequence 236339, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 236339
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_147123C.1.pep
US-10-425-115-236339

Query Match 87.1%; Score 27; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFF 5
Db 23 KFPVFF 27

RESULT 42
US-10-425-115-200545
; Sequence 200545, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 200545
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_114485C.1.pep
US-10-425-115-200545

Query Match 87.1%; Score 27; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFF 5
Db 25 KFPVFF 29

RESULT 43
US-10-424-599-232761
; Sequence 232761, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 232761
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52207C.1.pep
US-10-424-599-232761

Query Match 87.1%; Score 27; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFPVFF 5
Db 11 KFPVFF 15

RESULT 44
US-10-425-115-206883
; Sequence 206883, Application US/10425115

```
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-21(53222)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/ SEQ ID NO 206883
/ LENGTH: 48
/ TYPE: PRT
/ ORGANISM: Zea mays
/ FEATURE:
/ OTHER INFORMATION: Clone ID: MRT4577_120267C.1.pap
US-10-425-115-206883

Query Match      87.1%; Score 27; DB 4; Length 48;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
DB 15 KPAFFA 20

RESULT 45
US-10-437-963-176215
/ Sequence 176215, Application US/10437963
/ Publication No. US20040123343A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 176215
/ LENGTH: 56
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_73986C.1.pap
US-10-437-963-176215

Query Match      87.1%; Score 27; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFF 5
DB 13 KVFVFF 17

RESULT 46
US-10-425-114-38807
/ Sequence 38807, Application US/10425114
/ Publication No. US20040034888A1
/ GENERAL INFORMATION:
/ APPLICANT: Liu, Jingdong
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Kovalic, David K.

/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: Screen, Steven E
/ APPLICANT: Tabaska, Jack E
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53313)B
/ CURRENT APPLICATION NUMBER: US/10/425,114
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 73128
/ SEQ ID NO 38807
/ LENGTH: 57
/ TYPE: PRT
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: 700684806_FLI.pap
US-10-425-114-38807

Query Match      87.1%; Score 27; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
DB 29 KVFVF 33

RESULT 47
US-09-764-877-1136
/ Sequence 1136, Application US/09764877
/ Patent No. US20020147140A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC005
/ CURRENT APPLICATION NUMBER: US/09/764,877
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - refer to PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 4031
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1136
/ LENGTH: 62
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: SITE
/ LOCATION: (55)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
/ NAME/KEY: SITE
/ LOCATION: (60)
/ OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-877-1136

Query Match      87.1%; Score 27; DB 3; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVF 5
DB 31 KVFVF 35

RESULT 48
US-10-242-515-1136
/ Sequence 1136, Application US/10242515
/ Publication No. US20040009488A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC005C1
/ CURRENT APPLICATION NUMBER: US/10/242,515
/ CURRENT FILING DATE: 2002-09-13
/ PRIOR APPLICATION NUMBER: 09/764,877
/ PRIOR FILING DATE: 2001-01-17
```



```
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1136
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (55)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-242-515-1136

Query Match      87.1%; Score 27; DB 4; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
        |||||
Db      31 KVFVF 35

RESULT 49
US-10-424-599-146372
; Sequence 146372, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 146372
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_103191C.1.pep
US-10-424-599-146372

Query Match      87.1%; Score 27; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
        |||||
```

```
Db      18 KVFVF 22

RESULT 50
US-10-425-115-248149
; Sequence 248149, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 248149
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_157899C.1.pep
US-10-425-115-248149

Query Match      87.1%; Score 27; DB 4; Length 72;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
        |||||
Db      67 KVFVF 71

RESULT 51
US-10-425-115-229605
; Sequence 229605, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 229605
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_140993C.1.pep
US-10-425-115-229605

Query Match      87.1%; Score 27; DB 4; Length 73;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFVF 5
        |||||
Db      1 KVFVF 5

RESULT 52
US-10-425-115-259222
```

; Sequence 259222, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 259222
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_167996C.1.pep
US-10-425-115-259222

Query Match 87.1%; Score 27; DB 4; Length 80;
Best Local Similarity 83.3%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
DB 66 KFTFFA 71

RESULT 53
US-10-425-115-215979
; Sequence 215979, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215979
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_128569C.1.pep
US-10-425-115-215979

Query Match 87.1%; Score 27; DB 4; Length 81;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 5
|||
DB 30 KVFVFA 34

RESULT 54
US-10-424-599-195261
; Sequence 195261, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 275005
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Zea mays

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 195261
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_18348C.1.pep
US-10-424-599-195261

Query Match 87.1%; Score 27; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 5
|||
DB 66 KVFVFA 70

RESULT 55
US-10-450-763-44156
; Sequence 44156, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 44156
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-450-763-44156

Query Match 87.1%; Score 27; DB 5; Length 82;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVFA 6
|||
DB 11 EFVFFA 16

RESULT 56
US-10-425-115-275005
; Sequence 275005, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 275005
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Zea mays

; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_182395C.1.pep
US-10-425-115-275005

Query Match 87.1%; Score 27; DB 4; Length 83;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVPF 5
|||
Db 49 KVFVPF 53

RESULT 57

US-10-424-599-259257
; Sequence 259257, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 259257
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_76133C.1.pep
US-10-424-599-259257

Query Match 87.1%; Score 27; DB 4; Length 88;
Best Local Similarity 66.7%; Pred. No. 4.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFPPA 6
:|:|
Db 13 RFIFFA 18

RESULT 58

US-10-424-599-246138
; Sequence 246138, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 246138
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(92)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64294C.1.pep
US-10-424-599-246138

Query Match 87.1%; Score 27; DB 4; Length 92;

Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVPF 5
|||
Db 71 KVFVPF 75

RESULT 59

US-10-424-599-207674
; Sequence 207674, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207674
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_29556C.1.pep
US-10-424-599-207674

Query Match 87.1%; Score 27; DB 4; Length 96;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVPF 5
|||
Db 5 KVFVPF 9

RESULT 60

US-10-425-115-221194
; Sequence 221194, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 221194
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_133318C.1.pep
US-10-425-115-221194

Query Match 87.1%; Score 27; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVFVPF 5
|||
Db 20 KVFVPF 24

RESULT 61

US-10-424-599-182454
; Sequence 182454, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 182454
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_135769C.1.pep
US-10-424-599-182454

Query Match 87.1%; Score 27; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
|||||
DB 30 KVVFF 34

RESULT 62
US-10-437-963-201763
; Sequence 201763, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201763
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_97105C.1.pep
US-10-437-963-201763

Query Match 87.1%; Score 27; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 5
|||||
DB 43 KVVFF 47

RESULT 63
US-09-823-153-4
; Sequence 4, Application US/09823153
; Patent No. US20020025540A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company

; APPLICANT: Roberts, Susan
; APPLICANT: Pak, Roger
; APPLICANT: Lewis, Martin
; APPLICANT: Smith, David
; APPLICANT: Hendrick, Joseph
; APPLICANT: Vinitzky, Alexander
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004
; CURRENT APPLICATION NUMBER: US/09/823,153
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Human Beta App
US-09-823-153-4

Query Match 87.1%; Score 27; DB 3; Length 104;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 6
|||||
DB 21 EFVFFA 26

RESULT 64
US-10-713-981-4
; Sequence 4, Application US/10713981
; Publication No. US20040121411A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Roberts, Susan
; APPLICANT: Pak, Roger
; APPLICANT: Lewis, Martin
; APPLICANT: Smith, David
; APPLICANT: Hendrick, Joseph
; APPLICANT: Vinitzky, Alexander
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN COMPLEX
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004 DIV
; CURRENT APPLICATION NUMBER: US/10/713,981
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Human Beta App
US-10-713-981-4

Query Match 87.1%; Score 27; DB 4; Length 104;
Best Local Similarity 83.3%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVVFF 6
|||||
DB 21 EFVFFA 26

RESULT 65
US-10-425-115-215097
; Sequence 215097, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 215097
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_127767C.1.pep
US-10-425-115-215097

Query Match 87.1%; Score 27; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
Db 97 KFVFF 101

RESULT 66
US-10-424-599-207673
; Sequence 207673, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 207673
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_29555C.1.pep
US-10-424-599-207673

Query Match 87.1%; Score 27; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
Db 16 KFVFF 20

RESULT 67
US-10-437-963-146282
; Sequence 146282, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 146282

; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_46920C.1.pep
US-10-437-963-146282

Query Match 87.1%; Score 27; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
Db 18 KFVFF 22

RESULT 68
US-10-424-599-278159
; Sequence 278159, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 278159
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_93200C.1.pep
US-10-424-599-278159

Query Match 87.1%; Score 27; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFVFF 5
Db 5 KFVFF 9

RESULT 69
US-10-425-115-208261
; Sequence 208261, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 208261
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_121527C.1.pep
US-10-425-115-208261

Query Match 87.1%; Score 27; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFVFF 5
Db 33 KFVFF 37

RESULT 70
US-10-425-115-286779
; Sequence 286779, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 286779
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(110)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_24637C.1.pep
US-10-425-115-286779

Query Match 87.1%; Score 27; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.7e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KFVFF 5
Db 96 KFVFF 100

RESULT 71
US-09-864-408A-4214
; Sequence 4214, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shinkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4214
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(11)
; OTHER INFORMATION: Wherein Xaa may be any naturally occurring amino acid
US-09-864-408A-4214

Query Match 87.1%; Score 27; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 5.9e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KFVFF 5

Db 67 KFVFF 71

RESULT 72
US-10-425-115-256025
; Sequence 256025, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 256025
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_165087C.1.pep
US-10-425-115-256025

Query Match 87.1%; Score 27; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 6e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KFVFF 5
Db 47 KFVFF 51

RESULT 73
US-10-425-115-289631
; Sequence 289631, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 289631
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_27231C.1.pep
US-10-425-115-289631

Query Match 87.1%; Score 27; DB 4; Length 125;
Best Local Similarity 100.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

QY 1 KFVFF 5
Db 26 KFVFF 30

RESULT 74
US-10-424-599-208184
; Sequence 208184, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 208184
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_30014C.1.pep
US-10-424-599-208184

Query Match 87.1%; Score 27; DB 4; Length 131;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
|||:
Db 118 KFIFFS 123

RESULT 75
US-10-424-599-221174
; Sequence 221174, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 221174
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_41750C.1.pep
US-10-424-599-221174

Query Match 87.1%; Score 27; DB 4; Length 131;
Best Local Similarity 83.3%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFVFA 6
|||:
Db 83 KFAFFA 88

Search completed: December 29, 2005, 18:49:46
Job time : 67.2903 secs

THIS PAGE BLANK (USPTO)